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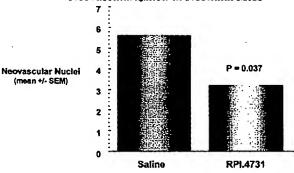
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(54) Title: NUCLEIC ACID BASED MODULATION OF FEMALE REPRODUCTIVE DISEASES AND CONDITIONS

# RPI.4731 Reduces Hypoxia-Induced Retinal Neovascularization in Neonatal Mice



SEQ ID NO: 5978
Results: ~40% decrease in retinal neovascularization following two intraocular injections of RPI.4731

(57) Abstract: The present invention relates to nucleic acid molecules, including dsRNA, siRNA, antisense, 2,5-A chimeras, aptamers, and enzymatic nucleic acid molecules, such as hammerhead ribozymes, DNAzymes, and allozymes, which modulate the expression of vascular endothelial growth factor receptor (VEGF) and/or vascular endothelial growth factor receptor (VEGF) genes for the treatment and/or diagnosis of diseases and conditions associated with angiogenesis, such as cancer, tumor angiogenesis, or ocular indications such as diabetic retinopathy, or age related macular degeneration, proliferative diabetic retinopathy, hypoxia-induced angiogenesis, rheumatoid arthritis, psoriasis, wound healing, and female reproductive disorders and conditions, including but not limited to endometriosis, endometrial carcinoma, gynecologic bleeding disorders, irregular menstrual cycles, ovulation, premenstrual syndrome (PMS), and menopausal dysfunction.

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# NUCLEIC ACID BASED MODULATION OF FEMALE REPRODUCTIVE DISEASES AND CONDITIONS

This patent application claims priority from Sandberg et al., USSN 60/334,461, filed November 30, 2001, entitled "Method and Reagent for the Modulation of Female Reproductive Diseases and Conditions" and Pavco et al., USSN 10/138,674, filed May 3, 2002, which is a continuation in part of Pavco et al., USSN 09/870,161, which is a continuation-in-part of Pavco et al., USSN 09/708,690, filed November 7, 2000, which is a continuation-in-part of Pavco et al., USSN 09/371,722, filed August 10, 1999, which is a continuation-in-part of Pavco et al., USSN 08/584,040, filed January 11, 1996, which claims the benefit of Pavco et al., USSN 60/005,974, filed on October 26, 1995; these earlier applications are entitled "Method and Reagent for Treatment of Diseases or Conditions Related to Levels of Vascular Endothelial Growth Factor Receptor". Each of these applications is hereby incorporated by reference herein in it's entirety including the drawings and tables.

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#### Technical Field Of The Invention

This invention relates to methods and reagents for the treatment of diseases or conditions relating to the levels of expression of vascular endothelial growth factor (VEGF) and vascular endothelial growth factor receptor(s). Specifically, the instant invention features nucleic-acid based molecules and methods that modulate the expression of vascular endothelial growth factor and/or vascular endothelial growth factor receptors, such as VEGFR1 and/or VEGFR2, that are useful in preventing, treating, controlling and/or diagnosing disorders and conditions related to angiogenesis, including but not limited to cancer, tumor angiogenesis, or ocular indications such as diabetic retinopathy, or age related macular degeneration, proliferative diabetic retinopathy, hypoxia-induced angiogenesis, rheumatoid arthritis, psoriasis, wound healing, endometriosis, endometrial carcinoma, gynecologic bleeding disorders, irregular menstrual cycles, ovulation, premenstrual syndrome (PMS), and menopausal dysfunction.

#### Background Of The Invention

The following is a discussion of relevant art, none of which is admitted to be prior art to the present invention.

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VEGF, also referred to as vascular permeability factor (VPF) and vasculotropin, is a potent and highly specific mitogen of vascular endothelial cells (for a review see Ferrara, 1993 Trends Cardiovas. Med. 3, 244; Neufeld et al., 1994, Prog. Growth Factor Res. 5, 89). VEGF-induced neovascularization is implicated in various pathological conditions such as tumor angiogenesis, or ocular indications such as diabetic retinopathy, or age related macular degeneration, proliferative diabetic retinopathy, hypoxia-induced angiogenesis, rheumatoid arthritis, psoriasis, wound healing and others.

VEGF, an endothelial cell-specific mitogen, is a 34-45 kDa glycoprotein with a wide range of activities that include promotion of angiogenesis, enhancement of vascular-permeability and others. VEGF belongs to the platelet-derived growth factor (PDGF) family of growth factors with approximately 18% homology with the A and B chain of PDGF at the amino acid level. Additionally, VEGF contains the eight conserved cysteine residues common to all growth factors belonging to the PDGF family (Neufeld et al., supra). VEGF protein is believed to exist predominantly as disulfide-linked homodimers; monomers of VEGF have been shown to be inactive (Plouet et al., 1989 EMBO J. 8, 3801).

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VEGF exerts its influence on vascular endothelial cells by binding to specific high-affinity cell surface receptors. Covalent cross-linking experiments with <sup>125</sup>I-labeled VEGF protein have led to the identification of three high molecular weight complexes of 225, 195 and 175 kDa presumed to be VEGF and VEGF receptor complexes (Vaisman et al., 1990 J. Biol. Chem. 265, 19461). Based on these studies VEGF-specific receptors of 180, 150 and 130 kDa molecular mass were predicted. In endothelial cells, receptors of 150 and 130 kDa have been identified. The VEGF receptors belong to the superfamily of receptor tyrosine kinases (RTKs) characterized by a conserved cytoplasmic catalytic kinase domain and a hydrophilic kinase sequence. The extracellular domains of the VEGF receptors consist of seven immunoglobulin-like domains that are thought to be involved in VEGF binding functions.

The two most abundant and high-affinity receptors of VEGF are flt-1 (VEGFR1) (fms-like tyrosine kinase) cloned by Shibuya et al., 1990 Oncogene 5, 519 and KDR (VEGFR2) (kinase-insert-domain-containing receptor) cloned by Terman et al., 1991 Oncogene 6, 1677. The murine homolog of KDR, cloned by Mathews et al., 1991, Proc. Natl. Acad. Sci., USA, 88, 9026, shares 85% amino acid homology with KDR and is termed as flk-1 (fetal liver kinase-1). The high-affinity binding of VEGF to its receptors is modulated by cell surface-associated heparin and heparin-like molecules (Gitay-Goren et al., 1992 J. Biol. Chem. 267, 6093).

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VEGF expression has been associated with several pathological states such as tumor angiogenesis, several forms of blindness, rheumatoid arthritis, psoriasis and others. In addition, a number of studies have demonstrated that VEGF is both necessary and sufficient for neovascularization. Takashita et al., 1995 J. Clin. Invest. 93, 662, demonstrated that a single injection of VEGF augmented collateral vessel development in a rabbit model of ischemia. VEGF also can induce neovascularization when injected into the comea. Expression of the VEGF gene in CHO cells is sufficient to confer tumorigenic potential to the cells. Kim et al., supra and Millauer et al., supra used monoclonal antibodies against VEGF or a dominant negative form of VEGFR2 receptor to inhibit tumor-induced neovascularization.

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During development, VEGF and its receptors are associated with regions of new vascular growth (Millauer et al., 1993 Cell 72, 835; Shalaby et al., 1993 J. Clin. Invest. 91, 2235). Furthermore, transgenic mice lacking either of the VEGF receptors are defective in blood vessel formation and these mice do not survive; VEGFR2 appears to be required for differentiation of endothelial cells, while VEGFR1 appears to be required at later stages of vessel formation (Shalaby et al., 1995 Nature 376, 62; Fung et al., 1995 Nature 376, 66). Thus, these receptors apparently need to be present to properly signal endothelial cells or their precursors to respond to vascularization-promoting stimuli.

Increasing evidence suggests that the VEGF family may also be involved with both the etiology and maintenance of peritoneal endometriosis. Peritoneal endometriosis is a significant debilitating gynecological problem of widespread prevalence. It is now generally accepted that the pathogenesis of peritoneal endometriosis involves the implantation of exfoliated endometrium. Maintenance of exfoliated endometrial tissue is dependent upon the generation and maintenance of an extensive blood supply both within and surrounding the ectopic tissue.

Endometriosis is a disease affecting an estimated 77 million women and teenagers worldwide. Endometriosis is a leading cause of infertility, chronic pelvic pain and hysterectomy. Endometriosis can be characterized when endometrial tissue (the tissue inside the uterus which builds up and is shed each month during menses) is found outside the uterus, in other areas of the body. The endometrial tissue can respond to hormonal commands each month and break down and bleed. However, unlike the endometrium, these tissue deposits have no way of leaving the body. The result is internal bleeding, degeneration of blood and tissue shed from the growths, inflammation of the surrounding areas, expression of irritating enzymes and formation of scar tissue. In addition, depending on the location of the growths.

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interference with the bowel, bladder, intestines and other areas of the pelvic cavity can occur. Endometrial tissue has even been found lodged in the skin and at other extrapelvic locations like the arm, leg and even brain.

Currently, the presence of Endometriosis can only be confirmed through surgery such as laparoscopy, but can be suspected based on symptoms, physical findings and diagnostic tests. Endometriosis can be treated in many different ways, both surgically and medically. Most commonly, surgery will be performed during which the disease will be excised, ablated, fulgarated, cauterized or otherwise removed, and adhesions will also be freed. Surgeries include but are not limited to laparoscopy; laparotomy; presacral and uterosacral and various levels of hysterectomies, where some or all of the reproductive organs are removed. Often, this method will only relieve the symptoms associated with growths on the reproductive organs, not the bowels or kidneys and related areas where Endometriosis can be present.

There are several drugs used to treat Endometriosis that are utilized either alone or in combination with surgery. These include contraceptives, GnRH agonists, and/or synthetic hormones. GnRH agonists are commonly used on women in all stages of the disease and may sometimes have serious side affects. GnRH (gonadotropin releasing hormone) analogues are classified into 2 groups: agonists and antagonists. Agonists are commonly used in the treatment of Endometriosis by suppressing the manufacture of follicle stimulating hormone (FSH) and luteinizing hormone (LH), common hormones required in ovulation. When they are not secreted, the body will go into "pseudo-menopause," stalling the growth of more implants. However, these are again only stop-gap measures that can be utilized only for short term intervals. Once the body returns to it's normal state, the Endometriosis will again begin to implant itself.

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Angiogenesis is likely to be involved in the pathogenesis of endometriosis. According to the transplantation theory, when the exfoliated endometrium is attached to the peritoneal layer, the establishment of a new blood supply is essential for the survival of the endometrial implant and development of endometriosis (Donnez et al., 1998, Hum. Reprod., 13, 1686-1690). Endometrial growth and repair after menstruation are associated with profound angiogenesis. Abnormalities in these processes result in excessive or unpredictable bleeding patterns and are common in many women. It is therefore important to understand which factors regulate normal endometrial angiogenesis. Vascular endothelial growth factor (VEGF) is an endothelial cell-specific mitogen that plays an important role in normal and pathological angiogenesis (Fasciani et al., 2000, Mol. Hum. Reprod., 6, 50-54; Sharkey et al., 2000, J. Clin. Endocrinol. Metab., 85, 402-409). Sources of this factor include the eutopic

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endometrium, ectopic endometriotic tissue and peritoneal fluid macrophages. Important to its etiology is the correct peritoneal environment in which the exfoliated endometrium is seeded and implants. Established ectopic tissue is then dependent on the peritoneal environment for its survival, an environment that supports angiogenesis. The increasing knowledge of the involvement of the VEGF family in endometriotic angiogenesis raises the possibility of novel approaches to its medical management, with particular focus on the anti-angiogenic control of the action of VEGF (McLaren, 2001, Hum. Reprod. Update, 6, 45-55).

Pavco et al., International PCT Publication No. WO 97/15662, describes methods and reagents for treating diseases or conditions related to levels of vascular endothelial growth factor receptor.

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Robinson, International PCT Publication No. WO 95/04142, describes the use of certain antisense oligonucleotides targeted against VEGF RNA to inhibit VEGF expression.

Jellinek et al., 1994 Biochemistry 33, 10450 describe the use of specific VEGF-specific high-affinity RNA aptamers to inhibit the binding of VEGF to its receptors.

Rockwell and Goldstein, International PCT Publication No. WO 95/21868, describe the use of certain anti-VEGF receptor monoclonal antibodies to neutralize the effect of VEGF on endothelial cells.

Pappa, International PCT Publication No. WO 01/32920, describes inhibitors, including certain ribozyme and antisense nucleic acid molecules, of specific genes, including cathepsin D, AEBP-1, stromelysin-3, cystatin B, protease inhibitor 1, sFRP4, gelsolin, IGFBP-3, dual specificity phosphatase 1, PAEP, Ig gamma chain, ferritin, complement component 3, proalpha-1 type III collagen, proline 4-hydroxylase, alpha-2 type I collagen, claudin-4, melanoma adhesion protein, procollagen C-endopeptidase enhancer, nascent-polypeptide-associated complex alpha polypeptide, elongation factor 1 alpha (EF-1-alpha), vitamin D3 25 hydroxylase, CSRP-1, steroidogenic acute regulatory protein, apolipoprotein E, transcobalamin II, prosaposin, early growth response 1 (EGR1), ribosomal protein S6, adenosine deaminase RNA-specific protein, RAD21, guanine nucleotide binding protein beta polypeptide 2-like 1 (RACK1) and podocalyxin genes which are all differentially expressed in tissues within individual patients with endometriosis.

30 Labarbera et al., International PCT Publication No. WO 00/73416, describes specific antisense nucleic acid molecules targeting follicle-stimulating hormone receptor.

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Storella et al., International PCT Publication No. WO 99/63116, describes modulators of Prothymosin gene products for treating endometriosis, including certain ribozymes and antisense nucleic acid molecules.

#### Summary Of The Invention

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This invention features nucleic acid-based molecules, for example, enzymatic nucleic acid molecules, allozymes, antisense nucleic acids, 2-5A antisense chimeras, triplex forming oligonucleotides, decoy RNA, dsRNA, siRNA, aptamers, and antisense nucleic acids containing nucleic acid cleaving chemical groups, and methods to modulate vascular endothelial growth factor (VEGF) and/or vascular endothelial growth factor receptor (VEGFr) gene expression. Non-limiting examples of genes that encode vascular endothelial growth factor receptors of the invention include VEGFR1, VEGFR2 or combinations thereof. In particular, the instant invention features nucleic acid-based molecules and methods that modulate the expression of vascular endothelial growth factor and/or vascular endothelial growth factor receptors, such as VEGFR1 and/or VEGFR2, that are useful in preventing, treating, controlling, and/or diagnosing angiogenesis related diseases and conditions, including but not limited to tumor angiogenesis, cancers such as breast cancer, lung cancer, colorectal cancer, renal cancer, pancreatic cancer, or melanoma, or ocular indications such as diabetic retinopathy, or age related macular degeneration, and female reproductive disorders and conditions, including but not limited to endometriosis, endometrial carcinoma, gynecologic bleeding disorders, irregular menstrual cycles, ovulation, premenstrual syndrome (PMS), and menopausal dysfunction.

In one embodiment, the invention features one or more nucleic acid-based molecules and methods that independently or in combination modulate the expression of gene(s) encoding vascular endothelial growth factor receptors. Specifically, the present invention features nucleic acid molecules that modulate the expression of VEGF (for example Genbank Accession No. NM\_003376), VEGFR1 receptor (for example Genbank Accession No. NM\_002019), and VEGFR2 receptor (for example Genbank Accession No. NM\_002253) that are useful in preventing, treating, controlling, and/or diagnosing tumor angiogenesis, cancers such as breast cancer, lung cancer, colorectal cancer, renal cancer, pancreatic cancer, or melanoma, or ocular indications such as diabetic retinopathy, or age related macular degeneration, and female reproductive disorders and conditions, including but not limited to

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endometriosis, endometrial carcinoma, gynecologic bleeding disorders, irregular menstrual cycles, ovulation, premenstrual syndrome (PMS), and menopausal dysfunction.

In one embodiment, the present invention features a compound having Formula I: (SEQ ID NO: 5977)

### 5' gsasgsusugcUGAuGagg ccgaaa ggccGaaAgucugB 3'

wherein each a is 2'-O-methyl adenosine nucleotide, each g is a 2'-O-methyl guanosine nucleotide, each c is a 2'-O-methyl cytidine nucleotide, each u is a 2'-O-methyl uridine nucleotide, each A is adenosine, each G is guanosine, each s individually represents a phosphorothioate internucleotide linkage, U is 2'-deoxy-2'-C-allyl uridine, and B is an inverted deoxyabasic moiety. This compound is also referred to as ANGIOZYMETM ribozyme.

In another embodiment, the present invention features a compound having Formula II: (SEO ID NO: 5978).

### 5'-usascs asau ucU GAu Gag gcg aaa gcc Gaa Aag aca aB-3'

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wherein each a is 2'-O-methyl adenosine nucleotide, each g is a 2'-O-methyl guanosine nucleotide, each c is a 2'-O-methyl cytidine nucleotide, each u is a 2'-O-methyl uridine nucleotide, each A is adenosine, each G is guanosine, each s individually represents a phosphorothicate internucleotide linkage,  $\underline{U}$  is 2'-deoxy-2'-C-allyl uridine, and B is an inverted deoxyabasic moiety.

In one embodiment, the invention features a composition comprising a nucleic acid molecule of the invention in a pharmaceutically acceptable carrier. In another embodiment, the invention features a composition comprising a compound of Formula I and/or Formula II in a pharmaceutically acceptable carrier or diluent.

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In one embodiment, the invention features a method of administering to a cell, for example a mammalian cell, including a human cell, a nucleic acid molecule of the invention comprising contacting the cell with the nucleic acid molecule under conditions suitable for administration, for example in the presence of a delivery reagent such as a lipid, cationic lipid, phospholipid, or liposome. In another embodiment, the invention features a method of administering to a cell, for example a mammalian cell, including a human cell, a compound of Formula I and/or Formula IIcomprising contacting the cell with the compound under

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conditions suitable for administration, for example in the presence of a delivery reagent such as a lipid, cationic lipid, phospholipid, or liposome.

In one embodiment, the present invention features a mammalian cell comprising a nucleic acid molecule of the invention, wherein the mammalian cell is, for example, a human cell. In another embodiment, the present invention also features a mammalian cell comprising the compound of Formula I and/or Formula II, wherein the mammalian cell is, for example, a human cell.

In one embodiment, the invention features a method of inhibiting angiogenesis, for example tumor angiogenesis, or ocular indications such as diabetic retinopathy, or age related macular degeneration, or endometrial neovascularization, in a subject comprising contacting the subject with a nucleic acid molecule of the invention, under conditions suitable for the inhibition. In another embodiment, the invention features a method of inhibiting angiogenesis, for example tumor angiogenesis, or ocular indications such as diabetic retinopathy, or age related macular degeneration, or endometrial neovascularization, in a subject, comprising contacting the subject with a compound of Formula I and/or Formula II, under conditions suitable for the inhibition.

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In another embodiment, the invention features a method of treatment of a subjecthaving an ocular condition associated with the increased level of a VEGF receptor, for example diabetic retinopathy, or age related macular degeneration, comprising contacting cells of the subjectwith a nucleic acid molecule, such as an enzymatic nucleic acid molecule targeted against a VEGF receptor RNA, e.g., molecule according to Formula I and/or II, under conditions suitable for the treatment.

In another embodiment, the invention features a method of treatment of a subjecthaving a condition associated with an increased level of VEGR and/or a VEGF receptor, for example tumor angiogenesis, cancers such as breast cancer, lung cancer, colorectal cancer, renal cancer, pancreatic cancer, or melanoma, ocular diseases or ocular indications such as diabetic retinopathy, or age related macular degeneration, rhuematoid arthritis, psoriasis endometriosis, endometrial carcinoma, gynecologic bleeding disorders, irregular menstrual cycles, ovulation, premenstrual syndrome (PMS), or menopausal dysfunction, comprising contacting cells of the subject with a nucleic acid molecule of the invention, such as a compound of Formula I and/or Formula II, under conditions suitable for the treatment.

In yet another embodiment, the inventive method of treatment further comprises the use of one or more drug therapies under conditions suitable for the treatment. Non-limiting

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examples of other drug therapies that can be used in combination with nucleic acid molecules of the invention include to 5-fluoro uridine, Leucovorin, Irinotecan (CAMPTOSAR® or CPT-11 or Camptothecin-11 or Campto), Paclitaxel, or Carboplatin, GnRH (gonadotropin releasing hormone) agonists, Lupron Depot (Leuprolide Acetate), Synarel (naferalin acetate), Zolodex (goserelin acetate), Suprefact (buserelin acetate), Danazol, or oral contraceptives including but not limited to Depo-Provera or Provera (medroxyprogesterone acetate), or any other estrogen/progesterone contraceptive.

In one embodiment, the invention features a method of administering to a mammal, for example a human, a nucleic acid molecule of the invention comprising contacting the mammal with the nucleic acid molecule under conditions suitable for the administration, for example, in the presence of a delivery reagent such as a lipid, cationic lipid, phospholipid, or liposome. In another embodiment, the invention features a method of administering to a mammal, for example a human, a compound of Formula I and/or Formula II comprising contacting the mammal with the compound under conditions suitable for the administration, for example, in the presence of a delivery reagent such as a lipid, cationic lipid, phospholipid, or liposome.

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In one embodiment, the invention features a nucleic acid molecule which down regulates expression of a vascular endothelial growth factor (VEGF) and/or vascular endothelial growth factor receptor (VEGFr) gene, for example, wherein the VEGFr gene comprises VEGFR1 or VEGFR2 and any combination thereof.

In one embodiment, a nucleic acid molecule of the invention, such as an enzymatic nucleic acid molecule, antisense nucleic acid molecule, 2-5A antisense chimera, triplex forming oligonucleotide, decoy RNA, dsRNA, siRNA, aptamer, or antisense nucleic acid containing nucleic acid cleaving chemical groups, is adapted to treat, control and/or diagnose tumor angiogenesis, cancers such as breast cancer, lung cancer, colorectal cancer, renal cancer, pancreatic cancer, or melanoma, ocular diseases or ocular indications, such as diabetic retinopathy, or age related macular degeneration, rhuematoid arthritis, psoriasis endometriosis, endometrial carcinoma, gynecologic bleeding disorders, irregular menstrual cycles, ovulation, premenstrual syndrome (PMS), or menopausal dysfunction.

Such nucleic acid molecules are also useful for the prevention of the diseases and conditions including diabetic retinopathy, macular degeneration, neovascular glaucoma, myopic degeneration, vertuca vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome

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and other diseases or conditions that are related to the levels of VEGFR1 or VEGFR2 in a cell or tissue.

In another embodiment, the invention features a composition in a pharmaceutically acceptable carrier or diluent, comprising the nucleic acid molecule of the instant invention.

In another embodiment, an enzymatic nucleic acid molecule, antisense nucleic acid molecule, 2-5A antisense chimera, triplex forming oligonucleotide, decoy RNA, dsRNA, siRNA, aptamer, or antisense nucleic acid containing nucleic acid cleaving chemical groups of the invention is adapted for birth control.

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In one embodiment, an enzymatic nucleic acid molecule of the invention is in a hammerhead, Inozyme, Zinzyme, DNAzyme, Amberzyme, or G-cleaver configuration.

In one embodiment, an enzymatic nucleic acid molecule of the invention comprises between 8 and 100 bases complementary to RNA of VEGFR1 and/or VEGFR2 gene. In another embodiment, an enzymatic nucleic acid molecule of the invention comprises between 14 and 24 bases complementary to RNA of VEGFR1 and/or VEGFR2 gene.

In one embodiment, a siRNA molecule of the invention comprises a double stranded RNA wherein one strand of the RNA is complementary to RNA of a VEGFR1 and/or VEGFR2 gene. In another embodiment, a siRNA molecule of the invention comprises a double stranded RNA wherein one strand of the RNA comprises a portion of a sequence of RNA having a VEGFR1 and/or VEGFR2 sequence. In yet another embodiment, a siRNA molecule of the invention comprises a double stranded RNA wherein both strands of RNA are connected by a non-nucleotide linker. Alternately, a siRNA molecule of the invention comprises a double stranded RNA wherein both strands of RNA are connected by a nucleotide linker, such as a loop or stem loop structure.

In one embodiment, a single strand component of a siRNA molecule of the invention is from about 14 to about 50 nucleotides in length. In another embodiment, a single strand component of a siRNA molecule of the invention is about 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides in length. In yet another embodiment, a single strand component of a siRNA molecule of the invention is about 23 nucleotides in length. In one embodiment, a siRNA molecule of the invention is from about 28 to about 56 nucleotides in length. In another embodiment, a siRNA molecule of the invention is about 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, or 52 nucleotides in length. In yet another embodiment, a siRNA molecule of the invention is about 46 nucleotides in length.

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In one embodiment, an enzymatic nucleic acid molecule, antisense nucleic acid molecule, 2-5A antisense chimera, triplex forming oligonucleotide, decoy RNA, dsRNA, siRNA, aptamer, or antisense nucleic acid containing nucleic acid cleaving chemical groups of the invention is chemically synthesized.

In another embodiment, an enzymatic nucleic acid molecule, antisense nucleic acid molecule, 2-5A antisense chimera, triplex forming oligonucleotide, decoy RNA, dsRNA, siRNA, aptamer, or antisense nucleic acid containing nucleic acid cleaving chemical groups of the invention comprises at least one 2'-sugar modification.

In another embodiment, an enzymatic nucleic acid molecule, antisense nucleic acid molecule, 2-5A antisense chimera, triplex forming oligonucleotide, decoy RNA, dsRNA, siRNA, aptamer, or antisense nucleic acids containing nucleic acid cleaving chemical groups of the invention comprises at least one nucleic acid base modification.

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In another embodiment, an enzymatic nucleic acid molecule, antisense nucleic acid molecule, 2-5A antisense chimera, triplex forming oligonucleotide, decoy RNA, dsRNA, siRNA, aptamer, or antisense nucleic acid containing nucleic acid cleaving chemical groups of the invention comprises at least one phosphate backbone modification.

In one embodiment, the invention features a mammalian cell, for example a human cell, comprising a nucleic acid molecule of the invention.

In another embodiment, the invention features a method of reducing VEGF and/or VEGFr, such as VEGFR1 and/or VEGFR2 expression or activity in a cell comprising contacting the cell with a nucleic acid molecule of the invention that modulates the expression and/or activity of VEGF and/or VEGFr, under conditions suitable for the reduction.

In another embodiment, a method of treatment of a subject having a condition associated with the level of VEGF and/or VEGFr, such as VEGFR1 and/or VEGFR2 is featured, wherein the method further comprises the use of one or more drug therapies under conditions suitable for the treatment.

In one embodiment, the invention features a method for treatment of a subject having tumor angiogenesis, tumor angiogenesis, cancers including but not limited to tumor and cancer types shown under Diagnosis in **Table III**, ocular diseases or ocular indications such as diabetic retinopathy, or age related macular degeneration, rhuematoid arthritis, psoriasis and/or endometriosis, endometrial carcinoma, gynecologic bleeding disorders, irregular

menstrual cycles, ovulation, premenstrual syndrome (PMS), or menopausal dysfunction, comprising administering to the subject a nucleic acid molecule of the invention that modulates the expression and/or activity of VEGF and/or VEGFr under conditions suitable for the treatment.

In another embodiment, the invention features a method for birth control in a subject comprising administering to the subject a nucleic acid molecule of the invention that modulates the expression and/or activity of VEGF and/or VEGFr under conditions suitable for the treatment.

In another embodiment, the invention features a method of cleaving RNA encoded by a VEGF, VEGFR1 and/or VEGFR2 gene comprising contacting an enzymatic nucleic acid molecule of the invention having endonuclease activity with RNA encoded by a VEGFR1 and/or VEGFR2 gene under conditions suitable for the cleavage, for example, wherein the cleavage is carried out in the presence of a divalent cation, such as Mg<sup>2+</sup>.

In one embodiment, a nucleic acid molecule of the invention comprises a cap structure, for example a 3',3'-linked or 5',5'-linked deoxyabasic ribose derivative, wherein the cap structure is at the 5'-end, or 3'-end, or both the 5'-end and the 3'-end of the enzymatic nucleic acid molecule.

In another embodiment, a nucleic acid molecule of the invention comprises a cap structure, for example a 3',3'-linked or 5',5'-linked deoxyabasic ribose derivative, wherein the cap structure is at the 5'-end, or 3'-end, or both the 5'-end and the 3'-end of the antisense nucleic acid molecule.

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In one embodiment, the invention features an expression vector comprising a nucleic acid sequence encoding at least one nucleic acid molecule of the invention such that the vector allows expression of the nucleic acid molecule.

In another embodiment, the invention features a mammalian cell, for example, a human cellcomprising an expression vector of the invention.

In yet another embodiment, an expression vector of the invention further comprises a sequence for a nucleic acid molecule complementary to RNA encoded by a VEGF and/or VEGFR, such as VEGFR1 and/or VEGFR2 gene.

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In one embodiment, an expression vector of the invention comprises a nucleic acid sequence encoding two or more nucleic acid molecules of the invention, which can be the same or different.

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In another embodiment, the invention features a method for treatment or control of tumor angiogenesis, cancers such as breast cancer, lung cancer, colorectal cancer, renal cancer, pancreatic cancer, or melanoma, or ocular indications such as diabetic retinopathy, or age related macular degeneration, and/or endometriosis, endometrial carcinoma, gynecologic bleeding disorders, irregular menstrual cycles, ovulation, premenstrual syndrome (PMS), or menopausal dysfunction, comprising administering to a subject a nucleic acid molecule of the invention that modulates the expression and/or activity of VEGF and/or VEGFr, such as an enzymatic nucleic acid molecule, antisense nucleic acid molecule, 2-5A antisense chimera, triplex forming oligonucleotide, decoy RNA, dsRNA, siRNA, aptamer, or antisense nucleic acid containing nucleic acid cleaving chemical groups of the invention, under conditions suitable for the treatment, including administering to the subject one or more other therapies, for example, 5-fluoro uridine, Leucovorin, Irinotecan (CAMPTOSAR® or CPT-11 or Camptothecin-11 or Campto), Paclitaxel, or Carboplatin GnRH (gonadotropin releasing hormone) agonists, Lupron Depot (Leuprolide Acetate), Synarel (naferalin acetate), Zolodex (goserelin acetate), Suprefact (buserelin acetate), Danazol, or oral contraceptives including but not limited to Depo-Provera or Provera (medroxyprogesterone acetate), or any other estrogen/progesterone contraceptive.

In one embodiment, the method of treatment features a nucleic acid molecule of the invention, such as an enzymatic nucleic acid or antisense nucleic acid molecule, that comprises at least five ribose residues, at least ten 2'-O-methyl modifications, and a 3'- end modification, such as a 3'-3' inverted abasic moiety. In another embodiment, a nucleic acid molecule of the invention further comprises phosphorothioate linkages on at least three of the 5' terminal nucleotides.

In another embodiment, the invention features a method of administering to a mammal, for example a human, an enzymatic nucleic acid molecule, antisense nucleic acid molecule, 2-5A antisense chimera, triplex forming oligonucleotide, decoy RNA, dsRNA, siRNA, aptamer, or antisense nucleic acid containing nucleic acid cleaving chemical groups of the invention, comprising contacting the mammal with the nucleic acid molecule under conditions suitable for the administration, for example, in the presence of a delivery reagent such as a lipid, cationic lipid, phospholipid, or liposome.

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In yet another embodiment, the invention features a method of administering to a mammal an enzymatic nucleic acid molecule, antisense nucleic acid molecule, 2-5A antisense chimera, triplex forming oligonucleotide, decoy RNA, dsRNA, siRNA, aptamer, or antisense nucleic acid containing nucleic acid cleaving chemical groups of the invention in conjunction with other therapies, comprising contacting the mammal, for example a human, with the nucleic acid molecule and the other therapy under conditions suitable for the administration.

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In another embodiment, other therapies contemplated by the instant invention that can be used in conjunction with the nucleic acid molecules of the instant invention include, but are not limited to, 5-fluoro uridine, Leucovorin, Irinotecan (CAMPTOSAR® or CPT-11 or Camptothecin-11 or Campto), Paclitaxel, or Carboplatin, GnRH (gonadotropin releasing hormone) agonists, Lupron Depot (Leuprolide Acetate), Synarel (naferalin acetate), Zolodex (goserelin acetate), Suprefact (buserelin acetate), Danazol, or oral contraceptives including but not limited to Depo-Provera or Provera (medroxyprogesterone acetate), or other estrogen/progesterone contraceptive.

In one embodiment, the invention features the use of an enzymatic nucleic acid molecule, to down-regulate the expression of VEGFR1 and/or VEGFR2 genes in the treatment or control of tumor angiogenesis, cancers such as breast cancer, lung cancer, colorectal cancer, renal cancer, pancreatic cancer, or melanoma, or ocular indications such as diabetic retinopathy, or age related macular degeneration, and/or endometriosis, endometrial carcinoma, gynecologic bleeding disorders, irregular menstrual cycles, ovulation, premenstrual syndrome (PMS), or menopausal dysfunction. Such enzymatic nucleic acid molecule can be in the hammerhead, NCH, G-cleaver, Amberzyme, Zinzyme, and/or DNAzyme motif.

In another embodiment, the invention features the use of an enzymatic nucleic acid moleculeto down-regulate the expression of VEGF and/or VEGFR, such as VEGFR1 and/or VEGFR2 genes, as a method of birth control. Such enzymatic nucleic acid molecule can be in the hammerhead, NCH, G-cleaver, Amberzyme, Zinzyme, and/or DNAzyme motif. In one embodiment, the nucleic acid molecules of the invention have complementarity to the substrate sequences in Tables V and VI. Examples of enzymatic nucleic acid molecules of the invention are shown in Tables V and VI. Examples of such enzymatic nucleic acid molecules consist essentially of sequences defined in these Tables.

By "inhibit", "down-regulate", or "reduce", it is meant that the expression of the gene, or level of nucleic acids or equivalent nucleic acids encoding one or more proteins or protein subunits, or activity of one or more proteins or protein subunits, such as VEGFR1, VEGFR2

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and/or flk-1, is reduced below that observed in the absence of the nucleic acid molecules of the invention. In one embodiment, inhibition, down-regulation or reduction with enzymatic nucleic acid molecule preferably is below that level observed in the presence of an enzymatically inactive or attenuated molecule that is able to bind to the same site on the target nucleic acid, but is unable to cleave that nucleic acid. In another embodiment, inhibition, down-regulation, or reduction with antisense oligonucleotides is preferably below that level observed in the presence of, for example, an oligonucleotide with scrambled sequence or with mismatches. In another embodiment, inhibition, down-regulation, or reduction of VEGF and/or VEGFr, such as VEGFR1 and/or VEGFR2 with the nucleic acid molecule of the instant invention is greater in the presence of the nucleic acid molecule than in its absence.

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By "up-regulate" is meant that the expression of a gene, or level of nucleic acids or equivalent nucleic acids encoding one or more proteins or protein subunits, or activity of one or more proteins or protein subunits, such as VEGFR1 and/or VEGFR2, is greater than that observed in the absence of the nucleic acid molecules of the invention. For example, the expression of a gene, such as VEGF and/or VEGFr, such as VEGFR1 and/or VEGFR2 gene, can be increased in order to treat, prevent, ameliorate, or modulate a pathological condition caused or exacerbated by an absence or low level of gene expression.

By "modulate" is meant that the expression of a gene, or level of nucleic acids or equivalent nucleic acids encoding one or more proteins or protein subunits, or activity of one or more proteins protein subunit(s) is up-regulated or down-regulated, such that the expression, level, or activity is greater than or less than that observed in the absence of the nucleic acid molecules of the invention.

By "enzymatic nucleic acid molecule" it is meant a nucleic acid molecule which has complementarity in a substrate binding region to a specified gene target, and also has an enzymatic activity which is active to specifically cleave a target nucleic acid. That is, the enzymatic nucleic acid molecule is able to intermolecularly cleave a nucleic acid and thereby inactivate a target nucleic acid molecule. These complementary regions allow sufficient hybridization of the enzymatic nucleic acid molecule to the target nucleic acid and thus permit cleavage. One hundred percent complementarity is preferred, but complementarity as low as 50-75% can also be useful in this invention (see for example Werner and Uhlenbeck, 1995, Nucleic Acids Research, 23, 2092-2096; Hammann et al., 1999, Antisense and Nucleic Acid Drug Dev., 9, 25-31). The nucleic acids can be modified at the base, sugar, and/or phosphate groups. The term enzymatic nucleic acid is used interchangeably with phrases such

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as ribozyme, catalytic RNA, enzymatic RNA, catalytic DNA, aptazyme or aptamer-binding ribozyme, regulatable ribozyme, catalytic oligonucleotides, nucleozyme, DNAzyme, RNA enzyme, endoribonuclease, endonuclease, minizyme, leadzyme, oligozyme or DNA enzyme. All of these terminologies describe nucleic acid molecules with enzymatic activity. The specific enzymatic nucleic acid molecules described in the instant application are not limiting in the invention and those skilled in the art will recognize that all that is important in an enzymatic nucleic acid molecule of this invention is that it has a specific substrate binding site which is complementary to one or more of the target nucleic acid regions, and that it have nucleotide sequences within or surrounding that substrate binding site which impart a nucleic acid cleaving and/or ligation activity to the molecule (Cech et al., U.S. Patent No. 4,987,071; Cech et al., 1988, 260 JAMA 3030).

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Several varieties of naturally-occurring enzymatic nucleic acids are known presently. Each can catalyze the hydrolysis of nucleic acid phosphodiester bonds in trans (and thus can cleave other nucleic acid molecules) under physiological conditions. Table I summarizes some of the characteristics of these ribozymes. In general, enzymatic nucleic acids act by first binding to a target nucleic acid. Such binding occurs through the target binding portion of a enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target nucleic acid. Thus, the enzymatic nucleic acid first recognizes and then binds a target nucleic acid through complementary base-pairing, and once bound to the correct site, acts enzymatically to cut the target nucleic acid. Strategic cleavage of such a target nucleic acid will destroy its ability to direct synthesis of an encoded protein. After an enzymatic nucleic acid has bound and cleaved its nucleic acid target, it is released from that nucleic acid to search for another target and can repeatedly bind and cleave new targets. Thus, a single ribozyme molecule is able to cleave many molecules of target nucleic acid. In addition, the ribozyme is a highly specific inhibitor of gene expression, with the specificity of inhibition depending not only on the base-pairing mechanism of binding to the target nucleic acid, but also on the mechanism of target nucleic acid cleavage. Single mismatches, or base-substitutions, near the site of cleavage can completely eliminate catalytic activity of a ribozyme.

In one embodiment of the inventions described herein, an enzymatic nucleic acid molecule of the invention is formed in a hammerhead or hairpin motif, but can also be formed in the motif of a hepatitis delta virus, group I intron, group II intron or RNase P RNA (in association with an RNA guide sequence), *Neurospora* VS RNA, DNAzymes, NCH cleaving motifs, or G-cleavers. Examples of such hammerhead motifs are described by Dreyfus, supra, Rossi et al., 1992, AIDS Research and Human Retroviruses 8, 183; of hairoin motifs

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by Hampel et al., EP0360257, Hampel and Tritz, 1989 Biochemistry 28, 4929, Feldstein et al., 1989, Gene 82, 53, Haseloff and Gerlach, 1989, Gene, 82, 43, and Hampel et al., 1990 Nucleic Acids Res. 18, 299; Chowrira & McSwiggen, US. Patent No. 5,631,359; an examples of a hepatitis delta virus motif is described by Perrotta and Been, 1992 Biochemistry 31, 16; examples of RNase P motifs are described by Guerrier-Takada et al., 1983 Cell 35, 849; Forster and Altman, 1990, Science 249, 783; Li and Altman, 1996, Nucleic Acids Res. 24, 835; examples of Neurospora VS RNA ribozyme motifs are described by Collins (Saville and Collins, 1990 Cell 61, 685-696; Saville and Collins, 1991 Proc. Natl. Acad. Sci. USA 88, 8826-8830; Collins and Olive, 1993 Biochemistry 32, 2795-2799; Guo and Collins, 1995, EMBO. J. 14, 363); examples of Group II introns are described by Griffin et al., 1995, Chem. Biol. 2, 761; Michels and Pyle, 1995, Biochemistry 34, 2965; Pyle et al., International PCT Publication No. WO 96/22689; an example of a Group I intron is described by Cech et al., U.S. Patent 4,987,071; and examples of DNAzymes are described by Usman et al., International PCT Publication No. WO 95/11304; Chartrand et al., 1995, NAR 23, 4092; Breaker et al., 1995, Chem. Bio. 2, 655; Santoro et al., 1997, PNAS 94, 4262, and Beigelman et al., International PCT publication No. WO 99/55857. NCH cleaving motifs are described in Ludwig & Sproat, International PCT Publication No. WO 98/58058; and G-cleavers are described in Kore et al., 1998, Nucleic Acids Research 26, 4116-4120 and Eckstein et al., International PCT Publication No. WO 99/16871. Additional motifs such as the Aptazyme (Breaker et al., WO 98/43993), Amberzyme (Beigelman et al., U.S. Serial No. 09/301,511) and Zinzyme (Figure 7) (Beigelman et al., U.S. Serial No. 09/918,728), all included by reference herein including drawings, can also be used in the present invention. These specific motifs or configurations are not limiting in the invention and those skilled in the art will recognize that all that is important in an enzymatic nucleic acid molecule of this invention is that it have a specific substrate binding site which is complementary to one or more of the target gene RNA regions, and that it have nucleotide sequences within or surrounding that substrate binding site which impart a RNA cleaving activity to the molecule (Cech et al., U.S. Patent No. 4,987,071).

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By "nucleic acid molecule" as used herein is meant a molecule having nucleotides. The nucleic acid can be single, double, or multiple stranded and can comprise modified or unmodified nucleotides or non-nucleotides or various mixtures and combinations thereof.

By "enzymatic portion" or "catalytic domain" is meant that portion/region of a enzymatic nucleic acid molecule essential for cleavage of a nucleic acid substrate (for example see Figure 6).

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By "substrate binding arm" or "substrate binding domain" is meant that portion/region of a enzymatic nucleic acid which is able to interact, for example via complementarity (i.e., able to base-pair with), with a portion of its substrate. Preferably, such complementarity is 100%, but can be less if desired. For example, as few as 10 bases out of 14 can be base-paired (see for example Werner and Uhlenbeck, 1995, Nucleic Acids Research, 23, 2092-2096; Hammann et al., 1999, Antisense and Nucleic Acid Drug Dev., 9, 25-31). Examples of such arms are shown generally in Figures 6-8. That is, these arms contain sequences within a enzymatic nucleic acid which are intended to bring enzymatic nucleic acid and target nucleic acid together through complementary base-pairing interactions. An enzymatic nucleic acid of the invention can have binding arms that are contiguous or non-contiguous and can be of varying lengths. The length of the binding arm(s) are preferably greater than or equal to four nucleotides and of sufficient length to stably interact with the target nucleic acid; preferably 12-100 nucleotides; more preferably 14-24 nucleotides long (see for example Werner and Uhlenbeck, supra; Hamman et al., supra; Hampel et al., EP0360257; Berzal-Herranz et al., 1993, EMBO J., 12, 2567-73) or between 8 and 14 nucleotides long. If two binding arms are chosen, the design is such that the length of the binding arms are symmetrical (i.e., each of the binding arms is of the same length; e.g., four and four, five and five nucleotides, or six and six nucleotides, or seven and seven nucleotides long) or asymmetrical (i.e., the binding arms are of different length; e.g., three and five, six and three nucleotides; three and six nucleotides long; four and five nucleotides long; four and six nucleotides long; four and seven nucleotides long; and the like).

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By "Inozyme" or "NCH" motif or configuration is meant, an enzymatic nucleic acid molecule comprising a motif as is generally described as NCH Rz in Figure 6 and in Ludwig et al., International PCT Publication No. WO 98/58058 and US Patent Application Serial No. 08/878,640. Inozymes possess endonuclease activity to cleave nucleic acid substrates having a cleavage triplet NCH/, where N is a nucleotide, C is cytidine and H is adenosine, uridine or cytidine, and "/" represents the cleavage site. H is used interchangeably with X. Inozymes can also possess endonuclease activity to cleave nucleic acid substrates having a cleavage triplet NCN/, where N is a nucleotide, C is cytidine, and "/" represents the cleavage site. "T" in Figure 6 represents an Inosine nucleotide, preferably a ribo-Inosine or xylo-Inosine nucleoside.

By "G-cleaver" motif or configuration is meant, an enzymatic nucleic acid molecule comprising a motif as is generally described as G-cleaver Rz in Figure 6 and in Eckstein et al., US 6,127,173. G-cleavers possess endonuclease activity to cleave nucleic acid substrates having a cleavage triplet NYN/, where N is a nucleotide, Y is uridine or cytidine and "/"

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represents the cleavage site. G-cleavers can be chemically modified as is generally shown in Figure 6.

By "amberzyme" motif or configuration is meant, an enzymatic nucleic acid molecule comprising a motif as is generally described in Beigelman et al., International PCT publication No. WO 99/55857 and US Patent Application Serial No. 09/476,387. Amberzymes possess endonuclease activity to cleave nucleic acid substrates having a cleavage triplet NG/N, where N is a nucleotide, G is guanosine, and "/" represents the cleavage site. Amberzymes can be chemically modified to increase nuclease stability through substitutions using modified nucleotides. In addition, differing nucleoside and/or non-nucleoside linkers can be used to substitute the 5'-gaaa-3' loops shown in the figure. Amberzymes represent a non-limiting example of an enzymatic nucleic acid molecule that does not require a ribonucleotide (2'-OH) group within its own nucleic acid sequence for activity.

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By "zinzyme" motif or configuration is meant, an enzymatic nucleic acid molecule comprising a motif as is generally described in Figure 7 and in Beigelman et al., International PCT publication No. WO 99/55857 and US Patent Application Serial No. 09/918,728. Zinzymes possess endonuclease activity to cleave nucleic acid substrates having a cleavage triplet including but not limited to YG/Y, where Y is uridine or cytidine, and G is guanosine and "/" represents the cleavage site. Zinzymes can be chemically modified to increase nuclease stability through substitutions as are generally shown in Figure 7, including substituting 2'-O-methyl guanosine nucleotides for guanosine nucleotides. In addition, differing nucleotide and/or non-nucleotide linkers can be used to substitute the 5'-gaaa-2' loop shown in the figure. Zinzymes represent a non-limiting example of an enzymatic nucleic acid molecule that does not require a ribonucleotide (2'-OH) group within its own nucleic acid sequence for activity.

By 'DNAzyme' is meant, an enzymatic nucleic acid molecule that does not require the presence of a 2'-OH group within its own nucleic acid sequence for activity. In particular embodiments the enzymatic nucleic acid molecule can have an attached linker or linkers or other attached or associated groups, moieties, or chains containing one or more nucleotides with 2'-OH groups. DNAzymes can be synthesized chemically or expressed endogenously in vivo, by means of a single stranded DNA vector or equivalent thereof. An example of a DNAzyme is shown in Figure 8 and is generally reviewed in Usman et al., US patent No., 6,159,714; Chartrand et al., 1995, NAR 23, 4092; Breaker et al., 1995, Chem. Bio. 2, 655; Santoro et al., 1997, PNAS 94, 4262; Breaker, 1999, Nature Biotechnology, 17, 422-423; and

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Santoro et. al., 2000, J. Am. Chem. Soc., 122, 2433-39. The "10-23" DNAzyme motif is one particular type of DNAzyme that was evolved using in vitro selection, see Santoro et al., supra and as generally described in Joyce et al., US 5,807,718. Additional DNAzyme motifs can be selected for using techniques similar to those described in these references, and hence, are within the scope of the present invention.

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By "sufficient length" is meant a nucleic acid molecule of the invention is long enough to provide the intended function under the expected condition. For example, a nucleic acid molecule of the invention needs to be of "sufficient length" to provide stable interaction with a target nucleic acid molecule under the expected binding conditions and environment. In another non-limiting example, for the binding arms of an enzymatic nucleic acid, "sufficient length" means that the binding arm sequence is long enough to provide stable binding to a target site under the expected reaction conditions and environment. The binding arms are not so long as to prevent useful turnover of the nucleic acid molecule.

By "stably interact" is meant interaction of an oligonucleotides with target nucleic acid (e.g., by forming hydrogen bonds with complementary nucleotides in the target under physiological conditions) that is sufficient to the intended purpose (e.g., cleavage of target nucleic acid by an enzyme).

By "equivalent" RNA to VEGF, VEGFR1 and/or VEGFR2 is meant to include nucleic acid molecules having homology (partial or complete) to a nucleic acid encoding VEGF, VEGFR1 and/or VEGFR2 proteins or encoding proteins with similar function as VEGF, VEGFR1 and/or VEGFR2 proteins in various organisms, including human, rodent, primate, rabbit, pig, protozoans, fungi, plants, and other microorganisms and parasites. The equivalent nucleic acid sequence also includes, in addition to the coding region, regions such as 5'-untranslated region, 3'-untranslated region, intron-exon junction and the like.

By "homology" is meant the nucleotide sequence of two or more nucleic acid molecules is partially or completely identical.

By "antisense nucleic acid", it is meant a non-enzymatic nucleic acid molecule that binds to target nucleic acid by means of RNA-RNA or RNA-DNA or RNA-PNA (protein nucleic acid; Egholm et al., 1993 Nature 365, 566) interactions and alters the activity of the target nucleic acid (for a review, see Stein and Cheng, 1993 Science 261, 1004 and Woolf et al., US patent No. 5,849,902). Typically, antisense molecules are complementary to a target sequence along a single contiguous sequence of the antisense molecule. However, in certain embodiments, an antisense molecule can bind to substrate such that the substrate molecule

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forms a loop, and/or an antisense molecule can bind such that the antisense molecule forms a loop. Thus, an antisense molecule can be complementary to two (or even more) non-contiguous substrate sequences or two (or even more) non-contiguous sequence portions of an antisense molecule can be complementary to a target sequence or both. For a review of current antisense strategies, see Schmajuk et al., 1999, J. Biol. Chem., 274, 21783-21789, Delihas et al., 1997, Nature, 15, 751-753, Stein et al., 1997, Antisense N. A. Drug Dev., 7, 151, Crooke, 2000, Methods Enzymol., 313, 3-45; Crooke, 1998, Biotech. Genet. Eng. Rev., 15, 121-157, Crooke, 1997, Ad. Pharmacol., 40, 1-49. In addition, antisense DNA can be used to target nucleic acid by means of DNA-RNA interactions, thereby activating RNase H, which digests the target nucleic acid in the duplex. The antisense oligonucleotides can comprise one or more RNAse H activating region, which is capable of activating RNAse H cleavage of a target nucleic acid. Antisense DNA can be synthesized chemically or expressed via the use of a single stranded DNA expression vector or equivalent thereof.

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By "RNase H activating region" is meant a region (generally greater than or equal to 4-25 nucleotides in length, preferably from 5-11 nucleotides in length) of a nucleic acid molecule capable of binding to a target nucleic acid to form a non-covalent complex that is recognized by cellular RNase H enzyme (see for example Arrow et al., US 5,849,902; Arrow et al., US 5,989,912). The RNase H enzyme binds to a nucleic acid molecule-target nucleic acid complex and cleaves the target nucleic acid sequence. The RNase H activating region comprises, for example, phosphodiester, phosphorothioate (preferably at least four of the nucleotides are phosphorothiote substitutions; more specifically, 4-11 of the nucleotides are phosphorothiote substitutions); phosphorodithioate, 5'-thiophosphate, or methylphosphonate backbone chemistry or a combination thereof. In addition to one or more backbone chemistries described above, the RNase H activating region can also comprise a variety of sugar chemistries. For example, the RNase H activating region can comprise deoxyribose, arabino, fluoroarabino or a combination thereof, nucleotide sugar chemistry. Those skilled in the art will recognize that the foregoing are non-limiting examples and that any combination of phosphate, sugar and base chemistry of a nucleic acid that supports the activity of RNase H enzyme is within the scope of the definition of the RNase H activating region and the instant invention.

By "2-5A antisense chimera" is meant an antisense oligonucleotide containing a 5'-phosphorylated 2'-5'-linked adenylate residue. These chimeras bind to target nucleic acid in a sequence-specific manner and activate a cellular 2-5A-dependent ribonuclease which, in turn, cleaves the target nucleic acid (Torrence et al., 1993 Proc. Natl. Acad. Sci. USA 90, 1300;

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Silverman et al., 2000, Methods Enzymol., 313, 522-533; Player and Torrence, 1998, Pharmacol. Ther., 78, 55-113).

By "triplex forming oligonucleotides" is meant an oligonucleotide that can bind to a double-stranded polynucleotide, such as DNA, in a sequence-specific manner to form a triple-strand helix. Formation of such triple helix structure has been shown to inhibit transcription of the targeted gene (Duval-Valentin et al., 1992 Proc. Natl. Acad. Sci. USA 89, 504; Fox, 2000, Curr. Med. Chem., 7, 17-37; Praseuth et. al., 2000, Biochim. Biophys. Acta, 1489, 181-206).

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By "gene" it is meant a nucleic acid that encodes an RNA, for example, nucleic acid sequences including but not limited to structural genes encoding a polypeptide.

The term "complementarity" as used herein refers to the ability of a nucleic acid to form hydrogen bond(s) with another nucleic acid sequence by either traditional Watson-Crick or other non-traditional types. In reference to nucleic molecules of the present invention, the binding free energy for a nucleic acid molecule with its target or complementary sequence is sufficient to allow the relevant function of the nucleic acid to proceed, e.g., enzymatic nucleic acid cleavage, antisense or triple helix inhibition. Determination of binding free energies for nucleic acid molecules is well known in the art (see, e.g., Turner et al., 1987, CSH Symp. Quant. Biol. LII pp.123-133; Frier et al., 1986, Proc. Nat. Acad. Sci. USA 83:9373-9377; Turner et al., 1987, J. Am. Chem. Soc. 109:3783-3785). A percent complementarity indicates the percentage of contiguous residues in a nucleic acid molecule which can form hydrogen bonds (e.g., Watson-Crick base pairing) with a second nucleic acid sequence (e.g., 5, 6, 7, 8, 9, 10 out of 10 being 50%, 60%, 70%, 80%, 90%, and 100% complementary). "Perfectly complementary" means that all the contiguous residues of a nucleic acid sequence will hydrogen bond with the same number of contiguous residues in a second nucleic acid sequence.

By "RNA" is meant a molecule comprising at least one ribonucleotide residue. By "ribonucleotide" or "2'-OH" is meant a nucleotide with a hydroxyl group at the 2' position of a  $\beta$ -D-ribo-furanose moiety.

By "nucleic acid decoy molecule", or "decoy" as used herein is meant a nucleic acid molecule that mimics the natural binding domain for a ligand. The decoy therefore competes with the natural binding target for the binding of a specific ligand. For example, it has been shown that over-expression of HIV trans-activation response (TAR) RNA can act as a

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"decoy" and efficiently binds HIV tat protein, thereby preventing it from binding to TAR sequences encoded in the HIV RNA (Sullenger et al., 1990, Cell, 63, 601-608).

By "aptamer" or "nucleic acid aptamer" as used herein is meant a nucleic acid molecule that binds specifically to a target molecule wherein the nucleic acid molecule has sequence that is distinct from sequence recognized by the target molecule in its natural setting. Alternately, an aptamer can be a nucleic acid molecule that binds to a target molecule where the target molecule does not naturally bind to a nucleic acid. The target molecule can be any molecule of interest. For example, the aptamer can be used to bind to a ligand binding domain of a protein, thereby preventing interaction of the naturally occurring ligand with the protein. Similarly, the nucleic acid molecules of the instant invention can bind to VEGFR1 or VEGFR2 receptors to block activity of the receptor. This is a non-limiting example and those in the art will recognize that other embodiments can be readily generated using techniques generally known in the art, see for example Gold et al., US 5,475,096 and 5,270,163; Gold et al., 1995, Annu. Rev. Biochem., 64, 763; Brody and Gold, 2000, J. Biotechnol., 74, 5; Sun, 2000, Curr. Opin. Mol. Ther., 2, 100; Kusser, 2000, J. Biotechnol., 74, 27; Hermann and Patel, 2000, Science, 287, 820; and Jayasena, 1999, Clinical Chemistry, 45, 1628.

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The term "double stranded RNA" or "dsRNA" as used herein refers to a double stranded RNA molecule capable of RNA interference "RNAi", including short interfering RNA "siRNA" see for example Bass, 2001, Nature, 411, 428-429; Elbashir et al., 2001, Nature, 411, 494-498; and Kreutzer et al., International PCT Publication No. WO 00/44895; Zernicka-Goetz et al., International PCT Publication No. WO 01/36646; Fire, International PCT Publication No. WO 99/32619; Plaetinck et al., International PCT Publication No. WO 01/29058; Deschamps-Depaillette, International PCT Publication No. WO 99/07409; and Li et al., International PCT Publication No. WO 00/44914.

By "nucleic acid sensor molecule" or "allozyme" as used herein is meant a nucleic acid molecule comprising an enzymatic domain and a sensor domain, where the enzymatic nucleic acid domain's ability to catalyze a chemical reaction is dependent on the interaction with a target signaling molecule, such as a nucleic acid, polynucleotide, oligonucleotide, peptide, polypeptide, or protein, for example VEGF, VEGFR1 and/or VEGFR2. The introduction of chemical modifications, additional functional groups, and/or linkers, to the nucleic acid sensor molecule can provide enhanced catalytic activity of the nucleic acid sensor molecule, increased binding affinity of the sensor domain to a target nucleic acid, and/or improved nuclease/chemical stability of the nucleic acid sensor molecule, and are

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hence within the scope of the present invention (see for example Usman et al., US Patent Application No. 09/877,526, George et al., US Patent Nos. 5,834,186 and 5,741,679, Shih et al., US Patent No. 5,589,332, Nathan et al., US Patent No 5,871,914, Nathan and Ellington, International PCT publication No. WO 00/24931, Breaker et al., International PCT Publication Nos. WO 00/26226 and 98/27104, and Sullenger et al., US Patent Application Serial No. 09/205,520).

By "sensor component" or "sensor domain" of the nucleic acid sensor molecule as used herein is meant, a nucleic acid sequence (e.g., RNA or DNA or analogs thereof) which interacts with a target signaling molecule, for example a nucleic acid sequence in one or more regions of a target nucleic acid molecule or more than one target nucleic acid molecule, and which interaction causes the enzymatic nucleic acid component of the nucleic acid sensor molecule to either catalyze a reaction or stop catalyzing a reaction. In the presence of target signaling molecule of the invention, such as VEGF, VEGFR1 and/or VEGFR2, the ability of the sensor component, for example, to modulate the catalytic activity of the nucleic acid sensor molecule, is inhibited or diminished. The sensor component can comprise recognition properties relating to chemical or physical signals capable of modulating the nucleic acid sensor molecule via chemical or physical changes to the structure of the nucleic acid sensor molecule. The sensor component can be derived from a naturally occurring nucleic acid binding sequence, for example, RNAs that bind to other nucleic acid sequences in vivo. Alternately, the sensor component can be derived from a nucleic acid molecule (aptamer) which is evolved to bind to a nucleic acid sequence within a target nucleic acid molecule (see for example Gold et al., US 5,475,096 and 5,270,163). The sensor component can be covalently linked to the nucleic acid sensor molecule, or can be non-covalently associated. A person skilled in the art will recognize that all that is required is that the sensor component is able to selectively inhibit the activity of the nucleic acid sensor molecule to catalyze a reaction.

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By "target molecule" or "target signaling molecule" is meant a molecule capable of interacting with a nucleic acid sensor molecule, specifically a sensor domain of a nucleic acid sensor molecule, in a manner that causes the nucleic acid sensor molecule to be active or inactive. The interaction of the signaling agent with a nucleic acid sensor molecule can result in modification of the enzymatic nucleic acid component of the nucleic acid sensor molecule via chemical, physical, topological, or conformational changes to the structure of the molecule, such that the activity of the enzymatic nucleic acid component of the nucleic acid sensor molecule is modulated, for example is activated or deactivated. Signaling agents can comprise target signaling molecules such as macromolecules, ligands, small molecules.

metals and ions, nucleic acid molecules including but not limited to RNA and DNA or analogs thereof, proteins, peptides, antibodies, polysaccharides, lipids, sugars, microbial or cellular metabolites, pharmaceuticals, and organic and inorganic molecules in a purified or unpurified form, for example VEGF, VEGFR1 and/or VEGFR2.

The term "triplex forming oligonucleotides" as used herein refers to an oligonucleotide that can bind to a double-stranded DNA in a sequence-specific manner to form a triple-strand helix. Formation of such a triple helix structure has been shown to inhibit transcription of a targeted gene (Duval-Valentin et al., 1992 Proc. Natl. Acad. Sci. USA 89, 504; Fox, 2000, Curr. Med. Chem., 7, 17-37; Praseuth et. al., 2000, Biochim. Biophys. Acta, 1489, 181-206).

The nucleic acid molecules that modulate the expression of VEGF and/or VEGFr, such as VEGFR1 and/or VEGFR2 specific nucleic acids, represent a novel therapeutic approach to treat or control a variety of angiogenesis related disorders and conditions, including but not limited to tumor angiogenesis, cancers such as breast cancer, lung cancer, colorectal cancer, renal cancer, pancreatic cancer, or melanoma, or ocular indications such as diabetic retinopathy, or age related macular degeneration, and/or endometriosis, endometrial carcinoma, gynecologic bleeding disorders, irregular menstrual cycles, ovulation, premenstrual syndrome (PMS), and/or menopausal dysfunction. The nucleic acid molecules that modulate the expression of VEGF and/or VEGFr, such as VEGFR1 and/or VEGFR2 specific nucleic acids also represent a novel approach to control ovulation or embryonic implantation and therefore provide a novel means of birth control.

In one embodiment of the present invention, a nucleic acid molecule of the instant invention can be between 12 and 100 nucleotides in length. An exemplary enzymatic nucleic acid molecule of the invention is shown as Formula I and/or Formula II. For example, enzymatic nucleic acid molecules of the invention are preferably between 15 and 50 nucleotides in length, more preferably between 25 and 40 nucleotides in length, e.g., 34, 36, or 38 nucleotides in length (for example see Jarvis et al., 1996, J. Biol. Chem., 271, 29107-29112). Exemplary DNAzymes of the invention are preferably between 15 and 40 nucleotides in length, more preferably between 25 and 35 nucleotides in length, e.g., 29, 30, 31, or 32 nucleotides in length (see for example Santoro et al., 1998, Biochemistry, 37, 13330-13342; Chartrand et al., 1995, Nucleic Acids Research, 23, 4092-4096). Exemplary antisense molecules of the invention are preferably between 15 and 75 nucleotides in length, more preferably between 20 and 35 nucleotides in length, e.g., 25, 26, 27, or 28 nucleotides in length (see for example Woolf et al., 1992, PNAS., 89, 7305-7309; Milner et al., 1997, Nature Biotechnology, 15, 537-541). Exemplary triplex forming oligonucleotide molecules of the invention are preferably between 10 and 40 nucleotides in length, more preferably

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between 12 and 25 nucleotides in length, e.g., 18, 19, 20, or 21 nucleotides in length (see for example Maher et al., 1990, Biochemistry, 29, 8820-8826; Strobel and Dervan, 1990, Science, 249, 73-75). Those skilled in the art will recognize that all that is required is that the nucleic acid molecule be of length and conformation sufficient and suitable for the nucleic acid molecule to catalyze a reaction contemplated herein. The length of the nucleic acid molecules of the instant invention are not limiting within the general limits stated.

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In a preferred embodiment, a nucleic acid molecule that modulates, for example, down-regulates, VEGF and/or VEGFr, such as VEGFR1 and/or VEGFR2 replication or expression comprises between 8 and 100 bases complementary to a nucleic acid molecule of VEGFR1 and/or VEGFR2. More preferably, a nucleic acid molecule that modulates VEGF and/or VEGFr, such as VEGFR1 and/or VEGFR2 replication or expression comprises between 14 and 24 bases complementary to a nucleic acid molecule of VEGFR1 and/or VEGFR2.

The invention provides a method for producing a class of nucleic acid—based gene modulating agents which exhibit a high degree of specificity for the nucleic acid of a desired target. For example, a nucleic acid molecule of the invention is preferably targeted to a highly conserved sequence region of target nucleic acids encoding VEGF and/or VEGFr, such as VEGFR1 and/or VEGFR2 (specifically VEGF, VEGFR1 and/or VEGFR2 genes) such that specific treatment of a disease or condition can be provided with either one or several nucleic acid molecules of the invention. Such nucleic acid molecules can be delivered exogenously to specific tissue or cellular targets as required. Alternatively, the nucleic acid molecules can be expressed from DNA and/or RNA vectors that are delivered to specific cells.

As used in herein "cell" is used in its usual biological sense, and does not refer to an entire multicellular organism. The cell can, for example, be *in vitro*, e.g., in cell culture, or present in a multicellular organism, including,, e.g., birds, plants and mammals such as humans, cows, sheep, apes, monkeys, swine, dogs, and cats. The cell may be prokaryotic (e.g., bacterial cell) or eukaryotic (e.g., mammalian or plant cell).

By "VEGFR1 and/or VEGFR2 proteins" is meant, protein receptor or a mutant protein derivative thereof, having vascular endothelial growth factor receptor activity, for example, having the ability to bind vascular endothelial growth factor and/or having tyrosine kinase activity.

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By "highly conserved sequence region" is meant, a nucleotide sequence of one or more regions in a target gene does not vary significantly from one generation to the other or from one biological system to the other.

"Angiogenesis" refers to formation of new blood vessels which is an essential process in reproduction, development and wound repair. "Tumor angiogenesis" refers to the induction of the growth of blood vessels from surrounding tissue into a solid tumor. Tumor growth and tumor metastasis are dependent on angiogenesis (for a review see Folkman, 1985 supra; Folkman 1990 J. Natl. Cancer Inst., 82, 4; Folkman and Shing, 1992 J. Biol. Chem. 267, 10931).

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Angiogenesis plays an important role in other diseases such as arthritis wherein new blood vessels have been shown to invade the joints and degrade cartilage (Folkman and Shing, supra).

"Retinopathy" refers to inflammation of the retina and/or degenerative condition of the retina which may lead to occlusion of the retina and eventual blindness. In "diabetic retinopathy" angiogenesis causes the capillaries in the retina to invade the vitreous resulting in bleeding and blindness which is also seen in neonatal retinopathy (for a review see Folkman, 1985 supra; Folkman 1990 supra; Folkman and Shing, 1992 supra).

Nucleic acid-based inhibitors of VEGF and/or VEGFr, such as VEGFR1 and/or VEGFR2, expression are useful for the prevention, treatment, and/or control of angiogenesis related disorders and conditions, including but not limited to, tumor angiogenesis, cancers such as breast cancer, lung cancer, colorectal cancer, renal cancer, pancreatic cancer, or melanoma, or ocular indications such as diabetic retinopathy, or age related macular degeneration, and/or endometriosis, endometrial carcinoma, gynecologic bleeding disorders, irregular menstrual cycles, ovulation, premenstrual syndrome (PMS), menopausal dysfunction, and other diseases or conditions that are related to or will respond to the levels of VEGF, VEGFR1 and/or VEGFR2 in a cell or tissue, alone or in combination with other therapies. The reduction of VEGF and/or VEGFr, such as VEGFR1 and/or VEGFR2 expression (specifically VEGF, VEGFR1 and/or VEGFR2 gene RNA levels) and thus reduction in the level of the respective protein relieves, to some degree, the symptoms of the disease or condition. Nucleic acid-based inhibitors of VEGF and/or VEGFr, such as VEGFR1 and/or VEGFR2 expression are also useful as birth control agents, for example by inhibition of ovulation or embryonic uterine implantation.

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The nucleic acid molecules of the invention can be added directly, or can be complexed with cationic lipids, packaged within liposomes, or otherwise delivered to target cells or tissues. The nucleic acid complexes can be locally administered to relevant tissues ex vivo, or in vivo through injection or infusion pump, with or without their incorporation in biopolymers. In preferred embodiments, the nucleic acid inhibitors comprise sequences, which are complementary to polynucleotides, for example DNA and RNA, having VEGF and/or VEGFR, such as VEGFR1 and/or VEGFR2 sequence.

Triplex molecules of the invention can be provided targeted to DNA target regions, and containing the DNA equivalent of a target sequence or a sequence complementary to the specified target (substrate) sequence. Antisense molecules typically are complementary to a target sequence along a single contiguous sequence of the antisense molecule. However, in certain embodiments, an antisense molecule can bind to substrate such that the substrate molecule forms a loop, and/or an antisense molecule can bind such that the antisense molecule forms a loop. Thus, the antisense molecule can be complementary to two (or even more) non-contiguous substrate sequences or two (or even more) non-contiguous sequence portions of an antisense molecule can be complementary to a target sequence or both.

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By "consists essentially of" is meant that the active nucleic acid molecule of the invention, for example, an enzymatic nucleic acid molecule, contains an enzymatic center or core equivalent to those in the examples, and binding arms able to bind nucleic acid such that cleavage at the target site occurs. Other sequences can be present which do not interfere with such cleavage. Thus, a core region can, for example, include one or more loop, stem-loop structure, or linker which does not prevent enzymatic activity. Thus, a particular region of a nucleic acid molecule of the invention can be such a loop, stem-loop, nucleotide linker, and/or non-nucleotide linker and can be represented generally as sequence "X". Thus, a core region may, for example, include one or more loop or stem-loop structures which do not prevent enzymatic activity. For example, a core sequence for a hammerhead enzymatic nucleic acid can comprise a conserved sequence, such as 5'-CUGAUGAG-3' and 5'-CGAA-3' connected by "X", where X is 5'-GCCGUUAGGC-3' (SEQ ID NO 5979), or any other Stem II region known in the art, or a nucleotide and/or non-nucleotide linker. Similarly, for other nucleic acid molecules of the instant invention, such as Inozyme, G-cleaver, amberzyme, zinzyme, DNAzyme, antisense, 2-5A antisense, triplex forming nucleic acid, aptamers, decoy nucleic acids, dsRNA or siRNA, other sequences or non-nucleotide linkers can be present that do not interfere with the function of the nucleic acid molecule.

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Sequence X can be a linker of ≥ 2 nucleotides in length, preferably 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 26, 30, where the nucleotides can preferably be internally base-paired to form a stem of preferably ≥ 2 base pairs. Alternatively or in addition, sequence X can be a non-nucleotide linker. In yet another embodiment, the nucleotide linker X can be a nucleic acid aptamer, such as an ATP aptamer, HIV Rev aptamer (RRE), HIV Tat aptamer (TAR) and others (for a review see Gold et al., 1995, Annu. Rev. Biochem., 64, 763; and Szostak & Ellington, 1993, in The RNA World, ed. Gesteland and Atkins, pp. 511, CSH Laboratory Press). A nucleic acid aptamer includes a nucleic acid sequence capable of interacting with a ligand. The ligand can be any natural or a synthetic molecule, including but not limited to a resin, metabolites, nucleosides, nucleic acid molecules, hormones, carbohydrates, receptors, cells, viruses, bacteria and others.

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In yet another embodiment, the non-nucleotide linker X is as defined herein. The term "non-nucleotide" as used herein include either abasic nucleotide, polyether, polyamine, polyamide, peptide, carbohydrate, lipid, or polyhydrocarbon compounds. Specific examples include those described by Seela and Kaiser, Nucleic Acids Res. 1990, 18:6353 and Nucleic Acids Res. 1987, 15:3113; Cload and Schepartz, J. Am. Chem. Soc. 1991, 113:6324; Richardson and Schepartz, J. Am. Chem. Soc. 1991, 113:5109; Ma et al., Nucleic Acids Res. 1993, 21:2585 and Biochemistry 1993, 32:1751; Durand et al., Nucleic Acids Res. 1990, 18:6353; McCurdy et al., Nucleosides & Nucleotides 1991, 10:287; Jschke et al., Tetrahedron Lett. 1993, 34:301; Ono et al., Biochemistry 1991, 30:9914; Arnold et al., International Publication No. WO 95/06731; Dudycz et al., International Publication No. WO 95/11910 and Ferentz and Verdine, J. Am. Chem. Soc. 1991, 113:4000, all hereby incorporated by reference herein.

A "non-nucleotide" further means any group or compound which can be incorporated into a nucleic acid chain in the place of one or more nucleotide units, including either sugar and/or phosphate substitutions, and allows the remaining bases to exhibit their enzymatic activity. The group or compound can be abasic in that it does not contain a commonly recognized nucleotide base, such as adenosine, guanine, cytosine, uracil or thymine. Thus, in one embodiment, the invention features an enzymatic nucleic acid molecule having one or more non-nucleotide moieties, and having enzymatic activity to cleave an RNA or DNA molecule.

In another aspect of the invention, nucleic acid molecules that interact with target nucleic acid molecules and down-regulate VEGF and/or VEGFr, such as VEGFR1 and/or

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VEGFR2 (specifically VEGF, VEGFR1 and/or VEGFR2 gene) activity are expressed from transcription units inserted into DNA or RNA vectors. The recombinant vectors are preferably DNA plasmids or viral vectors. Enzymatic nucleic acid molecule or antisense expressing viral vectors can be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. The recombinant vectors capable of expressing the enzymatic nucleic acid molecules or antisense are delivered as described above, and persist in target cells. Alternatively, viral vectors can be used that provide for transient expression of enzymatic nucleic acid molecules or antisense. Such vectors can be repeatedly administered as necessary. Once expressed, the enzymatic nucleic acid molecules or antisense bind to the target nucleic acid and down-regulate its function or expression. Delivery of enzymatic nucleic acid molecule or antisense expressing vectors can be systemic, such as by intravenous or intramuscular administration, by administration to target cells explanted from the patient followed by reintroduction into the patient, or by any other means that would allow for introduction into the desired target cell. Antisense DNA can be expressed via the use of a single stranded DNA intracellular expression vector.

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By "vectors" is meant any nucleic acid- and/or viral-based technique used to deliver a desired nucleic acid.

By "subject" or "patient" is meant an organism, which is a donor or recipient of explanted cells, or the cells themselves. "Subject" or "Patient" also refers to an organism to which the nucleic acid molecules of the invention can be administered. Preferably, a subject or patient is a mammal or mammalian cells. More preferably, a subject or patient is a human or human cells.

By "enhanced enzymatic activity" is meant to include activity measured in cells and/or in vivo where the activity is a reflection of both the catalytic activity and the stability of the nucleic acid molecules of the invention. In this invention, the product of these properties can be increased *in vivo* compared to an all RNA enzymatic nucleic acid or all DNA enzyme. In some cases, the activity or stability of the nucleic acid molecule can be decreased (i.e., less than ten-fold), but the overall activity of the nucleic acid molecule is enhanced, *in vivo*.

The nucleic acid molecules of the instant invention, individually, or in combination or in conjunction with other drugs, can be used to treat diseases or conditions discussed above. For example, to treat a disease or condition associated with the levels of VEGFR1 and/or VEGFR2, the patient can be treated, or other appropriate cells can be treated, as is evident to those skilled in the art, individually or in combination with one or more drugs under conditions suitable for the treatment.

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In a further embodiment, the described molecules of the invention can be used in combination with other known treatments to treat conditions or diseases discussed above. For example, the described molecules can be used in combination with one or more known therapeutic agents to treat angiogenesis related disorders and conditions, including but not limited to tumor angiogenesis, cancers such as breast cancer, lung cancer, colorectal cancer, renal cancer, pancreatic cancer, or melanoma, or ocular indications such as diabetic retinopathy, or age related macular degeneration, and/or endometriosis, birth control, endometrial tumors, gynecologic bleeding disorders, irregular menstrual cycles, ovulation, premenstrual syndrome (PMS), menopausal dysfunction, endometrial carcinoma, and/or other diseases or conditions which respond to the modulation of VEGF and/or VEGFr, such as VEGFR1 and/or VEGFR2 expression.

Other features and advantages of the invention will be apparent from the following description of the preferred embodiments thereof, and from the claims.

## Brief Description of the Drawings

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Figure 1 shows a secondary structure model of ANGIOZYME $^{\text{TM}}$  ribozyme bound to its RNA target.

Figure 2 shows a time course of inhibition of primary tumor growth following systemic administration of ANGIOZYME™ in the LLC mouse model.

Figure 3 shows inhibition of primary tumor growth following systemic administration of ANGIOZYME<sup>TM</sup> according to a certain dosing regimen in the LLC mouse model.

Figure 4 shows a dose-dependent inhibition of tumor metastases following systemic administration of ANGIOZYME™ in a mouse colorectal model.

Figure 5 is a graph showing the plasma concentration profile of ANGIOZYME™ after a single subcutaneous (SC) dose of 10, 30, 100 or 300 mg/m<sup>2</sup>.

Figure 6 shows examples of chemically stabilized ribozyme motifs. HH Rz, represents hammerhead ribozyme motif (Usman et al., 1996, Curr. Op. Struct. Bio., 1, 527); NCH Rz represents the NCH ribozyme motif (Ludwig et al., International PCT Publication No. WO 98/58058 and US Patent Application Serial No. 08/878,640); G-Cleaver, represents G-cleaver ribozyme motif (Kore et al., 1998, Nucleic Acids Research 26, 4116-4120, Eckstein et

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al., US 6,127,173). N or n, represent independently a nucleotide which can be same or different and have complementarity to each other; rI, represents ribo-Inosine nucleotide; arrow indicates the site of cleavage within the target. Position 4 of the HH Rz and the NCH Rz is shown as having 2'-C-allyl modification, but those skilled in the art will recognize that this position can be modified with other modifications well known in the art, so long as such modifications do not significantly inhibit the activity of the ribozyme.

Figure 7 shows an example of a Zinzyme A ribozyme motif that is chemically stabilized (see for example Beigelman *et al.*, International PCT publication No. WO 99/55857 and US Patent Application Serial No. 09/918,728).

Figure 8 shows an example of a DNAzyme motif described by Santoro et al., 1997, PNAS, 94, 4262 and Joyce et al., US 5,807,718.

Figure 9 shows data demonstrating the inhibition of soluble VEGFR1 in a clinical study using ANGIOZYME (SEQ ID NO: 5977).

Figure 10 shows an generalized outline for the mouse model of proliferative retinopathy showing the points of ribozyme administration.

Figure 11 shows a graph demonstrating the efficacy of a VEGF-receptor-targeted enzymatic nucleic acid molecule in a mouse model of proliferative retinopathy.

#### Detailed Description of the Invention

### Nucleic Acid Molecules and Mechanism of Action

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Enzymatic Nucleic Acid: Several varieties of naturally-occurring enzymatic nucleic acids are presently known. In addition, several in vitro selection (evolution) strategies (Orgel, 1979, Proc. R. Soc. London, B 205, 435) have been used to evolve new nucleic acid catalysts capable of catalyzing cleavage and ligation of phosphodiester linkages (Joyce, 1989, Gene, 82, 83-87; Beaudry et al., 1992, Science 257, 635-641; Joyce, 1992, Scientific American 267, 90-97; Breaker et al., 1994, TIBTECH 12, 268; Bartel et al., 1993, Science 261:1411-1418; Szostak, 1993, TIBS 17, 89-93; Kumar et al., 1995, FASEB J., 9, 1183; Breaker, 1996, Curr. Op. Biotech., 7, 442; Santoro et al., 1997, Proc. Natl. Acad. Sci., 94, 4262; Tang et al., 1997, RNA 3, 914; Nakamaye & Eckstein, 1994, supra; Long & Uhlenbeck, 1994, supra; Ishizaka et al., 1995, supra; Vaish et al., 1997, Biochemistry 36, 6495; all of these are incorporated by reference herein). Each can catalyze a series of reactions including the hydrolysis of

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phosphodiester bonds in trans (and thus can cleave other nucleic acid molecules) under physiological conditions.

The enzymatic nature of an enzymatic nucleic acid molecule has significant advantages, one advantage being that the concentration of enzymatic nucleic acid molecule necessary to affect a therapeutic treatment is lower. This advantage reflects the ability of the enzymatic nucleic acid molecule to act enzymatically. Thus, a single enzymatic nucleic acid molecule is able to cleave many molecules of target nucleic acid. In addition, the enzymatic nucleic acid molecule is a highly specific inhibitor, with the specificity of inhibition depending not only on the base-pairing mechanism of binding to the target nucleic acid, but also on the mechanism of target nucleic acid cleavage. Single mismatches, or base-substitutions, near the site of cleavage can be chosen to completely eliminate catalytic activity of a enzymatic nucleic acid molecule.

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Nucleic acid molecules having an endonuclease enzymatic activity are able to repeatedly cleave other separate nucleic acid molecules in a nucleotide base sequence-specific manner. With the proper design, such enzymatic nucleic acid molecules can be targeted to RNA transcripts, and achieve efficient cleavage in vitro (Zaug et al., 324, Nature 429 1986; Uhlenbeck, 1987 Nature 328, 596; Kim et al., 84 Proc. Natl. Acad. Sci. USA 8788, 1987; Dreyfus, 1988, Einstein Quart. J. Bio. Med., 6, 92; Haseloff and Gerlach, 334 Nature 585, 1988; Cech, 260 JAMA 3030, 1988; and Jefferies et al., 17 Nucleic Acids Research 1371, 1989; Santoro et al., 1997 supra).

Because of their sequence specificity, trans-cleaving enzymatic nucleic acid molecules can be used as therapeutic agents for human disease (Usman & McSwiggen, 1995 Ann. Rep. Med. Chem. 30, 285-294; Christoffersen and Marr, 1995 J. Med. Chem. 38, 2023-2037). Enzymatic nucleic acid molecules can be designed to cleave specific nucleic acid targets within the background of cellular nucleic acid. Such a cleavage event renders the nucleic acid non-functional and abrogates protein expression from that nucleic acid. In this manner, synthesis of a protein associated with a disease state can be selectively inhibited (Warashina et al., 1999, Chemistry and Biology, 6, 237-250).

Enzymatic nucleic acid molecules of the invention that are allosterically regulated ("allozymes") can be used to down-regulate VEGF and/or VEGFR, such as VEGFR1 and/or VEGFR2, expression. These allosteric enzymatic nucleic acids or allozymes (see for example Usman et al., US Patent Application No. 09/877,526, George et al., US Patent Nos. 5,834,186 and 5,741,679, Shih et al., US Patent No. 5,589,332, Nathan et al., US Patent No 5,871,914, Nathan and Ellington, International PCT publication No. WO 00/24931, Breaker

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et al., International PCT Publication Nos. WO 00/26226 and 98/27104, and Sullenger et al., US Patent Application Serial No. 09/205,520) are designed to respond to a signaling agent, for example, mutant VEGFR1 and/or VEGFR2 protein, wild-type VEGFR1 and/or VEGFR2 protein, mutant VEGFR1 and/or VEGFR2 RNA, wild-type VEGFR1 and/or VEGFR2 RNA, other proteins and/or RNAs involved in VEGF signal transduction, compounds, metals, polymers, molecules and/or drugs that are targeted to VEGFR1 and/or VEGFR2 expression. which in turn modulates the activity of the enzymatic nucleic acid molecule. In response to interaction with a predetermined signaling agent, the activity of the allosteric enzymatic nucleic acid is activated or inhibited such that the expression of a particular target is selectively down-regulated. The target can comprise wild-type VEGFR1 and/or VEGFR2. mutant VEGFR1 and/or VEGFR2, and/or a predetermined component of the VEGF signal transduction pathway. In a specific example, allosteric enzymatic nucleic acid molecules that are activated by interaction with a RNA encoding VEGF protein are used as therapeutic agents in vivo. The presence of RNA encoding the VEGF protein activates the allosteric enzymatic nucleic acid molecule that subsequently cleaves the RNA encoding a VEGFR1 and/or VEGFR2 protein resulting in the inhibition of VEGFR1 and/or VEGFR2 protein expression.

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In another non-limiting example, an allozyme can be activated by a VEGF and/or VEGFr, such as VEGFR1 and/or VEGFR2 protein, peptide, or mutant polypeptide that causes the allozyme to inhibit the expression of VEGF and/or VEGFr, such as VEGFR1 and/or VEGFR2 genes, by, for example, cleaving RNA encoded by VEGF, VEGFR1 and/or VEGFR2 gene. In this non-limiting example, the allozyme acts as a decoy to inhibit the function of VEGF, VEGFR1 and/or VEGFR2 and also inhibit the expression of VEGF, VEGFR1 and/or VEGFR2 protein.

Antisense: Antisense molecules can be modified or unmodified RNA, DNA, or mixed polymer oligonucleotides and primarily function by specifically binding to matching sequences resulting in inhibition of peptide synthesis (Wu-Pong, Nov 1994, BioPharm, 20-33). The antisense oligonucleotide binds to target RNA by Watson Crick base-pairing and blocks gene expression by preventing ribosomal translation of the bound sequences either by steric blocking or by activating RNase H enzyme. Antisense molecules can also alter protein synthesis by interfering with RNA processing or transport from the nucleus into the cytoplasm (Mukhopadhyay & Roth, 1996, Crit. Rev. in Oncogenesis 7, 151-190).

In addition, binding of single stranded DNA to RNA can result in nuclease degradation of the heteroduplex (Wu-Pong, supra; Crooke, supra). To date, the only backbone modified

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DNA chemistry which act as substrates for RNase H are phosphorothioates, phosphorodithioates, and borontrifluoridates. Recently it has been reported that 2'-arabino and 2'-fluoro arabino- containing oligos can also activate RNase H activity.

A number of antisense molecules have been described that utilize novel configurations of chemically modified nucleotides, secondary structure, and/or RNase H substrate domains (Woolf et al., International PCT Publication No. WO 98/13526; Thompson et al., International PCT Publication No. WO 99/54459; Hartmann et al., USSN 60/101,174 which was filed on September 21, 1998) all of these are incorporated by reference herein in their entirety.

In addition, antisense deoxyoligoribonucleotides can be used to target RNA by means of DNA-RNA interactions, thereby activating RNase H, which digests the target RNA in the duplex. Antisense DNA can be expressed via the use of a single stranded DNA intracellular expression vector or equivalents and variations thereof.

<u>Triplex Forming Oligonucleotides (TFO)</u>: Single stranded DNA can be designed to bind to genomic DNA in a sequence specific manner. TFOs are comprised of pyrimidine-rich oligonucleotides which bind DNA helices through Hoogsteen Base-pairing (Wu-Pong, *supra*). The resulting triple helix composed of the DNA sense, DNA antisense, and TFO disrupts RNA synthesis by RNA polymerase. The TFO mechanism can result in gene expression or cell death since binding can be irreversible (Mukhopadhyay & Roth, *supra*).

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2-5A Antisense Chimera: The 2-5A system is an interferon mediated mechanism for RNA degradation found in higher vertebrates (Mitra et al., 1996, Proc Nat Acad Sci USA 93, 6780-6785). Two types of enzymes, 2-5A synthetase and RNase L, are required for RNA cleavage. The 2-5A synthetases require double stranded RNA to form 2'-5' oligoadenylates (2-5A). 2-5A then acts as an allosteric effector for utilizing RNase L which has the ability to cleave single stranded RNA. The ability to form 2-5A structures with double stranded RNA makes this system particularly useful for inhibition of viral replication.

(2'-5') oligoadenylate structures can be covalently linked to antisense molecules to form chimeric oligonucleotides capable of RNA cleavage (Torrence, *supra*). These molecules putatively bind and activate a 2-5A dependent RNase, the oligonucleotide/enzyme complex then binds to a target RNA molecule which can then be cleaved by the RNase enzyme.

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RNAi: Double-stranded RNAs can suppress expression of homologous genes through an evolutionarily conserved process named RNA interference (RNAi) or post-transcriptional gene silencing (PTGS). One mechanism underlying silencing is the degradation of target mRNAs by an RNP complex, which contains short interfering RNAs (siRNAs) as guides to substrate selection. Short interfering RNAs are typically 21 to 23 nucleotides in length. A bidentate nuclease called Dicer has been implicated as the protein responsible for siRNA production. For example, a double-stranded RNA (dsRNA) matching a gene sequence is synthesized in vitro and introduced into a cell. The dsRNA feeds into a biological pathway and is broken into short pieces of short interfering (si) RNAs. With the help of cellular enzymes such as Dicer, the siRNA triggers the degradation of the messenger RNA that matches its sequence (see for example Tuschl et al., International PCT Publication No. WO 01/75164; Bass, 2001, Nature, 411, 428-429; Elbashir et al., 2001, Nature, 411, 494-498; and Kreutzer et al., International PCT Publication No. WO 00/44895).

### Target sites

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Targets for useful nucleic acid molecules of the invention, such as enzymatic nucleic acid molecules, dsRNA, and antisense nucleic acids can be determined as disclosed in Draper et al., WO 93/23569; Sullivan et al., WO 93/23057; Thompson et al., WO 94/02595; Draper et al., WO 95/04818; McSwiggen et al., US Patent No. 5,525,468, and hereby incorporated by reference herein in totality. Other examples include the following PCT applications, which concern inactivation of expression of disease-related genes: WO 95/23225, WO 95/13380, WO 94/02595, incorporated by reference herein. Rather than repeat the guidance provided in those documents here, below are provided specific examples of such methods. not limiting to those in the art. Enzymatic nucleic acid molecules and antisense to such targets are designed as described in those applications and synthesized to be tested in vitro and in vivo, as also described. The sequences of human VEGF, VEGFR1 and/or VEGFR2 RNAs are screened for optimal nucleic acid target sites using a computer-folding algorithm. Potential nucleic acid binding/cleavage sites are identified. While human sequences can be screened and nucleic acid molecules thereafter designed, as discussed in Stinchcomb et al.. WO 95/23225, mouse targeted enzymatic nucleic acid molecules can be useful to test efficacy of action of the nucleic acid molecule prior to testing in humans.

Nucleic acid molecule binding/cleavage sites are identified, for example enzymatic nucleic acid, antisense, and dsRNA mediated binding sites are chosen. For enzymatic nucleic acid molecules of the invention, the nucleic acid molecules are individually analyzed by computer folding (Jaeger et al., 1989 Proc. Natl. Acad. Sci. USA, 86, 7706) to assess whether

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the sequences fold into the appropriate secondary structure. Those nucleic acid molecules with unfavorable intramolecular interactions such as between the binding arms and the catalytic core can be eliminated from consideration. Varying binding arm lengths can be chosen to optimize activity.

Nucleic acids, such as antisense, RNAi, and/or enzymatic nucleic acid molecule binding/cleavage sites are identified and are designed to anneal to various sites in the nucleic acid target. The binding arms of enzymatic nucleic acid molecules of the invention are complementary to the target site sequences described above. Antisense and RNAi sequences are designed to have partial or complete complementarity to the nucleic acid target. The nucleic acid molecules can be chemically synthesized. The method of synthesis used follows the procedure for normal DNA/RNA synthesis as described below and in Usman et al., 1987 J. Am. Chem. Soc., 109, 7845; Scaringe et al., 1990 Nucleic Acids Res., 18, 5433; and Wincott et al., 1995 Nucleic Acids Res. 23, 2677-2684; Caruthers et al., 1992, Methods in Enzymology 211,3-19.

## 15 Synthesis of Nucleic acid Molecules

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Synthesis of nucleic acids greater than 100 nucleotides in length is difficult using automated methods, and the therapeutic cost of such molecules is prohibitive. In this invention, small nucleic acid motifs ("small refers to nucleic acid motifs less than about 100 nucleotides in length, preferably less than about 80 nucleotides in length, and more preferably less than about 50 nucleotides in length; e.g., antisense oligonucleotides, enzymatic nucleic acids, aptamers, allozymes, decoys, siRNA etc.) are preferably used for exogenous delivery. The simple structure of these molecules increases the ability of the nucleic acid to invade targeted regions of RNA structure. Exemplary molecules of the instant invention are chemically synthesized, and others can similarly be synthesized.

DNA Oligonucleotides are synthesized using protocols known in the art as described in Caruthers et al., 1992, Methods in Enzymology 211, 3-19, Thompson et al., International PCT Publication No. WO 99/54459, Wincott et al., 1995, Nucleic Acids Res. 23, 2677-2684, Wincott et al., 1997, Methods Mol. Bio., 74, 59, Brennan et al., 1998, Biotechnol Bioeng., 61, 33-45, and Brennan, US patent No. 6,001,311. All of these references are incorporated herein by reference. The synthesis of oligonucleotides makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. In a non-limiting example, small scale syntheses are conducted on a 394 Applied Biosystems, Inc. synthesizer using a 0.2 µmol scale protocol with a 2.5 min coupling step for 2'-O-methylated nucleotides and a 45 sec coupling step for 2'-deoxy nucleotides. Table II

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outlines the amounts and the contact times of the reagents used in the synthesis cycle. Alternatively, syntheses at the 0.2 µmol scale can be performed on a 96-well plate synthesizer, such as the instrument produced by Protogene (Palo Alto, CA) with minimal modification to the cycle. A 33-fold excess (60 µL of 0.11 M = 6.6 µmol) of 2'-O-methyl phosphoramidite and a 105-fold excess of S-ethyl tetrazole (60  $\mu$ L of 0.25 M = 15  $\mu$ mol) can be used in each coupling cycle of 2'-O-methyl residues relative to polymer-bound 5'hydroxyl. A 22-fold excess (40  $\mu$ L of 0.11 M = 4.4  $\mu$ mol) of deoxy phosphoramidite and a 70-fold excess of S-ethyl tetrazole (40  $\mu$ L of 0.25 M = 10  $\mu$ mol) can be used in each coupling cycle of deoxy residues relative to polymer-bound 5'-hydroxyl. Average coupling yields on the 394 Applied Biosystems, Inc. synthesizer, determined by colorimetric quantitation of the trityl fractions, are typically 97.5-99%. Other oligonucleotide synthesis reagents for the 394 Applied Biosystems, Inc. synthesizer include; detritylation solution is 3% TCA in methylene chloride (ABI); capping is performed with 16% N-methyl imidazole in THF (ABI) and 10% acetic anhydride/10% 2,6-lutidine in THF (ABI); and oxidation solution is 16.9 mM I2, 49 mM pyridine, 9% water in THF (PERSEPTIVETM). Burdick & Jackson Synthesis Grade acetonitrile is used directly from the reagent bottle. S-Ethyltetrazole solution (0.25 M in acetonitrile) is made up from the solid obtained from American International Chemical, Inc. Alternately, for the introduction of phosphorothicate linkages, Beaucage reagent (3H-1,2-Benzodithiol-3-one 1,1-dioxide, 0.05 M in acetonitrile) is used.

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Deprotection of the DNA polynucleotides is performed as follows: the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 40% aq. methylamine (1 mL) at 65 °C for 10 min. After cooling to -20 °C, the supernatant is removed from the polymer support. The support is washed three times with 1.0 mL of EtOH:MeCN:H2O/3:1:1, vortexed and the supernatant is then added to the first supernatant. The combined supernatants, containing the oligoribonucleotide, are dried to a white powder.

The method of synthesis used for RNA oligonucleotides including certain nucleic acid molecules of the invention follows the procedure as described in Usman et al., 1987, J. Am. Chem. Soc., 109, 7845; Scaringe et al., 1990, Nucleic Acids Res., 18, 5433; and Wincott et al., 1995, Nucleic Acids Res. 23, 2677-2684 Wincott et al., 1997, Methods Mol. Bio., 74, 59, and makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. In a non-limiting example, small scale syntheses are conducted on a 394 Applied Biosystems, Inc. synthesizer using a 0.2 µmol scale protocol with a 7.5 min coupling step for alkylsilyl protected nucleotides and a 2.5 min coupling step for 2'-O-methylated nucleotides. Table II outlines the amounts and the

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contact times of the reagents used in the synthesis cycle. Alternatively, syntheses at the 0.2 µmol scale can be done on a 96-well plate synthesizer, such as the instrument produced by Protogene (Palo Alto, CA) with minimal modification to the cycle. A 33-fold excess (60 µL of 0.11 M = 6.6 µmol) of 2'-O-methyl phosphoramidite and a 75-fold excess of S-ethyl tetrazole (60 µL of 0.25 M = 15 µmol) can be used in each coupling cycle of 2'-O-methyl residues relative to polymer-bound 5'-hydroxyl. A 66-fold excess (120 µL of 0.11 M = 13.2 µmol) of alkylsilyl (ribo) protected phosphoramidite and a 150-fold excess of S-ethyl tetrazole (120 µL of 0.25 M = 30 µmol) can be used in each coupling cycle of ribo residues relative to polymer-bound 5'-hydroxyl. Average coupling yields on the 394 Applied Biosystems, Inc. synthesizer, determined by colorimetric quantitation of the trityl fractions. are typically 97.5-99%. Other oligonucleotide synthesis reagents for the 394 Applied Biosystems, Inc. synthesizer include; detritylation solution is 3% TCA in methylene chloride (ABI); capping is performed with 16% N-methyl imidazole in THF (ABI) and 10% acetic anhydride/10% 2,6-lutidine in THF (ABI); oxidation solution is 16.9 mM I2, 49 mM pyridine, 9% water in THF (PERSEPTIVETM). Burdick & Jackson Synthesis Grade acetonitrile is used directly from the reagent bottle. S-Ethyltetrazole solution (0.25 M in acetonitrile) is made up from the solid obtained from American International Chemical, Inc. Alternately, for the introduction of phosphorothioate linkages, Beaucage reagent (3H-1,2-Benzodithiol-3-one 1,1dioxide0.05 M in acetonitrile) is used.

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Deprotection of the RNA is performed using either a two-pot or one-pot protocol. For the two-pot protocol, the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 40% aq. methylamine (1 mL) at 65 °C for 10 min. After cooling to -20 °C, the supernatant is removed from the polymer support. The support is washed three times with 1.0 mL of EtOH:MeCN:H2O/3:1:1, vortexed and the supernatant is then added to the first supernatant. The combined supernatants, containing the oligoribonucleotide, are dried to a white powder. The base deprotected oligoribonucleotide is resuspended in anhydrous TEA/HF/NMP solution (300 µL of a solution of 1.5 mL N-methylpyrrolidinone, 750 µL TEA and 1 mL TEA•3HF to provide a 1.4 M HF concentration) and heated to 65 °C. After 1.5 h, the oligomer is quenched with 1.5 M NH<sub>4</sub>HCO<sub>3</sub>.

Alternatively, for the one-pot protocol, the polymer-bound trityl-on oligoribonucleotide is transferred to a 4 mL glass screw top vial and suspended in a solution of 33% ethanolic methylamine/DMSO: 1/1 (0.8 mL) at 65 °C for 15 min. The vial is brought to r.t. TEA•3HF (0.1 mL) is added and the vial is heated at 65 °C for 15 min. The sample is cooled at -20 °C and then quenched with 1.5 M NH<sub>4</sub>HCO<sub>3</sub>.

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For purification of the trityl-on oligomers, the quenched NH<sub>4</sub>HCO<sub>3</sub> solution is loaded onto a C-18 containing cartridge that had been prewashed with acetonitrile followed by 50 mM TEAA. After washing the loaded cartridge with water, the RNA is detritylated with 0.5% TFA for 13 min. The cartridge is then washed again with water, salt exchanged with 1 M NaCl and washed with water again. The oligonucleotide is then eluted with 30% acetonitrile.

Inactive hammerhead ribozymes or binding attenuated control (BAC) oligonucleotides) are synthesized by substituting a U for G5 and a U for A14 (numbering from Hertel, K. J., et al., 1992, Nucleic Acids Res., 20, 3252). Similarly, one or more nucleotide substitutions can be introduced in other enzymatic nucleic acid molecules to inactivate the molecule and such molecules can serve as a negative control.

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The average stepwise coupling yields are typically >98% (Wincott et al., 1995 Nucleic Acids Res. 23, 2677-2684). Those of ordinary skill in the art will recognize that the scale of synthesis can be adapted to be larger or smaller than the example described above including but not limited to 96 well format, all that is important is the ratio of chemicals used in the reaction.

Alternatively, the nucleic acid molecules of the present invention can be synthesized separately and joined together post-synthetically, for example by ligation (Moore et al., 1992, Science 256, 9923; Draper et al., International PCT publication No. WO 93/23569; Shabarova et al., 1991, Nucleic Acids Research 19, 4247; Bellon et al., 1997, Nucleosides & Nucleotides, 16, 951; Bellon et al., 1997, Bioconjugate Chem. 8, 204).

Preferably, the nucleic acid molecules of the present invention are modified extensively to enhance stability by modification with nuclease resistant groups, for example, 2'-amino, 2'-C-allyl, 2'-flouro, 2'-O-methyl, 2'-H (for a review see Usman and Cedergren, 1992, TIBS 17, 34; Usman et al., 1994, Nucleic Acids Symp. Ser. 31, 163). Ribozymes are purified by gel electrophoresis using general methods or are purified by high pressure liquid chromatography (HPLC; See Wincott et al., Supra, the totality of which is hereby incorporated herein by reference) and are re-suspended in water.

# Optimizing Activity of the nucleic acid molecule of the invention.

Chemically synthesizing nucleic acid molecules with modifications (base, sugar and/or phosphate) that prevent their degradation by serum ribonucleases can increase their potency (see e.g., Eckstein et al., International Publication No. WO 92/07065; Perrault et al., 1990 Nature 344, 565; Pieken et al., 1991, Science 253, 314; Usman and Cedergren, 1992, Trends

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in Biochem. Sci. 17, 334; Usman et al., International Publication No. WO 93/15187; and Rossi et al., International Publication No. WO 91/03162; Sproat, US Patent No. 5,334,711; Gold et al., US 6,300,074; and Burgin et al., supra; all of which are incorporated by reference herein). Modifications which enhance their efficacy in cells, and removal of bases from nucleic acid molecules to shorten oligonucleotide synthesis times and reduce chemical requirements are desired. (All these publications are hereby incorporated by reference herein).

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There are several examples in the art describing sugar, base and phosphate modifications that can be introduced into nucleic acid molecules with significant enhancement in their nuclease stability and efficacy. For example, oligonucleotides are modified to enhance stability and/or enhance biological activity by modification with nuclease resistant groups, for example, 2'-amino, 2'-C-allyl, 2'-flouro, 2'-O-methyl, 2'-H, nucleotide base modifications (for a review see Usman and Cedergren, 1992, TIBS, 17, 34; Usman et al., 1994, Nucleic Acids Symp. Ser. 31, 163; Burgin et al., 1996, Biochemistry, 35, 14090). Sugar modification of nucleic acid molecules have been extensively described in the art (see Eckstein et al., International Publication PCT No. WO 92/07065; Perrault et al. Nature, 1990, 344, 565-568; Pieken et al. Science, 1991, 253, 314-317; Usman and Cedergren, Trends in Biochem. Sci., 1992, 17, 334-339; Usman et al. International Publication PCT No. WO 93/15187; Sproat, US Patent No. 5,334,711 and Beigelman et al., 1995, J. Biol. Chem., 270, 25702; Beigelman et al., International PCT publication No. WO 97/26270; Beigelman et al., US Patent No. 5,716,824; Usman et al., US patent No. 5,627,053; Woolf et al., International PCT Publication No. WO 98/13526; Thompson et al., USSN 60/082,404 which was filed on April 20, 1998; Karpeisky et al., 1998, Tetrahedron Lett., 39, 1131; Earnshaw and Gait, 1998, Biopolymers (Nucleic acid Sciences), 48, 39-55; Verma and Eckstein, 1998, Annu. Rev. Biochem., 67, 99-134; and Burlina et al., 1997, Bioorg. Med. Chem., 5, 1999-2010; all of the references are hereby incorporated in their totality by reference herein). Such publications describe general methods and strategies to determine the location of incorporation of sugar, base and/or phosphate modifications and the like into ribozymes without inhibiting catalysis, and are incorporated by reference herein. In view of such teachings, similar modifications can be used as described herein to modify the nucleic acid molecules of the instant invention.

While chemical modification of oligonucleotide internucleotide linkages with phosphorothicate, phosphorothicate, and/or 5'-methylphosphonate linkages improves stability, too many of these modifications can cause some toxicity. Therefore when designing nucleic acid molecules the amount of these internucleotide linkages should be minimized.

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The reduction in the concentration of these linkages should lower toxicity resulting in increased efficacy and higher specificity of these molecules.

Nucleic acid molecules having chemical modifications that maintain or enhance activity are provided. Such nucleic acid is also generally more resistant to nucleases than unmodified nucleic acid. Thus, in a cell and/or in vivo the activity may not be significantly lowered. Therapeutic nucleic acid molecules delivered exogenously are optimally stable within cells until translation of the target RNA has been inhibited long enough to reduce the levels of the undesirable protein. This period of time varies between hours to days depending upon the disease state. Clearly, nucleic acid molecules must be resistant to nucleases in order to function as effective intracellular therapeutic agents. Improvements in the chemical synthesis of RNA and DNA (Wincott et al., 1995 Nucleic Acids Res. 23, 2677; Caruthers et al., 1992, Methods in Enzymology 211,3-19 (incorporated by reference herein) have expanded the ability to modify nucleic acid molecules by introducing nucleotide modifications to enhance their nuclease stability as described above.

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In one embodiment, nucleic acid molecules of the invention include one or more G-clamp nucleotides. A G-clamp nucleotide is a modified cytosine analog wherein the modifications confer the ability to hydrogen bond both Watson-Crick and Hoogsteen faces of a complementary guanine within a duplex, see for example Lin and Matteucci, 1998, J. Am. Chem. Soc., 120, 8531-8532. A single G-clamp analog substitution within an oligonucleotide can result in substantially enhanced helical thermal stability and mismatch discrimination when hybridized to complementary oligonucleotides. The inclusion of such nucleotides in nucleic acid molecules of the invention results in both enhanced affinity and specificity to nucleic acid targets. In another embodiment, nucleic acid molecules of the invention include one or more LNA "locked nucleic acid" nucleotides such as a 2', 4'-C mythylene bicyclo nucleotide (see for example Wengel et al., International PCT Publication No. WO 00/66604 and WO 99/14226).

In another embodiment, the invention features conjugates and/or complexes of nucleic acid molecules targeting VEGF receptors such as VEGFR1 and/or VEGFR2. Such conjugates and/or complexes can be used to facilitate delivery of molecules into a biological system, such as cells. The conjugates and complexes provided by the instant invention can impart therapeutic activity by transferring therapeutic compounds across cellular membranes, altering the pharmacokinetics, and/or modulating the localization of nucleic acid molecules of the invention. The present invention encompasses the design and synthesis of novel conjugates and complexes for the delivery of molecules, including but not limited to small

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molecules, lipids, phospholipids, nucleosides, nucleotides, nucleic acids, antibodies, toxins, negatively charged polymers and other polymers, for example proteins, peptides, hormones, carbohydrates, polyethylene glycols, or polyamines, across cellular membranes. In general, the transporters described are designed to be used either individually or as part of a multi-component system, with or without degradable linkers. These compounds are expected to improve delivery and/or localization of nucleic acid molecules of the invention into a number of cell types originating from different tissues, in the presence or absence of serum (see Sullenger and Cech, US 5,854,038). Conjugates of the molecules described herein can be attached to biologically active molecules via linkers that are biodegradable, such as biodegradable nucleic acid linker molecules.

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The term "biodegradable nucleic acid linker molecule" as used herein, refers to a nucleic acid molecule that is designed as a biodegradable linker to connect one molecule to another molecule, for example, a biologically active molecule. The stability of the biodegradable nucleic acid linker molecule can be modulated by using various combinations of ribonucleotides, deoxyribonucleotides, and chemically modified nucleotides, for example, 2'-O-methyl, 2'-fluoro, 2'-amino, 2'-O-amino, 2'-C-allyl, 2'-O-allyl, and other 2'-modified or base modified nucleotides. The biodegradable nucleic acid linker molecule can be a dimer, trimer, tetramer or longer nucleic acid molecule, for example, an oligonucleotide of about 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nucleotides in length, or can comprise a single nucleotide with a phosphorus based linkage, for example, a phosphoramidate or phosphodiester linkage. The biodegradable nucleic acid linker molecule can also comprise nucleic acid backbone, nucleic acid sugar, or nucleic acid base modifications.

The term "biodegradable" as used herein, refers to degradation in a biological system, for example enzymatic degradation or chemical degradation.

The term "biologically active molecule" as used herein, refers to compounds or molecules that are capable of eliciting or modifying a biological response in a system. Non-limiting examples of biologically active molecules contemplated by the instant invention include therapeutically active molecules such as antibodies, hormones, antivirals, peptides, proteins, chemotherapeutics, small molecules, vitamins, co-factors, nucleosides, nucleotides, oligonucleotides, enzymatic nucleic acids, antisense nucleic acids, triplex forming oligonucleotides, 2,5-A chimeras, siRNA, dsRNA, allozymes, aptamers, decoys and analogs thereof. Biologically active molecules of the invention also include molecules capable of modulating the pharmacokinetics and/or pharmacodynamics of other biologically active

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molecules, for example, lipids and polymers such as polyamines, polyamides, polyethylene glycol and other polyethers.

The term "phospholipid" as used herein, refers to a hydrophobic molecule comprising at least one phosphorus group. For example, a phospholipid can comprise a phosphorus containing group and saturated or unsaturated alkyl group, optionally substituted with OH, COOH, oxo, amine, or substituted or unsubstituted aryl groups.

Therapeutic nucleic acid molecules (e.g., enzymatic nucleic acid molecules and antisense nucleic acid molecules) delivered exogenously are optimally stable within cells until translation of the target RNA has been inhibited long enough to reduce the levels of the undesirable protein. This period of time varies between hours to days depending upon the disease state. These nucleic acid molecules should be resistant to nucleases in order to function as effective intracellular therapeutic agents. Improvements in the chemical synthesis of nucleic acid molecules described in the instant invention and in the art have expanded the ability to modify nucleic acid molecules by introducing nucleotide modifications to enhance their nuclease stability as described above.

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In another embodiment, nucleic acid catalysts having chemical modifications that maintain or enhance enzymatic activity are provided. Such nucleic acids are also generally more resistant to nucleases than unmodified nucleic acid. Thus, in a cell and/or in vivo the activity of the nucleic acid may not be significantly lowered. As exemplified herein such enzymatic nucleic acids are useful in a cell and/or in vivo even if activity over all is reduced 10 fold (Burgin et al., 1996, Biochemistry, 35, 14090). Such enzymatic nucleic acids herein are said to "maintain" the enzymatic activity of an all RNA ribozyme or all DNA DNAzyme.

In another aspect the nucleic acid molecules comprise a 5' and/or a 3'- cap structure.

By "cap structure" is meant chemical modifications, which have been incorporated at either terminus of the oligonucleotide (see for example Wincott et al., WO 97/26270, incorporated by reference herein). These terminal modifications protect the nucleic acid molecule from exonuclease degradation, and can help in delivery and/or localization within a cell. The cap can be present at the 5'-terminus (5'-cap) or at the 3'-terminus (3'-cap) or can be present on both terminus. In non-limiting examples, the 5'-cap includes inverted abasic residue (moiety), 4',5'-methylene nucleotide; 1-(beta-D-erythrofuranosyl) nucleotide, 4'-thio nucleotide, carbocyclic nucleotide; 1,5-anhydrohexitol nucleotide; L-nucleotides; alphanucleotides; modified base nucleotide; phosphorodithioate linkage; threo-pentofuranosyl nucleotide; acyclic 3',4'-seco nucleotide; acyclic 3,4-dihydroxybutyl nucleotide; acyclic 3,5-

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dihydroxypentyl nucleotide, 3'-3'-inverted nucleotide moiety; 3'-3'-inverted abasic moiety; 3'-2'-inverted nucleotide moiety; 3'-2'-inverted abasic moiety; 1,4-butanediol phosphate; 3'-phosphoramidate; hexylphosphate; aminohexyl phosphate; 3'-phosphorothioate; phosphorodithioate; or bridging or non-bridging methylphosphonate moiety (for more details see Wincott et al., International PCT publication No. WO 97/26270, incorporated by reference herein).

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In another embodiment the 3'-cap includes, for example 4',5'-methylene nucleotide; 1-(beta-D-erythrofuranosyl) nucleotide; 4'-thio nucleotide, carbocyclic nucleotide; 5'-amino-alkyl phosphate; 1,3-diamino-2-propyl phosphate, 3-aminopropyl phosphate; 6-aminohexyl phosphate; 1,2-aminododecyl phosphate; hydroxypropyl phosphate; 1,5-anhydrohexitol nucleotide; L-nucleotide; alpha-nucleotide; modified base nucleotide; phosphorodithioate; threo-pentofuranosyl nucleotide; acyclic 3',4'-seco nucleotide; 3,4-dihydroxybutyl nucleotide; 3,5-dihydroxypentyl nucleotide, 5'-5'-inverted nucleotide moiety; 5'-5'-inverted abasic moiety; 5'-phosphoramidate; 5'-phosphorothioate; 1,4-butanediol phosphate; 5'-amino; bridging and/or non-bridging 5'-phosphoramidate, phosphorothioate and/or phosphorodithioate, bridging or non bridging methylphosphonate and 5'-mercapto moieties (for more details see Beaucage and Iyer, 1993, Tetrahedron 49, 1925; incorporated by reference herein).

By the term "non-nucleotide" is meant any group or compound which can be incorporated into a nucleic acid chain in the place of one or more nucleotide units, including either sugar and/or phosphate substitutions, and allows the remaining bases to exhibit their enzymatic activity. The group or compound is abasic in that it does not contain a commonly recognized nucleotide base, such as adenosine, guanine, cytosine, uracil or thymine.

An "alkyl" group refers to a saturated aliphatic hydrocarbon, including straight-chain, branched-chain, and cyclic alkyl groups. Preferably, the alkyl group has 1 to 12 carbons. More preferably it is a lower alkyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkyl group can be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =0, =S, NO<sub>2</sub> or N(CH<sub>3</sub>)<sub>2</sub>, amino, or SH. The term also includes alkenyl groups which are unsaturated hydrocarbon groups containing at least one carbon-carbon double bond, including straight-chain, branched-chain, and cyclic groups. Preferably, the alkenyl group has 1 to 12 carbons. More preferably it is a lower alkenyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkenyl group can be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =0, =S, NO<sub>2</sub>, halogen, N(CH<sub>3</sub>)<sub>2</sub>, amino, or SH. The term "alkyl" also includes alkynyl groups which have an unsaturated hydrocarbon group containing at least

one carbon-carbon triple bond, including straight-chain, branched-chain, and cyclic groups. Preferably, the alkynyl group has 1 to 12 carbons. More preferably it is a lower alkynyl of from 1 to 7 carbons, more preferably 1 to 4 carbons. The alkynyl group can be substituted or unsubstituted. When substituted the substituted group(s) is preferably, hydroxyl, cyano, alkoxy, =0,=S, NO<sub>2</sub> or N(CH<sub>3</sub>)<sub>2</sub>, amino or SH.

Such alkyl groups can also include aryl, alkylaryl, carbocyclic aryl, heterocyclic aryl, amide and ester groups. An "aryl" group refers to an aromatic group which has at least one ring having a conjugated p electron system and includes carbocyclic aryl, heterocyclic aryl and biaryl groups, all of which can be optionally substituted. The preferred substituent(s) of aryl groups are halogen, trihalomethyl, hydroxyl, SH, OH, cyano, alkoxy, alkyl, alkenyl, alkynyl, and amino groups. An "alkylaryl" group refers to an alkyl group (as described above) covalently joined to an aryl group (as described above). Carbocyclic aryl groups are groups wherein the ring atoms on the aromatic ring are all carbon atoms. The carbon atoms are optionally substituted. Heterocyclic aryl groups are groups having from 1 to 3 heteroatoms as ring atoms in the aromatic ring and the remainder of the ring atoms are carbon atoms. Suitable heteroatoms include oxygen, sulfur, and nitrogen, and include furanyl, thienyl, pyrrolyl, N-lower alkyl pyrrolo, pyrimidyl, pyrazinyl, imidazolyl and the like, all optionally substituted. An "amide" refers to an -C(O)-NH-R, where R is either alkyl, aryl, alkylaryl or hydrogen. An "ester" refers to an -C(O)-OR', where R is either alkyl, aryl, alkylaryl or hydrogen.

By "nucleotide" is meant a heterocyclic nitrogenous base in N-glycosidic linkage with a phosphorylated sugar. Nucleotides are recognized in the art to include natural bases (standard), and modified bases well known in the art. Such bases are generally located at the 1' position of a nucleotide sugar moiety. Nucleotides generally comprise a base, sugar and a phosphate group. The nucleotides can be unmodified or modified at the sugar, phosphate and/or base moiety, (also referred to interchangeably as nucleotide analogs, modified nucleotides, non-natural nucleotides, non-standard nucleotides and other; see for example, Usman and McSwiggen, supra; Eckstein et al., International PCT Publication No. WO 92/07065; Usman et al., International PCT Publication No. WO 93/15187; Uhlman & Peyman, supra all are hereby incorporated by reference herein). There are several examples of modified nucleic acid bases known in the art as summarized by Limbach et al., 1994, Nucleic Acids Res. 22, 2183. Some of the non-limiting examples of chemically modified and other natural nucleic acid bases that can be introduced into nucleic acids include, for example, inosine, purine, pyridin-4-one, pyridin-2-one, phenyl, pseudouracil, 2, 4, 6-trimethoxy benzene, 3-methyl uracil, dihydrouridine, naphthyl, aminophenyl, 5-alkylcytidines (e.g.,

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5-methylcytidine), 5-alkyluridines (e.g., ribothymidine), 5-halouridine (e.g., 5-bromouridine) or 6-azapyrimidines or 6-alkylpyrimidines (e.g. 6-methyluridine), propyne, quesosine, 2thiouridine, 4-thiouridine, wybutosine, wybutoxosine, 4-acetylcytidine, 5-(carboxyhydroxymethyl)uridine, 5'-carboxymethylaminomethyl-2-thiouridine, 5carboxymethylaminomethyluridine, beta-D-galactosylqueosine, 1-methyladenosine, 1-2,2-dimethylguanosine, 3-methylcytidine, 2-methyladenosine, 2methylguanosine. 7-methylguanosine, N6-methyladenosine, 5-methoxyaminomethyl-2-5-methylaminomethyluridine, thiouridine, 5-methylcarbonylmethyluridine. 5methyloxyuridine, 5-methyl-2-thiouridine, 2-methylthio-N6-isopentenyladenosine, beta-Dmannosylqueosine, uridine-5-oxyacetic acid, 2-thiocytidine, threonine derivatives and others (Burgin et al., 1996, Biochemistry, 35, 14090; Uhlman & Peyman, supra). By "modified bases" in this aspect is meant nucleotide bases other than adenine, guanine, cytosine and uracil at 1' position or their equivalents; such bases can be used at any position, for example, within the catalytic core of an enzymatic nucleic acid molecule and/or in the substrate-binding regions of the nucleic acid molecule.

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By "nucleoside" is meant a heterocyclic nitrogenous base in N-glycosidic linkage with a sugar. Nucleosides are recognized in the art to include natural bases (standard), and modified bases well known in the art. Such bases are generally located at the 1' position of a nucleoside sugar moiety. Nucleosides generally comprise a base and sugar group. The nucleosides can be unmodified or modified at the sugar, and/or base moiety, (also referred to interchangeably as nucleoside analogs, modified nucleosides, non-natural nucleosides, nonstandard nucleosides and other; see for example, Usman and McSwiggen, supra; Eckstein et al., International PCT Publication No. WO 92/07065; Usman et al., International PCT Publication No. WO 93/15187; Uhlman & Peyman, supra all are hereby incorporated by reference herein). There are several examples of modified nucleic acid bases known in the art as summarized by Limbach et al., 1994, Nucleic Acids Res. 22, 2183. Some of the nonlimiting examples of chemically modified and other natural nucleic acid bases that can be introduced into nucleic acids include, inosine, purine, pyridin-4-one, pyridin-2-one, phenyl, pseudouracil, 2, 4, 6-trimethoxy benzene, 3-methyl uracil, dihydrouridine, naphthyl, aminophenyl, 5-alkylcytidines (e.g., 5-methylcytidine), 5-alkylcytidines (e.g., ribothymidine), 5-halouridine (e.g., 5-bromouridine) or 6-azapyrimidines or 6-alkylpyrimidines (e.g. 6methyluridine), propyne, quesosine, 2-thiouridine, 4-thiouridine, wybutosine, wybutoxosine, 4-acetylcytidine, 5-(carboxyhydroxymethyl)uridine, 5'-carboxymethylaminomethyl-2thiouridine, 5-carboxymethylaminomethyluridine, beta-D-galactosylqueosine. 1methyladenosine. 1-methylinosine. 2,2-dimethylguanosine, 3-methylcytidine. 2methyladenosine, 2-methylguanosine, N6-methyladenosine, 7-methylguanosine. 5-

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methoxyaminomethyl-2-thiouridine, 5-methylaminomethyluridine, 5-methylcarbonylmethyluridine, 5-methylcarbonylmethyluridine, 5-methylcarbonylmethyluridine, 5-methylcarbonylmethyluridine, 5-methylcarbonylmethyluridine, 5-methylcarbonylmethyluridine, 2-methylthio-N6-isopentenyladenosine, beta-D-mannosylqueosine, uridine-5-oxyacetic acid, 2-thiocytidine, threonine derivatives and others (Burgin et al., 1996, Biochemistry, 35, 14090; Uhlman & Peyman, supra). By "modified bases" in this aspect is meant nucleoside bases other than adenine, guanine, cytosine and uracil at 1' position or their equivalents; such bases can be used at any position, for example, within the catalytic core of an enzymatic nucleic acid molecule and/or in the substrate-binding regions of the nucleic acid molecule.

In one embodiment, the invention features modified enzymatic nucleic acid molecules with phosphate backbone modifications comprising one or more phosphorothioate, phosphorodithioate, methylphosphonate, morpholino, amidate carbamate, carboxymethyl, acetamidate, polyamide, sulfonate, sulfonamide, sulfamate, formacetal, thioformacetal, and/or alkylsilyl, substitutions. For a review of oligonucleotide backbone modifications see Hunziker and Leumann, 1995, Nucleic Acid Analogues: Synthesis and Properties, in Modern Synthetic Methods, VCH, 331-417, and Mesmaeker et al., 1994, Novel Backbone Replacements for Oligonucleotides, in Carbohydrate Modifications in Antisense Research, ACS, 24-39. These references are hereby incorporated by reference herein.

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By "abasic" is meant sugar moieties lacking a base or having other chemical groups in place of a base at the 1' position, for example a 3',3'-linked or 5',5'-linked deoxyabasic ribose derivative (for more details see Wincott *et al.*, International PCT publication No. WO 97/26270).

By "unmodified nucleoside" is meant one of the bases adenine, cytosine, guanine, thymine, uracil joined to the 1' carbon of  $\beta$ -D-ribo-furanose.

By "modified nucleoside" is meant any nucleotide base which contains a modification in the chemical structure of an unmodified nucleotide base, sugar and/or phosphate.

In connection with 2'-modified nucleotides as described for the present invention, by "amino" is meant 2'-NH<sub>2</sub> or 2'-O- NH<sub>2</sub>, which can be modified or unmodified. Such modified groups are described, for example, in Eckstein *et al.*, U.S. Patent 5,672,695 and Matulic-Adamic *et al.*, WO 98/28317, respectively, which are both incorporated by reference in their entireties.

Various modifications to nucleic acid (e.g., antisense and ribozyme) structure can be made to enhance the utility of these molecules. For example, such modifications can enhance

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shelf-life, half-life in vitro, stability, and ease of introduction of such oligonucleotides to the target site, including, e.g., enhancing penetration of cellular membranes and conferring the ability to recognize and bind to targeted cells.

Use of the nucleic acid-based molecules of the invention can lead to better treatment of the disease progression by affording the possibility of combination therapies (e.g., multiple enzymatic nucleic acid molecules targeted to different genes, enzymatic nucleic acid molecules coupled with known small molecule inhibitors, or intermittent treatment with combinations of enzymatic nucleic acid molecules (including different enzymatic nucleic acid molecule motifs) and/or other chemical or biological molecules). The treatment of patients with nucleic acid molecules can also include combinations of different types of nucleic acid molecules. Therapies can be devised which include a mixture of enzymatic nucleic acid molecules (including different enzymatic nucleic acid molecules (including different enzymatic nucleic acid molecules (including different enzymatic nucleic acid molecules one or more targets to alleviate symptoms of a disease.

## 15 Administration of Nucleic Acid Molecules

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Methods for the delivery of nucleic acid molecules are described in Akhtar et al., 1992. Trends Cell Bio., 2, 139; and Delivery Strategies for Antisense Oligonucleotide Therapeutics. ed. Akhtar, 1995 which are both incorporated herein by reference. Sullivan et al., PCT WO 94/02595, further describes the general methods for delivery of enzymatic RNA molecules. These protocols can be utilized for the delivery of virtually any nucleic acid molecule. Nucleic acid molecules can be administered to cells by a variety of methods known to those familiar to the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable nanocapsules, and bioadhesive microspheres. Alternatively, the nucleic acid/vehicle combination is locally delivered by direct injection or by use of an infusion pump. Other routes of delivery include, but are not limited to oral (tablet or pill form) and/or intrathecal delivery (Gold, 1997, Neuroscience, 76, 1153-1158). Other approaches include the use of various transport and carrier systems, for example though the use of conjugates and biodegradable polymers. For a comprehensive review on drug delivery strategies including CNS delivery, see Ho et al., 1999, Curr. Opin. Mol. Ther., 1, 336-343 and Jain, Drug Delivery Systems: Technologies and Commercial Opportunities, Decision Resources, 1998 and Groothuis et al., 1997, J. Neuro Virol., 3, 387-400. More detailed descriptions of nucleic acid delivery and administration are provided in Sullivan et al., supra, Draper et al., PCT

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WO93/23569, Beigelman et al., PCT WO99/05094, and Klimuk et al., PCT WO99/04819 all of which have been incorporated by reference herein.

The molecules of the instant invention can be used as pharmaceutical agents. Pharmaceutical agents prevent, inhibit the occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) of a disease state in a patient.

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The polynucleotides of the invention can be administered (e.g., RNA, DNA or protein) and introduced into a patient by any standard means, with or without stabilizers, buffers, and the like, to form a pharmaceutical composition. When it is desired to use a liposome delivery mechanism, standard protocols for formation of liposomes can be followed. The compositions of the present invention can also be formulated and used as tablets, capsules or elixirs for oral administration; suppositories for rectal administration; sterile solutions; suspensions for injectable administration; and the other compositions known in the art.

The present invention also includes pharmaceutically acceptable formulations of the compounds described. These formulations include salts of the above compounds, e.g., acid addition salts, for example, salts of hydrochloric, hydrobromic, acetic acid, and benzene sulfonic acid.

A pharmacological composition or formulation refers to a composition or formulation in a form suitable for administration, e.g., systemic administration, into a cell or patient, preferably a human. Suitable forms, in part, depend upon the use or the route of entry, for example oral, transdermal, or by injection. Such forms should not prevent the composition or formulation from reaching a target cell (i.e., a cell to which the negatively charged polymer is desired to be delivered to). For example, pharmacological compositions injected into the blood stream should be soluble. Other factors are known in the art, and include considerations such as toxicity and forms which prevent the composition or formulation from exerting its effect.

By "systemic administration" is meant in vivo systemic absorption or accumulation of drugs in the blood stream followed by distribution throughout the entire body. Administration routes which lead to systemic absorption include, without limitations: intravenous, subcutaneous, intraperitoneal, inhalation, oral, intrapulmonary and intramuscular. Each of these administration routes expose the desired negatively charged polymers, e.g., nucleic acids, to an accessible diseased tissue. The rate of entry of a drug into the circulation has been shown to be a function of molecular weight or size. The use of a liposome or other drug carrier comprising the compounds of the instant invention can

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potentially localize the drug, for example, in certain tissue types, such as the tissues of the reticular endothelial system (RES). A liposome formulation which can facilitate the association of drug with the surface of cells, such as, lymphocytes and macrophages is also useful. This approach can provide enhanced delivery of the drug to target cells by taking advantage of the specificity of macrophage and lymphocyte immune recognition of abnormal cells, such as cells implicated in endometriosis, birth control, endometrial tumors, gynecologic bleeding disorders, irregular menstrual cycles, ovulation, premenstrual syndrome (PMS), menopausal dysfunction, and endometrial carcinoma.

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By pharmaceutically acceptable formulation is meant, a composition or formulation that allows for the effective distribution of the nucleic acid molecules of the instant invention in the physical location most suitable for their desired activity. Non-limiting examples of agents suitable for formulation with the nucleic acid molecules of the instant invention include: PEG conjugated nucleic acids, phospholipid conjugated nucleic acids, nucleic acids containing lipophilic moieties, phosphorothioates, P-glycoprotein inhibitors (such as Pluronic P85) which can enhance entry of drugs into various tissues, for example the CNS (Jolliet-Riant and Tillement, 1999, Fundam. Clin. Pharmacol., 13, 16-26); biodegradable polymers, such as poly (DL-lactide-coglycolide) microspheres for sustained release delivery after implantation (Emerich, DF et al, 1999, Cell Transplant, 8, 47-58) Alkermes, Inc. Cambridge, MA; and loaded nanoparticles, such as those made of polybutylcyanoacrylate, which can deliver drugs across the blood brain barrier and can alter neuronal uptake mechanisms (Prog Neuropsychopharmacol Biol Psychiatry, 23, 941-949, 1999). Other non-limiting examples of delivery strategies, including CNS delivery of the nucleic acid molecules of the instant invention include material described in Boado et al., 1998, J. Pharm. Sci., 87, 1308-1315; Tyler et al., 1999, FEBS Lett., 421, 280-284; Pardridge et al., 1995, PNAS USA., 92, 5592-5596; Boado, 1995, Adv. Drug Delivery Rev., 15, 73-107; Aldrian-Herrada et al., 1998, Nucleic Acids Res., 26, 4910-4916; and Tyler et al., 1999, PNAS USA., 96, 7053-7058. All these references are hereby incorporated herein by reference.

The invention also features the use of the composition comprising surface-modified liposomes containing poly (ethylene glycol) lipids (PEG-modified, or long-circulating liposomes or stealth liposomes). Nucleic acid molecules of the invention can also comprise covalently attached PEG molecules of various molecular weights. These formulations offer a method for increasing the accumulation of drugs in target tissues. This class of drug carriers resists opsonization and elimination by the mononuclear phagocytic system (MPS or RES), thereby enabling longer blood circulation times and enhanced tissue exposure for the encapsulated drug (Lasic et al. Chem. Rev. 1995, 95, 2601-2627; Ishiwata et al., Chem.

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Pharm. Bull. 1995, 43, 1005-1011). Such liposomes have been shown to accumulate selectively in tumors, presumably by extravasation and capture in the neovascularized target tissues (Lasic et al., Science 1995, 267, 1275-1276; Oku et al., 1995, Biochim. Biophys. Acta, 1238, 86-90). The long-circulating liposomes enhance the pharmacokinetics and pharmacodynamics of DNA and RNA, particularly compared to conventional cationic liposomes which are known to accumulate in tissues of the MPS (Liu et al., J. Biol. Chem. 1995, 42, 24864-24870; Choi et al., International PCT Publication No. WO 96/10391; Ansell et al., International PCT Publication No. WO 96/10392; all of which are incorporated by reference herein). Long-circulating liposomes are also likely to protect drugs from nuclease degradation to a greater extent compared to cationic liposomes, based on their ability to avoid accumulation in metabolically aggressive MPS tissues such as the liver and spleen. All of these references are incorporated by reference herein.

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The present invention also includes compositions prepared for storage or administration which include a pharmaceutically effective amount of the desired compounds in a pharmaceutically acceptable carrier or diluent. Acceptable carriers or diluents for therapeutic use are well known in the pharmaceutical art, and are described, for example, in *Remington's Pharmaceutical Sciences*, Mack Publishing Co. (A.R. Gennaro edit. 1985) hereby incorporated by reference herein. For example, preservatives, stabilizers, dyes and flavoring agents can be provided. These include sodium benzoate, sorbic acid and esters of phydroxybenzoic acid. In addition, antioxidants and suspending agents can be used.

A pharmaceutically effective dose is that dose required to prevent, inhibit the occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) of a disease state. The pharmaceutically effective dose depends on the type of disease, the composition used, the route of administration, the type of mammal being treated, the physical characteristics of the specific mammal under consideration, concurrent medication, and other factors which those skilled in the medical arts will recognize. Generally, an amount between 0.1 mg/kg and 100 mg/kg body weight/day of active ingredients is administered dependent upon potency of the negatively charged polymer.

The nucleic acid molecules of the invention and formulations thereof can be administered orally, topically, parenterally, by inhalation or spray or rectally in dosage unit formulations containing conventional non-toxic pharmaceutically acceptable carriers, adjuvants and vehicles. The term parenteral as used herein includes percutaneous, subcutaneous, intravascular (e.g., intravenous), intramuscular, or intrathecal injection or

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infusion techniques and the like. In addition, there is provided a pharmaceutical formulation comprising a nucleic acid molecule of the invention and a pharmaceutically acceptable carrier. One or more nucleic acid molecules of the invention can be present in association with one or more non-toxic pharmaceutically acceptable carriers and/or diluents and/or adjuvants, and if desired other active ingredients. The pharmaceutical compositions containing nucleic acid molecules of the invention can be in a form suitable for oral use, for example, as tablets, troches, lozenges, aqueous or oily suspensions, dispersible powders or granules, emulsion, hard or soft capsules, or syrups or elixirs.

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Compositions intended for oral use can be prepared according to any method known to the art for the manufacture of pharmaceutical compositions and such compositions can contain one or more such sweetening agents, flavoring agents, coloring agents or preservative agents in order to provide pharmaceutically elegant and palatable preparations. Tablets contain the active ingredient in admixture with non-toxic pharmaceutically acceptable excipients that are suitable for the manufacture of tablets. These excipients can be for example, inert diluents, such as calcium carbonate, sodium carbonate, lactose, calcium phosphate or sodium phosphate; granulating and disintegrating agents, for example, corn starch, or alginic acid; binding agents, for example starch, gelatin or acacia, and lubricating agents, for example magnesium stearate, stearic acid or talc. The tablets can be uncoated or they can be coated by known techniques. In some cases such coatings can be prepared by known techniques to delay disintegration and absorption in the gastrointestinal tract and thereby provide a sustained action over a longer period. For example, a time delay material such as glyceryl monosterate or glyceryl distearate can be employed.

Formulations for oral use can also be presented as hard gelatin capsules wherein the active ingredient is mixed with an inert solid diluent, for example, calcium carbonate, calcium phosphate or kaolin, or as soft gelatin capsules wherein the active ingredient is mixed with water or an oil medium, for example peanut oil, liquid paraffin or olive oil.

Aqueous suspensions contain the active materials in admixture with excipients suitable for the manufacture of aqueous suspensions. Such excipients are suspending agents, for example sodium carboxymethylcellulose, methylcellulose, hydropropyl-methylcellulose, sodium alginate, polyvinylpyrrolidone, gum tragacanth and gum acacia; dispersing or wetting agents can be a naturally-occurring phosphatide, for example, lecithin, or condensation products of an alkylene oxide with fatty acids, for example polyoxyethylene stearate, or condensation products of ethylene oxide with long chain aliphatic alcohols, for example heptadecaethyleneoxycetanol, or condensation products of ethylene oxide with partial esters

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derived from fatty acids and a hexitol such as polyoxyethylene sorbitol monooleate, or condensation products of ethylene oxide with partial esters derived from fatty acids and hexitol anhydrides, for example polyethylene sorbitan monooleate. The aqueous suspensions can also contain one or more preservatives, for example ethyl, or n-propyl p-hydroxybenzoate, one or more coloring agents, one or more flavoring agents, and one or more sweetening agents, such as sucrose or saccharin.

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Oily suspensions can be formulated by suspending the active ingredients in a vegetable oil, for example arachis oil, olive oil, sesame oil or coconut oil, or in a mineral oil such as liquid paraffin. The oily suspensions can contain a thickening agent, for example beeswax, hard paraffin or cetyl alcohol. Sweetening agents and flavoring agents can be added to provide palatable oral preparations. These compositions can be preserved by the addition of an anti-oxidant such as ascorbic acid.

Dispersible powders and granules suitable for preparation of an aqueous suspension by the addition of water provide the active ingredient in admixture with a dispersing or wetting agent, suspending agent and one or more preservatives. Suitable dispersing or wetting agents or suspending agents are exemplified by those already mentioned above. Additional excipients, for example sweetening, flavoring and coloring agents, can also be present.

Pharmaceutical compositions of the invention can also be in the form of oil-in-water emulsions. The oily phase can be a vegetable oil or a mineral oil or mixtures of these. Suitable emulsifying agents can be naturally-occurring gums, for example gum acacia or gum tragacanth, naturally-occurring phosphatides, for example soy bean, lecithin, and esters or partial esters derived from fatty acids and hexitol, anhydrides, for example sorbitan monocleate, and condensation products of the said partial esters with ethylene oxide, for example polyoxyethylene sorbitan monocleate. The emulsions can also contain sweetening and flavoring agents.

Syrups and elixirs can be formulated with sweetening agents, for example glycerol, propylene glycol, sorbitol, glucose or sucrose. Such formulations can also contain a demulcent, a preservative and flavoring and coloring agents. The pharmaceutical compositions can be in the form of a sterile injectable aqueous or oleaginous suspension. This suspension can be formulated according to the known art using those suitable dispersing or wetting agents and suspending agents that have been mentioned above. The sterile injectable preparation can also be a sterile injectable solution or suspension in a non-toxic parentally acceptable diluent or solvent, for example as a solution in 1,3-butanediol. Among the acceptable vehicles and solvents that can be employed are water, Ringer's solution and

isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose any bland fixed oil can be employed including synthetic mono-or diglycerides. In addition, fatty acids such as oleic acid find use in the preparation of injectables.

The nucleic acid molecules of the invention can also be administered in the form of suppositories, e.g., for rectal administration of the drug. These compositions can be prepared by mixing the drug with a suitable non-irritating excipient that is solid at ordinary temperatures but liquid at the rectal temperature and will therefore melt in the rectum to release the drug. Such materials include cocoa butter and polyethylene glycols.

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Nucleic acid molecules of the invention can be administered parenterally in a sterile medium. The drug, depending on the vehicle and concentration used, can either be suspended or dissolved in the vehicle. Advantageously, adjuvants such as local anesthetics, preservatives and buffering agents can be dissolved in the vehicle.

Dosage levels of the order of from about 0.1 mg to about 140 mg per kilogram of body weight per day are useful in the treatment of the above-indicated conditions (about 0.5 mg to about 7 g per patient per day). The amount of active ingredient that can be combined with the carrier materials to produce a single dosage form varies depending upon the host treated and the particular mode of administration. Dosage unit forms generally contain between from about 1 mg to about 500 mg of an active ingredient.

It is understood that the specific dose level for any particular patient depends upon a variety of factors including the activity of the specific compound employed, the age, body weight, general health, sex, diet, time of administration, route of administration, and rate of excretion, drug combination and the severity of the particular disease undergoing therapy.

For administration to non-human animals, the composition can also be added to the animal feed or drinking water. It can be convenient to formulate the animal feed and drinking water compositions so that the animal takes in a therapeutically appropriate quantity of the composition along with its diet. It can also be convenient to present the composition as a premix for addition to the feed or drinking water.

The nucleic acid molecules of the present invention can also be administered to a patient in combination with other therapeutic compounds to increase the overall therapeutic effect. The use of multiple compounds to treat an indication can increase the beneficial effects while reducing the presence of side effects.

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Alternatively, certain of the nucleic acid molecules of the instant invention can be expressed within cells from eukaryotic promoters (e.g., Izant and Weintraub, 1985, Science, 229, 345; McGarry and Lindquist, 1986, Proc. Natl. Acad. Sci., USA 83, 399; Scanlon et al., 1991, Proc. Natl. Acad. Sci. USA, 88, 10591-5; Kashani-Sabet et al., 1992, Antisense Res. Dev., 2, 3-15; Dropulic et al., 1992, J. Virol., 66, 1432-41; Weerasinghe et al., 1991, J. Virol., 65, 5531-4; Ojwang et al., 1992, Proc. Natl. Acad. Sci. USA, 89, 10802-6; Chen et al., 1992, Nucleic Acids Res., 20, 4581-9; Sarver et al., 1990 Science, 247, 1222-1225; Thompson et al., 1995, Nucleic Acids Res., 23, 2259; Good et al., 1997, Gene Therapy, 4, 45; all of these references are hereby incorporated in their totalities by reference herein). Those skilled in the art realize that any nucleic acid can be expressed in eukaryotic cells from the appropriate DNA/RNA vector. The activity of such nucleic acids can be augmented by their release from the primary transcript by a enzymatic nucleic acid (Draper et al., PCT WO 93/23569, and Sullivan et al., PCT WO 94/02595; Ohkawa et al., 1992, Nucleic Acids Symp. Ser., 27, 15-6; Taira et al., 1991, Nucleic Acids Res., 19, 5125-30; Ventura et al., 1993, Nucleic Acids Res., 21, 3249-55; Chowrira et al., 1994, J. Biol. Chem., 269, 25856; all of these references are hereby incorporated in their totalities by reference herein). Gene therapy approaches specific to the CNS are described by Blesch et al., 2000, Drug News Perspect., 13, 269-280; Peterson et al., 2000, Cent. Nerv. Syst. Dis., 485-508; Peel and Klein, 2000, J. Neurosci. Methods, 98, 95-104; Hagihara et al., 2000, Gene Ther., 7, 759-763; and Herrlinger et al., 2000, Methods Mol. Med., 35, 287-312. AAV-mediated delivery of nucleic acid to cells of the nervous system is further described by Kaplitt et al., US 6,180,613.

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In another aspect of the invention, RNA molecules of the present invention are preferably expressed from transcription units (see for example Couture et al., 1996, TIG., 12, 510) inserted into DNA or RNA vectors. The recombinant vectors are preferably DNA plasmids or viral vectors. Ribozyme expressing viral vectors can be constructed based on, but not limited to, adeno-associated virus, retrovirus, adenovirus, or alphavirus. Preferably, the recombinant vectors capable of expressing the nucleic acid molecules are delivered as described above, and persist in target cells. Alternatively, viral vectors can be used that provide for transient expression of nucleic acid molecules. Such vectors can be repeatedly administered as necessary. Once expressed, the nucleic acid molecule binds to the target mRNA. Delivery of nucleic acid molecule expressing vectors can be systemic, such as by intravenous or intra-muscular administration, by administration to target cells ex-planted from the patient followed by reintroduction into the patient, or by any other means that would allow for introduction into the desired target cell (for a review see Couture et al., 1996, TIG., 12, 510).

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In one aspect the invention features an expression vector comprising a nucleic acid sequence encoding at least one of the nucleic acid molecules of the instant invention. The nucleic acid sequence encoding the nucleic acid molecule of the instant invention is operably linked in a manner which allows expression of that nucleic acid molecule.

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In another aspect the invention features an expression vector comprising: a) a transcription initiation region (e.g., eukaryotic pol I, II or III initiation region); b) a transcription termination region (e.g., eukaryotic pol I, II or III termination region); c) a nucleic acid sequence encoding at least one of the nucleic acid catalyst of the instant invention; and wherein said sequence is operably linked to said initiation region and said termination region, in a manner which allows expression and/or delivery of said nucleic acid molecule. The vector can optionally include an open reading frame (ORF) for a protein operably linked on the 5' side or the 3'-side of the sequence encoding the nucleic acid catalyst of the invention; and/or an intron (intervening sequences).

Transcription of the nucleic acid molecule sequences are driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase III (pol III). Transcripts from pol II or pol III promoters are expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type depends on the nature of the gene regulatory sequences (enhancers, silencers, etc.) present nearby. Prokaryotic RNA polymerase promoters are also used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells (Elroy-Stein and Moss, 1990, Proc. Natl. Acad. Sci. US A, 87, 6743-7; Gao and Huang 1993, Nucleic Acids Res., 21, 2867-72; Lieber et al., 1993, Methods Enzymol., 217, 47-66; Zhou et al., 1990, Mol. Cell. Biol., 10, 4529-37). All of these references are incorporated by reference herein. Several investigators have demonstrated that nucleic acid molecules, such as ribozymes expressed from such promoters can function in mammalian cells (e.g. Kashani-Sabet et al., 1992, Antisense Res. Dev., 2, 3-15; Ojwang et al., 1992, Proc. Natl. Acad. Sci. U S A, 89, 10802-6; Chen et al., 1992, Nucleic Acids Res., 20, 4581-9; Yu et al., 1993, Proc. Natl. Acad. Sci. U S A, 90, 6340-4; L'Huillier et al., 1992, EMBO J., 11, 4411-8; Lisziewicz et al., 1993, Proc. Natl. Acad. Sci. U. S. A, 90, 8000-4; Thompson et al., 1995, Nucleic Acids Res., 23, 2259; Sullenger & Cech, 1993, Science, 262, 1566). More specifically, transcription units such as the ones derived from genes encoding U6 small nuclear (snRNA), transfer RNA (tRNA) and adenovirus VA RNA are useful in generating high concentrations of desired RNA molecules such as ribozymes in cells (Thompson et al., supra; Couture and Stinchcomb, 1996, supra; Noonberg et al., 1994, Nucleic Acid Res., 22, 2830; Noonberg et al., US Patent No. 5,624,803; Good et al., 1997, Gene Ther., 4, 45; Beigelman et al., International PCT Publication No. WO

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96/18736; all of these publications are incorporated by reference herein. The above ribozyme transcription units can be incorporated; into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or adeno-associated virus vectors), or viral RNA vectors (such as retroviral or alphavirus vectors) (for a review see Couture and Stinchcomb, 1996, supra).

In another aspect the invention features an expression vector comprising nucleic acid sequence encoding at least one of the nucleic acid molecules of the invention, in a manner which allows expression of that nucleic acid molecule. The expression vector comprises in one embodiment; a) a transcription initiation region; b) a transcription termination region; c) a nucleic acid sequence encoding at least one said nucleic acid molecule; and wherein said sequence is operably linked to said initiation region and said termination region, in a manner which allows expression and/or delivery of said nucleic acid molecule.

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In another embodiment the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an open reading frame; d) a nucleic acid sequence encoding at least one said nucleic acid molecule, wherein said sequence is operably linked to the 3'-end of said open reading frame; and wherein said sequence is operably linked to said initiation region, said open reading frame and said termination region, in a manner which allows expression and/or delivery of said nucleic acid molecule. In yet another embodiment the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an intron; d) a nucleic acid sequence encoding at least one said nucleic acid molecule; and wherein said sequence is operably linked to said initiation region, said intron and said termination region, in a manner which allows expression and/or delivery of said nucleic acid molecule.

In another embodiment, the expression vector comprises: a) a transcription initiation region; b) a transcription termination region; c) an intron; d) an open reading frame; e) a nucleic acid sequence encoding at least one said nucleic acid molecule, wherein said sequence is operably linked to the 3'-end of said open reading frame; and wherein said sequence is operably linked to said initiation region, said intron, said open reading frame and said termination region, in a manner which allows expression and/or delivery of said nucleic acid molecule.

Flt-1 (VEGFR1), KDR (VEGFR2) and/or flk-1 are attractive nucleic acid-based therapeutic targets by several criteria. The interaction between VEGF and VEGF-R is well-established. Efficacy can be tested in well-defined and predictive animal models. Finally, the disease conditions are serious and current therapies are inadequate. Whereas protein-based

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therapies are designed to affect VEGF activity, nucleic acid-based therapy based on the molecules and methods described herein provides a direct and elegant approach to directly modulate flt-1, KDR and/or flk-1 expression.

Because VEGFR1 and VEGFR2 mRNAs are highly homologous in certain regions, some nucleic acid target sites are also homologous. In this case, a single nucleic acid molecule of the invention can target both VEGFR1 and VEGFR2 mRNAs. At partially homologous sites, a single nucleic acid molecule can sometimes be designed to accommodate a site on both mRNAs by including G/U base pairing. For example, if there is a G present in a enzymatic nucleic acid target site in VEGFR1 mRNA at the same position there is an A in the VEGFR2 enzymatic nucleic acid target site, the enzymatic nucleic acid can be synthesized with a U at the complementary position and it will bind both to sites. The advantage of one enzymatic nucleic acid that targets both VEGFR1 and VEGFR2 mRNAs is clear, especially in cases where both VEGF receptors may contribute to the progression of angiogenesis in the disease state.

15 Examples

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The following are non-limiting examples showing the selection, isolation, synthesis and activity of exemplary nucleic acids of the instant invention.

The following examples demonstrate the selection and design of antisense, aptamer, dsRNA, allozyme, hammerhead, DNAzyme, NCH, Amberzyme, Zinzyme, or G-Cleaver ribozyme molecules and binding/cleavage sites within VEGF, VEGFR1 and/or VEGFR2 RNA.

## Example 1: Enzymatic nucleic acid-mediated inhibition of angiogenesis in vivo

The study described below was performed to assess the anti-angiogenic activity of hammerhead ribozymes targeted against flt-1 4229 site (SED ID NO: 5977) in the rat cornea model of VEGF induced angiogenesis (see above). These ribozymes have either active or inactive catalytic core and either bind and cleave or just bind to VEGF-R mRNA of the flt-1 subtype. The active ribozymes, that are able to bind and cleave the target RNA, have been shown to inhibit (125I-labeled) VEGF binding in cultured endothelial cells and produce a dose-dependent decrease in VEGF induced endothelial cell proliferation in these cells. The catalytically inactive forms of these ribozymes, which can only bind to the RNA but cannot catalyze RNA cleavage, failed to inhibit VEGF binding and failed to decrease VEGF induced endothelial cell proliferation. The ribozymes and VEGF were co-delivered using the filter

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disk method: Nitrocellulose filter disks (Millipore®) of 0.057 diameter were immersed in appropriate solutions and were surgically implanted in rat cornea as described by Pandey et al., supra. This delivery method has been shown to deliver rhodamine-labeled free ribozyme to scleral cells and, in all likelihood cells of the pericorneal vascular plexus. Since the active ribozymes show cell culture efficacy and can be delivered to the target site using the disk method, it is essential that these ribozymes be assessed for in vivo anti-angiogenic activity.

The stimulus for angiogenesis in this study was the treatment of the filter disk with 30 µM VEGF which is implanted within the cornea's stroma. This dose yields reproducible neovascularization stemming from the pericorneal vascular plexus growing toward the disk in a dose-response study 5 days following implant. Filter disks treated only with the vehicle for VEGF show no angiogenic response. The ribozymes were co-adminstered with VEGF on a disk in two different ribozyme concentrations. One concern with the simultaneous administration is that the ribozymes will not be able to inhibit angiogenesis since VEGF receptors can be stimulated. However, we have observed that in low VEGF doses, the neovascular response reverts to normal suggesting that the VEGF stimulus is essential for maintaining the angiogenic response. Blocking the production of VEGF receptors using simultaneous administration of anti-VEGF-R mRNA ribozymes could attenuate the normal neovascularization induced by the filter disk treated with VEGF.

#### Materials and Methods:

## 20 1. Stock hammerhead ribozyme solutions:

a. flt-1 4229 (786 µM)- Active

b. flt-1 4229 (736 µM)- Inactive

## 2. Experimental solutions/groups:

Group 1 Solution 1 Control VEGF solution: 30 µM in 82mM Tris base

25 Group 2 Solution 2 flt-1 4229 (1 μg/μL) in 30 μM VEGF/82 mM Tris base

Group 3 Solution 3 flt-1 4229 (10 µg/µL) in 30 µM VEGF/82 mM Tris base

Group 4 Solution 4 No VEGF, flt-1 4229 (10 μg/μL) in 82 mM Tris base

Group 5 Solution 5 No VEGF, No ribozyme in 82 mM Tris base

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10 eyes per group, 5 animals (Since they have similar molecular weights, the molar concentrations should be essentially similar).

Each solution (VEGF and RIBOZYMES) were prepared as a 2X solution for 1:1 mixing for final concentrations above, with the exception of solution 1 in which VEGF was 2X and diluted with ribozyme diluent (sterile water).

#### 3. VEGF Solutions

The 2X VEGF solution (60  $\mu$ M) was prepared from a stock of 0.82  $\mu$ g/ $\mu$ L in 50 mM Tris base. 200  $\mu$ L of VEGF stock was concentrated by speed vac to a final volume of 60.8  $\mu$ L, for a final concentration of 2.7  $\mu$ g/ $\mu$ L or 60  $\mu$ M. Six 10  $\mu$ L aliquots was prepared for daily mixing. 2X solutions for VEGF and Ribozyme was stored at 4°C until the day of the surgery. Solutions were mixed for each day of surgery. Original 2X solutions was prepared on the day before the first day of the surgery.

## 4. <u>Surgical Solutions:</u>

#### Anesthesia:

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stock ketamine hydrochloride 100 mg/mL

stock xylazine hydrochloride 20 mg/mL

stock acepromazine 10 mg/mL

Final anesthesia solution: 50 mg/mL ketamine, 10 mg/mL xylazine, and 0.5 mg/mL acepromazine

20 5% povidone iodine for opthalmic surgical wash

2% lidocaine (sterile) for opthalmic administration (2 drops per eye)

sterile 0.9% NaCl for opthalmic irrigation

### 5. Surgical Methods:

Standard surgical procedure as described in Pandey et al., supra. Filter disks were incubated in 1 µL of each solution for approximately 30 minutes prior to implantation.

## 6. Experimental Protocol:

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The animal comea were treated with the treatment groups as described above. Animals were allowed to recover for 5 days after treatment with daily observation (scoring 0 - 3). On the fifth day animals were euthanized and digital images of each eye was obtained for quantitation using Image Pro Plus. Quantitated neovascular surface area were analyzed by ANOVA followed by two post-hoc tests including Dunnets and Tukey-Kramer tests for significance at the 95% confidence level. Dunnets provide information on the significance between the differences within the means of treatments vs. controls while Tukey-Kramer provide information on the significance of differences within the means of each group.

The fit-1 4229 (SEQ ID NO: 5977) active hammerhead ribozyme at both concentrations was effective at inhibiting angiogenesis while the inactive ribozyme did not show any significant reduction in angiogenesis. A statistically signifiant reduction in neovascular surface area was observed only with active ribozymes. This result clearly shows that the ribozymes are capable of significantly inhibiting angiogenesis *in vivo*. Specifically, given ribozyme mechanism of action, the observed inhibition is by the binding and cleavage of target RNA by ribozymes.

## Example 2: Bioactivity of anti-angiogenesis ribozymes targeting flt-1 and kdr RNA

### MATERIALS AND METHODS

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Ribozymes: Hammerhead ribozymes and controls designed to have attenuated activity (attenuated controls) were synthesized and purified as previously described above. The attenuated ribozyme controls maintain the binding arm sequence of the parent ribozyme and thus are still capable of binding to the mRNA target. However, they have two nucleotide changes in the core sequence that substantially reduce their ability to carry out the cleavage reaction. Ribozymes were designed to target Flt-1 or KDR mRNA sites conserved in human, mouse, and rat. In general, ribozymes with binding arms of seven nucleotides were designed and tested. If, however, only six nucleotides surrounding the cleavage site were conserved in all three species, six nucleotide binding arms were used. Data are presented herein for 2'-NH2 uridine modified ribozymes in cell proliferation studies and for 2'-C-allyl uridine modified ribozymes in RNAse protection, in vitro cleavage and corneal studies.

In vitro ribozyme cleavage assays: In vitro RNA cleavage rates on a 15 nucleotide synthetic RNA substrate were measured as previously described above.

Cell culture: Human dermal microvascular endothelial cells (HMVEC-d, Clonetics Corp.) were maintained at 37°C in flasks or plates coated with 1.5% porcine skin gelatin (300

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bloom, Sigma) in Growth medium (Clonetics Corp.) supplemented with 10-20% fetal bovine serum (FBS, Hyclone). Cells were grown to confluency and used up to the seventh passage. Stimulation medium consisted of 50% Sigma 99 media and 50% RPMI 1640 with L-glutamine and additional supplementation with 10 μg/mL Insulin-Transferrin-Selenium (Gibco BRL) and 10% FBS. Cell growth was stimulated by incubation in Stimulation medium supplemented with 20 ng/mL of either VEGF<sub>165</sub> or bFGF. VEGF<sub>165</sub> (165 amino acids) was selected for cell culture and animal studies because it is the predominant form of the four native forms of VEGF generated by alternative mRNA splicing. Cell culture assays were carried out in triplicate.

## 10 Ribozyme and ribozyme/LIPOFECTAMINETM formulations:

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Cell culture: Ribozymes or attenuated controls (50-200 nM) were formulated for cell culture studies and used immediately. Formulations were carried out with LIPOFECTAMINE<sup>TM</sup> (Gibco BRL) at a 3:1 lipid to phosphate charge ratio in serum-free medium (OPTI-MEM<sup>TM</sup>, Gibco BRL) by mixing for 20 minutes at room temperature. For example, a 3:1 lipid to phosphate charge ratio was established by complexing 200 nM ribozyme with 10.8 μg/μL LIPOFECTAMINE<sup>TM</sup> (13.5 μM DOSPA).

In vivo: For corneal studies, lyophilized ribozyme or attenuated controls were resuspended in sterile water at a final stock concentration of 170  $\mu$ g/ $\mu$ L (highest dose). Lower doses (1.7-50  $\mu$ g/ $\mu$ L) were prepared by serial dilution in sterile water.

Proliferation assay: HMVEC-d were seeded (5 x 10<sup>3</sup> cells/well) in 48-well plates (Costar) and incubated 24-30 hours in Growth medium at 37°C. After removal of the Growth medium, cells were treated with 50-200 nM LIPOFECTAMINE™ complexes of ribozyme or attenuated controls for 2 hours in OPTI-MEM™. The ribozyme/control-containing medium was removed and the cells were washed extensively in 1X PBS. The medium was then replaced with Stimulation medium or Stimulation medium supplemented with 20 ng/mL VEGF<sub>165</sub> or bFGF. After 48 hours, the cell number was determined using a Coulter™ cell counter. Data are presented as cell number per well following 48 hours of VEGF stimulation.

RNAse protection assay: HMVEC-d were seeded (2 x 10<sup>5</sup> cells/well) in 6-well plates (Costar) and allowed to grow 32-36 hours in Growth medium at 37°C. Cells were treated with LPOFECTAMINE™ complexes containing 200 nM ribozyme or attenuated control for 2 h as described under "Proliferation Assay" and then incubated in Growth medium containing 20 ng/mL VEGF<sub>165</sub> for 24 hours. Cells were harvested and an RNAse protection assay was carried out using the Ambion Direct Protect kit and protocol with the exception that 50 mM

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EDTA was added to the lysis buffer to eliminate the possibility of ribozyme cleavage during sample preparation. Antisense RNA probes targeting portions of Flt-1 and KDR were prepared by transcription in the presence of [ $^{32}$ P]-UTP. Samples were analyzed on polyacrylamide gels and the level of protected RNA fragments was quantified using a Molecular Dynamics PhosphorImager. The levels of Flt-1 and KDR were normalized to the level of cyclophilin (human cyclophilin probe template, Ambion) in each sample. The coefficient of variation for cyclophilin levels was 11% [265940 cpm  $\pm$  29386 (SD)] for all conditions tested here (i.e. in the presence of either active ribozymes or attenuated controls). Thus, cyclophilin is useful as an internal standard in these studies.

## Rat corneal pocket assay of VEGF-induced angiogenesis:

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Animal guidelines and anesthesia. Animal housing and experimentation adhered to standards outlined in the 1996 Guide for the Care and Use of Laboratory Animals (National Research Council). Male Sprague Dawley rats (250-300 g) were anesthetized with ketamine (50 mg/kg), xylazine (10 mg/kg), and acepromazine (0.5 mg/kg) administered intramuscularly (im). The level of anesthesia was monitored every 2-3 min by applying hind limb paw pressure and examining for limb withdrawal. Atropine (0.4 mg/kg, im) was also administered to prevent potential corneal reflex-induced bradycardia.

Preparation of VEGF soaked disk. For corneal implantation, 0.57 mm diameter nitrocellulose disks, prepared from 0.45  $\mu$ m pore diameter nitrocellulose filter membranes (Millipore Corporation), were soaked for 30 min in 1  $\mu$ L of 30  $\mu$ M VEGF<sub>165</sub> in 82 mM TrisHCl (pH 6.9) in covered petri dishes on ice.

Corneal surgery. The rat corneal model used in this study was a modified from Koch et al. Supra and Pandey et al., supra. Briefly, corneas were irrigated with 0.5% povidone iodine solution followed by normal saline and two drops of 2% lidocaine. Under a dissecting microscope (Leica MZ-6), a stromal pocket was created and a presoaked filter disk (see above) was inserted into the pocket such that its edge was 1 mm from the corneal limbus.

Intraconjunctival injection of test solutions. Immediately after disk insertion, the tip of a 40-50 µm OD injector (constructed in our laboratory) was inserted within the conjunctival tissue 1 mm away from the edge of the corneal limbus that was directly adjacent to the VEGF-soaked filter disk. Six hundred nanoliters of test solution (ribozyme, attenuated control or sterile water vehicle) were dispensed at a rate of 1.2 µL/min using a syringe pump (Kd Scientific). The injector was then removed, scrially rinsed in 70% ethanol and sterile water and immersed in sterile water between each injection. Once the test solution was injected,

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closure of the eyelid was maintained using microaneurism clips until the animal began to recover gross motor activity. Following treatment, animals were warmed on a heating pad at 37°C.

Animal treatment groups/experimental protocol. Ribozymes targeting Flt-1 site 4229 (SEQ ID NO: 5977) and KDR mRNA site 726 (SEQ ID NO: 5978) were tested in the corneal model along with their attenuated controls. Five treatment groups were assigned to examine the effects of five doses of each test substance over a dose range of 1-100 µg on VEGF-stimulated angiogenesis. Negative (30 µM VEGF soaked filter disk and intraconjunctival injection of 600 nL sterile water) and no stimulus (Tris-soaked filter disk and intraconjunctival injection of sterile water) control groups were also included. Each group consisted of five animals (10 eyes) receiving the same treatment.

Quantitation of angiogenic response. Five days after disk implantation, animals were euthanized following im administration of 0.4 mg/kg atropine and corneas were digitally imaged. The neovascular surface area (NSA, expressed in pixels) was measured postmortem from blood-filled corneal vessels using computerized morphometry (Image Pro Plus, Media Cybernetics, v2.0). The individual mean NSA was determined in triplicate from three regions of identical size in the area of maximal neovascularization between the filter disk and the limbus. The number of pixels corresponding to the blood-filled corneal vessels in these regions was summated to produce an index of NSA. A group mean NSA was then calculated. Data from each treatment group were normalized to VEGF/ribozyme vehicle-treated control NSA and finally expressed as percent inhibition of VEGF-induced angiogenesis.

Statistics. After determining the normality of treatment group means, group mean percent inhibition of VEGF-induced angiogenesis was subjected to a one-way analysis of variance. This was followed by two post-hoc tests for significance including Dunnett's (comparison to VEGF control) and Tukey-Kramer (all other group mean comparisons) at alpha = 0.05. Statistical analyses were performed using JMP v.3.1.6 (SAS Institute).

## RESULTS

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Ribozyme-mediated reduction of VEGF-induced cell proliferation: Ribozyme cleavage of Flt-1 or KDR mRNA should result in a decrease in the density of cell surface VEGF receptors. This decrease should limit VEGF binding and consequently interfere with the mitogenic signaling induced by VEGF. To determine if cell proliferation was impacted by anti-Flt-1 and/or anti-KDR ribozyme treatment, proliferation assays using cultured human microvascular cells were carried out. Ribozymes included in the proliferation assays were

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initially chosen by their ability to decrease the level of VEGF binding to treated cells. In these initial studies, ribozymes targeting 20 sites in the coding region of each mRNA were screened. The most effective ribozymes against two sites in each target, Flt-1 sites 1358 and 4229 and KDR sites 726 and 3950, were included in the proliferation assays reported here. In addition, attenuated analogs of each ribozyme were used as controls. These attenuated controls are still capable of binding to the mRNA target since the binding arm sequence is maintained. However, these controls have two nucleotide changes in the core sequence that substantially reduce their ability to carry out the cleavage reaction.

The active ribozymes tested decreased the relative proliferation of HMVEC-d after VEGF stimulation, an effect that increased with ribozyme concentration. This concentration dependency was not observed following treatment with the attenuated controls designed for these sites. In fact, little or no change in cell growth was noted following treatment with the attenuated controls, even though these controls can still bind to the specific target sequences. At 200 nM, there was a distinct "window" between the anti-proliferative effects of each ribozyme and its attenuated control; a trend also observed at lower doses. This window of inhibition of proliferation (56-77% based on total cells/well) reflects the contribution of ribozyme-mediated activity. In comparison, no effect of anti-Flt-1 or anti-KDR ribozymes was noted on bFGF-stimulated cell proliferation. Moreover, an irrelevant, but active, ribozyme whose binding sequence is not found in either Flt-1 or KDR mRNA had no effect in this assay. These data are consistent with the basic ribozyme mechanism in which binding and cleavage are necessary components. Although the relative surface distribution of Flt-1 and KDR receptors in this cell type is not known, the antiproliferative effects of these ribozymes indicate that, at least in cell culture, both receptors are functionally coupled to proliferation.

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Specific reduction of Flt-1 or KDR mRNA by ribozyme treatment: To confirm that anti-Flt-1 and anti-KDR ribozymes reduce their respective mRNA targets, cellular levels of Flt-1 or KDR were quantified using an RNAse protection assay with specific Flt-1 or KDR probes. For each target, one ribozyme/attenuated control pair was chosen for continued study. Exposure of HMVEC-d to active ribozyme targeting Flt-1 site 4229 decreased Flt-1 mRNA, but not KDR mRNA. Likewise, treatment with the active ribozyme targeting KDR site 726 decreased KDR, but not Flt-1 mRNA. Both ribozymes decreased the level of their respective target RNA by greater than 50%. The degree of reduction associated with the corresponding attenuated controls was not greater than 13%.

In vitro activity of anti-Flt and anti-KDR ribozymes.

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To confirm further the necessity of an active ribozyme core, in vitro cleavage activities were determined for the Flt-1 site 4229 ribozyme and the KDR site 726 ribozyme as well as their paired attenuated controls. The first order rate constants calculated from the time-course of short substrate cleavage for the anti-Flt-1 ribozyme and its attenuated control were 0.081  $\pm$  0.0007 min<sup>-1</sup> and 0.001  $\pm$  6 x 10<sup>-5</sup> min<sup>-1</sup>, respectively. For the anti-KDR ribozyme and its paired control, the first order rate constants were 0.434  $\pm$  0.024 min<sup>-1</sup> and 0.002  $\pm$  1 x 10<sup>-4</sup> min<sup>-1</sup>, respectively. Although the attenuated controls retain a very slight level of cleavage activity under these optimized conditions, the decrease in *in vitro* cleavage activity between each active ribozyme and its paired attenuated control is about two orders of magnitude. Thus, an active core is essential for cleavage activity *in vitro* and is also necessary for ribozyme activity in cell culture.

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Ribozyme-mediated reduction of VEGF-induced angiogenesis in vivo. To assess whether ribozymes targeting VEGF receptor mRNA could impact the complex process of angiogenesis, prototypic anti-Flt-1 and KDR ribozymes that were identified in cell culture studies were screened in a rat corneal pocket assay of VEGF-induced angiogenesis. In this assay, comeas implanted with VEGF-containing filter disks exhibited a robust neovascular response in the corneal region between the disk and the corneal limbus (from which the new vessels emerge). Disks containing a vehicle solution elicited no angiogenic response. In separate studies, intraconjunctival injections of sterile water vehicle did not affect the magnitude of the VEGF-induced angiogenic response. In addition, ribozyme injections alone did not induce angiogenesis.

The dose-related effects of anti-Flt-1 or KDR ribozymes on the VEGF-induced angiogenic response were then examined. The antiangiogenic effect of the anti-Flt-1 (site 4229) and KDR (site 726) ribozymes and their attenuated controls over a dose range from 1 to 100  $\mu$ g, respectively was determined. For both ribozymes, the maximal antiangiogenic response (48 and 36% for anti-Flt-1 and KDR ribozymes, respectively) was observed at a dose of 10  $\mu$ g.

The anti-Flt-1 ribozyme produced a significantly greater antiangiogenic response than its attenuated control at 3 and 10  $\mu$ g (p<0.05). Its attenuated control exhibited a small but significant antiangiogenic response at doses above 10  $\mu$ g compared to vehicle treated VEGF controls (p<0.05). At its maximum, this response was not significantly greater than that observed with the lowest dose of active anti-Flt-1 ribozyme. The anti-KDR ribozyme significantly inhibited angiogenesis from 3 to 30  $\mu$ g (p<0.05). The anti-KDR attenuated control had no significant effect at any dose tested.

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## Example 3. In vivo inhibition of tumor growth and metastases by VEGF-R ribozymes.

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A. Lewis Lung Carcinoma Mouse Model: Ribozymes were chemically synthesized as described above. The sequence of ANGIOZYME™ bound to its target RNA is shown in Figure 1.

The tumors in this study were derived from a cell line (LLC-HM) which gives rise to reproducible numbers of spontaneous lung metastases when propagated in vivo. The LLC-HM line was obtained from Dr. Michael O'Reilly, Harvard University. neovascularization in Lewis lung carcinoma has been shown to be VEGF-dependent. Tumors from mice bearing LLC-HM (selected for the highly metastatic phenotype by serial propagation) were harvested 20 days post-inoculation. A tumor brei suspension was prepared from these tumors according to standard protocols. On day 0 of the study, 0.5 x 10<sup>6</sup> viable LLC-HM tumor cells were injected subcutaneously (sc) into the dorsum or flank of previously untreated mice (100 µL injectate). Tumors were allowed to grow for a period of 3 days prior to initiating continuous intravenous administration of saline or 30 mg/kg/d ANGIOZYME™ via Alzet mini-pumps. One set of animals was dosed from days 3 to 17, inclusive. Tumor length and width measurements and volumes were calculated according to the formula: Volume = 0.5(length)(width)<sup>2</sup>. At post-inoculation day 25, animals were euthanized and lungs harvested. The number of lung macrometastatic nodules was counted. It should be noted that metastatic foci were quantified 8 days after the cessation of dosing. Ribozyme solutions were prepared to deliver to another set of animals 100, 10, 3, or 1 mg/kg/day of ANGIOZYME™ via Alzet mini-pumps. A total of 10 animals per dose or saline control group were surgically implanted on the left flank with osmotic mini-pumps prefilled with the respective test solution three days following tumor inoculation. Pumps were attached to indwelling jugular vein catheters.

Figure 2 shows the antitumor effects of ANGIOZYME™. There is a statistically significant inhibition (p < 0.05) of primary LLC-HM tumor growth in tumors grown in the flank regions compared to saline control. ANGIOZYME™ significantly reduced (p < 0.05) the number of lung metastatic foci in animals inoculated either in the flank regions. Figure 3 illustrates the dose-dependent anti-metastatic effect of ANGIOZYME™ compared to saline control.

B. Mouse Colorectal Cancer Model. KM12L4a-16 is a human colorectal cancer cell line. On day 0 of the study, 0.5 x 10<sup>6</sup> KM12L4a-16 cells were implanted into the spleen of nude mice. Three days after tumor inoculation, Alzet minipumps were implanted and continuous subcutaneous delivery of either saline or 12, 36 or 100 mg/kg/ day of

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ANGIOZYME<sup>TM</sup> was initiated. On day 5, the spleens containing the primary tumors were removed. On day 18, the Alzet minipumps were replaced with fresh pumps so that delivery of saline or ANGIOZYME<sup>TM</sup> was continuous over a 28 day period from day 3 to day 32. Animals were euthanized on day 41 and the liver tumor burden was evaluated.

Following treatment with 100 mg/kg/day of ANGIOZYME<sup>TM</sup>, there was a significant reduction in the incidence and median number of liver metastasis (Figure 4). In saline-treated animals, the median number of metastases was 101. However, at the high dose of ANGIOZYME<sup>TM</sup> (100 mg/kg/day), the median number of metastases was zero.

Example 4: Effect of ANGIOZYME<sup>TM</sup> alone or in combination with chemotherapeutic agents in the mouse Lewis Lung Carcinoma Model.

## Methods

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Tumor inoculations. Male C57/BL6 mice, age 6 to 8 weeks, were inoculated subcutaneously in the flank with  $5 \times 10^5$  LLC-HM cells from brei preparations made from tumors grown in mice.

Ribozymes and controls. RPI.4610, also known as ANGIOZYME™ (SEQ ID NO: 5977), is an anti-Flt-1 ribozyme that targets site 4229 in the human Flt-1 receptor mRNA (EMBL accession no. X51602). The controls tested include RPI.13141, an attenuated version of RPI.4610 in which four nucleotides in the catalytic core are changed so that the cleavage activity is dramatically decreased. RPI.13141, however, maintains the base composition and binding arms of RPI.4610 and so is still capable of binding to the target site. The second control (RPI.13030) also has changes to the catalytic core (three) to inhibit cleavage activity, but in addition the sequence of the binding arms has been scrambled so that it can no longer bind to the target sequence. One nucleotide in the arm of RPI.13030 is also changed to maintain the same base composition as RPI.4610.

Ribozyme administrations. Ribozymes and controls were resuspended in normal saline. Administration was initiated seven days following tumor inoculation. Animals either received a daily subcutaneous injection (30 mg/kg test substance) from day 7 to day 20 or were instrumented with an Alzet osmotic minipump (12 μL/day flow rate) containing a solution of ribozyme or control. Subcutaneous infusion pumps delivered the test substances (30 mg/kg/day) from day 7 to 20 (14-day pumps, 420 mg/kg total test substance) or days 7-34 (28-day pumps, 840 mg/kg total test substance). Where indicated, chemotherapeutic agents were given in combination with ribozyme treatment. Cyclophosphamide was given by intraperitoneal administration on days 7, 9 and 11 (125 mg/kg). Gemcitabine was given by

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intraperitoneal administration on days 8, 11 and 14 (125 mg/kg). Untreated, uninstrumented animals were used as comparison. Five animals were included in each group.

#### Results

The antiangiogenic ribozyme, ANGIOZYMETM, was tested in a model of Lewis lung. carcinoma alone and in combination with two chemotherapeutic agents. Previously (see above), 30 mg/kg/day ANGIOZYME<sup>TM</sup> alone was determined to inhibit both primary tumor growth and lung metastases in a highly metastatic variant of Lewis lung (continuous 14-day iv deliveryvia Alzet minipump, manuscript in preparation).

In this study, 30 mg/kg/day ANGIOZYME™ delivered either as a daily subcutaneous bolus injection or as a continuous infusion from an Alzet minipump resulted in a delay in tumor growth. On average, tumor growth to 500 mm<sup>3</sup> was delayed by ~7 days in animals being treated with ANGIOZYME™ compared to an untreated group. Growth of tumors in animals being treated with either of two attenuated controls was delayed by only ~ 2 days.

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ANGIOZYME™ delivered by subcutaneous bolus was also tested in combination with either Gemcytabine or cyclophosphamide. Tumor growth delay increased by about 3 days in the presence of combination therapy with ANGIOZYMETM and Gemcytabine over the effects of either treatment alone. The combination of ANGIOZYME™ and cyclophosphamide did not increase tumor growth delay over that of cyclophosphamide alone, however, suboptimal doses of cyclophosphamide were not included in this study. Neither of the attenuated controls increased the effect of the chemotherapeutic agents.

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The effect of ANGIOZYME™ on metastases to the lung was also determined in the 25 presence and absence of additional chemotherapeutic treatment. Macrometastases to the lungs were counted in two animals in each treatment group on day 20. In the presence of ANGIOZYMETM, with or without a chemotherapeutic agent, the lung metastases were reduced to zero. Treatment with either Gemcytabine or cyclophosphamide alone (mean number of metastases 4.5 and 4, respectively) were not as effective as ANGIOZYME™ alone or when used in combination with ANGIOZYMETM. Neither of the attenuated controls increased the effect of the chemotherapeutic agents.

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The effect on metastases to the lung was also determined following continuous treatment with ANGIOZYMETM. At day 20, an average of ~8 macrometastases were noted in the treatment groups which had been instrumented with Alzet minipumps (either 14- or 28day pumps). This is a decrease in metastases of ~50% from the untreated group. Since

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ANGIOZYME<sup>TM</sup> delivered by a daily subcutaneous bolus resulted in zero metastases (Fig.4) in the two animals counted, it is possible that the additional burden of being instrumented with the minipump contributes to a slightly decreased response to ANGIOZYME<sup>TM</sup>.

#### Example 5: Identification of Potential Target Sites in Human VEGFR1 and/or VEGFR2 RNA

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The sequence of human VEGFR1 and/or VEGFR2 genes are screened for accessible sites using a computer-folding algorithm. Regions of the RNA that do not form secondary folding structures and contain potential enzymatic nucleic acid molecule and/or antisense binding/cleavage sites are identified. An exemplary sequence of an enzymatic nucleic acid molecule of the invention is shown in Formula I and/or Formula II (SEQ ID Nos: 5977 and 5978, respectively). Other nucleic acid molecules and targets contemplated by the invention are described in Pavco et al., US Patent Application No. 09/870,161, incorporated by reference herein in its entirety. Similarly, other nucleic acid molecules of the invention, including antisense, aptamers, dsRNA, siRNA, and/or 2,5-A chimeras, can be designed to modulate the expression of the nucleic acid targets described in Pavco et al., US Patent Application No. 09/870,161.

# Example 6: Selection of Enzymatic Nucleic Acid Cleavage Sites in Human VEGFR1 and/or VEGFR2 RNA

Enzymatic nucleic acid molecule target sites are chosen by analyzing sequences of human VEGFR1 receptor (for example Genbank Accession No. NM\_002019), and VEGFR2 receptor (for example Genbank Accession No. NM\_002253) genes and prioritizing the sites on the basis of folding. Enzymatic nucleic acid molecules are designed that can bind each target and are individually analyzed by computer folding (Christoffersen et al., 1994 J. Mol. Struc. Theochem, 311, 273; Jaeger et al., 1989, Proc. Natl. Acad. Sci. USA, 86, 7706) to assess whether the enzymatic nucleic acid molecule sequences fold into the appropriate secondary structure. Those enzymatic nucleic acid molecules with unfavorable intramolecular interactions between the binding arms and the catalytic core can be eliminated from consideration. As discussed herein, varying binding arm lengths can be chosen to optimize activity. Generally, at least 4 bases on each arm are able to bind to, or otherwise interact with, the target RNA.

30 Example 7: Chemical Synthesis and Purification of Ribozymes and Antisense for Efficient Cleavage and/or blocking of VEGFR1 and/or VEGFR2 RNA

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Enzymatic nucleic acid molecules and antisense constructs are designed to anneal to various sites in the RNA message. The binding arms of the enzymatic nucleic acid molecules are complementary to the target site sequences described above, while the antisense constructs are fully complementary to the target site sequences described above. RNAi molecules (dsRNA) likewise have one strand of RNA or a portion of RNA complementarity to the target site sequence or a portion of the target site sequence. For example, complementarity within the double-strand RNAi structure is formed from two separate individual RNA strands or from self-complementary areas of a topologically closed, individual RNA strand which can be optionally circular. The nucleic acid molecules were chemically synthesized. The method of synthesis used followed the procedure for normal RNA synthesis as described above and in Usman et al., (1987 J. Am. Chem. Soc., 109, 7845), Scaringe et al., (1990 Nucleic Acids Res., 18, 5433) and Wincott et al., supra, and made use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end, and phosphoramidites at the 3'-end. The average stepwise coupling yields were typically >98%.

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Nucleic acid molecules are also synthesized from DNA templates using bacteriophage T7 RNA polymerase (Milligan and Uhlenbeck, 1989, Methods Enzymol. 180, 51). Nucleic acid molecules of the invention are purified by gel electrophoresis using general methods or are purified by high pressure liquid chromatography (HPLC; See Wincott et al., supra; the totality of which is hereby incorporated herein by reference) and are resuspended in water. Examples of sequences of chemically synthesized enzymatic nucleic acid molecules are shown in Formula I (SEQ ID NO: 5977), Formula II (SEQ ID NO: 5978) and in Pavco et al., US Patent Application No. 09/870,161.

# Example 8: Enzymatic Nucleic Acid Molecule Cleavage of VEGFR1 and/or VEGFR2 RNA Target in vitro

Enzymatic nucleic acid molecules targeted to the human VEGFR1 and/or VEGFR2 RNA are designed and synthesized as described above. These enzymatic nucleic acid molecules can be tested for cleavage activity in vitro, for example, using the following procedure. The target sequences and the nucleotide location within the VEGFR1 and/or VEGFR2 RNA are described in Pavco et al., US Patent Application No. 09/870,161.

Cleavage Reactions: Full-length or partially full-length, internally-labeled target RNA for enzymatic nucleic acid molecule cleavage assay is prepared by in vitro transcription in the presence of [a-32p] CTP, passed over a G 50 Sephadex column by spin chromatography and used as substrate RNA without further purification. Alternately, substrates are 5'-32p-end

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labeled using T4 polynucleotide kinase enzyme. Assays are performed by pre-warming a 2X concentration of purified enzymatic nucleic acid molecule in enzymatic nucleic acid molecule cleavage buffer (50 mM Tris-HCl, pH 7.5 at 37°C, 10 mM MgCl<sub>2</sub>) and the cleavage reaction was initiated by adding the 2X enzymatic nucleic acid molecule mix to an equal volume of substrate RNA (maximum of 1-5 nM) that was also pre-warmed in cleavage buffer. As an initial screen, assays are carried out for 1 hour at 37°C using a final concentration of either 40 nM or 1 mM enzymatic nucleic acid molecule, *i.e.*, enzymatic nucleic acid molecule excess. The reaction is quenched by the addition of an equal volume of 95% formamide, 20 mM EDTA, 0.05% bromophenol blue and 0.05% xylene cyanol after which the sample is heated to 95°C for 2 minutes, quick chilled and loaded onto a denaturing polyacrylamide gel. Substrate RNA and the specific RNA cleavage products generated by enzymatic nucleic acid molecule cleavage are visualized on an autoradiograph of the gel. The percentage of cleavage is determined by Phosphor Imager<sup>®</sup> quantitation of bands representing the intact substrate and the cleavage products.

# 15 Example 9: Phase I/II Study of Repetitive Dosing of ANGIOZYME™ Targeting the VEGFR1 (FLT-1) Receptor of VEGF

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A ribozyme therapeutic agent ANGIOZYME™ (SEQ ID NO: 5977), was assessed by daily subcutaneous administration in a phase I/II trial for 31 patients with refractory solid tumors. Demographic information relating to patients enrolled in the study are shown in Table III. The primary study endpoint was to determine the safety and maximum tolerated dose of ANGIOZYME™. Secondary endpoints assessed ANGIOZYME™ pharmacokinetics and clinical response. Patients were treated at the following doses: 3 patients received doses of 10 mg/m<sup>2</sup>/day, 4 patients received 30 mg/m<sup>2</sup>/day, 20 patients received 100 mg/m<sup>2</sup>/day, and 4 patients received 300 mg/m<sup>2</sup>/day. All but one patient were dosed for a minimum of 29 consecutive days with 24-hour pharmacokinetic analyses on Day 1 and 29. Clinical response from was assessed monthly. Results The data 20 patients ANGIOZYME™ was well tolerated, with no systemic adverse events. Figure 5 shows the plasma concentration profile of ANGIOZYMETM after a single subcutaneous dose of 10, 30, 100, or 300 mg/m<sup>2</sup>. The pharmacokinetic parameters of ANGIOZYME<sup>™</sup> after subcutaneous bolus administration are outlined in Table IV. An MTD (maximum tolerated dose) could not be established. One patient in the 300 mg/m<sup>2</sup>/d group experienced a grade 3 injection site reaction. Patients in the other groups experienced intermittent grade 1 and grade 2 injection site reactions with erythema and induration. No systemic or laboratory toxicities were observed. Pharmacokinetic analyses demonstrated dose-dependent plasma concentrations with good bioavailability (70-90%), t1/2 = 209-384 min, and no accumulation after repeated

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doses. To date, 17/28 (61%) of evaluable patients have had stable disease for periods of one to six months and two patients (nasopharyngeal squamous cell carcinoma and melanoma) had minor clinical responses. The patient with nasopharyngeal carcinoma demonstrated central tumor necrosis as indicated by MRI. The longest period of treatment thus far has been 8 months for two patients at 100 mg/m<sup>2</sup>/d (breast, peritoneal mesothelioma).

# Example 10: Down-regulation of VEGFR1 gene expression to treat gynecologic neovascularization dependent conditions

One patient in the Phase I/II trial described in Example 19 was menstruating prior to enrollment in the ANGIOZYME™ monotherapy trial. After 1-2 months on trial, the patient's menstrual cycles ceased. The patient remained on trial for approximately 11 months and did not menstruate. The patient then went off the trial for about 4 months and the menstrual cycles resumed. Re-enrollment in the ANGIOZYMETM trial resulted in the patient's menstrual cycle stopping again. This clinical observation suggests that ANGIOZYMETM is interfering with the patient's menstrual cycle, perhaps by inhibiting neovascularization of uterine tissue. This data also suggests that ANGIOZYMETM has a direct effect on the endometrial tissue or an effect on LH/FSH stimulation. These results suggest the treatment or control, using ANGIOZYME™ (SEQ ID NO: 5977) and/or other nucleic acid molecules of the instant invention, of various clinical targets and/or processes associated with female reproduction and gynecologic neovascularization, such as endometriosis, birth control, gynecologic bleeding disorders, irregular menstrual cycles, ovulation, premenstrual syndrome (PMS), menopausal dysfunction, endometrial carcinoma or other condition associated with the expression of VEGFR1 and/or VEGFR2 VEGF receptors.

### Example 11: Down-regulation of VEGFR1 in clinical setting

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Twenty-seven of the patients enrolled in the Phase I/II trial described in Example 19 had day 1 (baseline) and day 43 (six-week) serum samples assayed for VEGFR1 biomarker. VEGFR1 levels were statistically different after six weeks of ANGIOZYME treatment (Figure 9). Although statistical testing involving all 27 patients showed statistical support for effects, not all patients presented with elevated levels of VEGF-R1. Since the effects of ANGIOZYME on VEGF-R1 may only be demonstrated when sufficient levels are present at baseline, a cutoff of 100 pg/mL was chosen and changes in this VEGF-R1 were re-analyzed. Ten of the 27 patients presented with baseline VEGF-R1 levels in excess of 100 pg/mL. For this subgroup VEGF-R1 levels were lower by 3-fold, p<.001. After six weeks of treatment the average (geometric mean) of VEGF-R1 decreased for this subgroup from 419 pg/ml to

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132pg/ml, p<.001. These results show that treatment with ANGIOZYME results in a statistically significant reduction in VEGFR1 expression.

Example 22: In vivo inhibition of neovascularization in an ocular animal model by VEGF-R ribozymes.

Summary of the Mouse Model: A mouse model of proliferative retinopathy (Aiello et al., 1995, Proc. Natl. Acad. Sci. USA 92: 10457-10461; Robinson et al., 1996, Proc. Natl. Acad. Sci. USA 93: 4851-4856; Pierce et al., 1996, Archives of Ophthalmology 114: 1219-1228) in which neovascularization of the mouse retina is induced by exposure of 7-day old mice to 75% oxygen followed by a return to normal room air. The initial period in high oxygen causes an obliteration of developing blood vessels in the retina. Exposure to room air five days later is perceived as hypoxia by the now underperfused retina. The result is an immediate upregulation of VEGF mRNA and VEGF protein (between 6-12 hours) followed by an extensive retinal neovascularization that peaks in ~5 days. Although this model is more representative of retinopathy of prematurity than diabetic retinopathy, it is an accepted small animal model in which to study neovascular pathophysiology of the retina. In fact, intravitreal injection of certain antisense DNA constructs targeting VEGF mRNA have been found to be antiangiogenic in this model, as were soluble VEGF receptor chimeric proteins designed to bind VEGF in the vitreous humor (Aiello et al., 1995, Proc. Natl. Acad. Sci. USA 92: 10457-10461; Robinson et al., 1996, Proc. Natl. Acad. Sci. USA 93: 4851-4856; Pierce et al., 1996, Archives of Ophthalmology 114: 1219-1228).

Summary of experiment: The effect of an anti-KDR/Flk-1 ribozyme on the peak level of neovascularization was tested in the mouse model described above. As shown in Figure 10, P7 mice were removed from the hyperoxic chamber and the mice received two intraocular injections (P12 and P13) in the right eye of 10 µg RPI.4731, the anti- KDR/Flk-1 ribozyme. The left eye of each mouse was treated as a control and received intraocular injections of saline. Five days after being exposed to room air, neovascular nuclei in the retina of both eyes were counted. Data are presented in Figure 11. There was a significant decrease in retinal neovascularization (~40%) compared to the control, saline-injected eyes.

RPL4731 sequence and chemical composition: 5'-u<sub>s</sub>a<sub>s</sub>c<sub>s</sub> a<sub>s</sub>au ucU GAu Gag gcg aaa gcc Gaa Aag aca aB-3' (SEQ ID NO: 5978)

where:

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uppercase G, A = ribonucleotides 10wercase = 2'-OMe U = 2'-C-allyl uridine

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B = inverted abasic nucleotide S = phosphorothioate internucleotide linkage

#### **Indications**

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1) Tumor angiogenesis: Angiogenesis has been shown to be necessary for tumors to grow into pathological size (Folkman, 1971, PNAS 76, 5217-5221; Wellstein & Czubayko, 1996, Breast Cancer Res and Treatment 38, 109-119). In addition, it allows tumor cells to travel through the circulatory system during metastasis. Increased levels of gene expression of a number of angiogenic factors such as vascular endothelial growth factor (VEGF) have been reported in vascularized and edema-associated brain tumors (Berkman et al., 1993 J. Clini. Invest. 91, 153). A more direct demostration of the role of VEGF in tumor angiogenesis was demonstrated by Jim Kim et al., 1993 Nature 362,841 wherein, monoclonal antibodies against VEGF were successfully used to inhibit the growth of rhabdomyosarcoma, glioblastoma multiforme cells in nude mice. Similarly, expression of a dominant negative mutated form of the flt-1 VEGF receptor inhibits vascularization induced by human glioblastoma cells in nude mice (Millauer et al., 1994, Nature 367, 576). Specific tumor/cancer types that can be targeted using the nucleic acid molecules of the invention include but are not limited to the tumor/cancer types described under Diagnosis in Table III.

- 2) Ocular diseases: Neovascularization has been shown to cause or exacerbate ocular diseases including but not limited to, macular degeneration, neovascular glaucoma, diabetic retinopathy, myopic degeneration, and trachoma (Norrby, 1997, APMIS 105, 417-437). Aiello et al., 1994 New Engl. J. Med. 331, 1480, showed that the ocular fluid, of a majority of patients suffering from diabetic retinopathy and other retinal disorders, contains a high concentration of VEGF. Miller et al., 1994 Am. J. Pathol. 145, 574, reported elevated levels of VEGF mRNA in patients suffering from retinal ischemia. These observations support a direct role for VEGF in ocular diseases. Other factors including those that stimulate VEGF synthesis may also contribute to these indications.
- 3) <u>Dermatological Disorders:</u> Many indications have been identified which may by angiogenesis dependent including but not limited to psoriasis, verruca vulgaris, angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber syndrome, Kippel-Trenaunay-Weber syndrome, and Osler-Weber-Rendu syndrome (Norrby, *supra*). Intradermal injection of the angiogenic factor b-FGF demonstrated angiogenesis in nude mice (Weckbecker et al., 1992, *Angiogenesis: Key principles-Science-Technology-Medicine*, ed R. Steiner) Detmar et al., 1994 J. Exp. Med. 180, 1141 reported that VEGF and its receptors were over-expressed in

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psoriatic skin and psoriatic dermal microvessels, suggesting that VEGF plays a significant role in psoriasis.

4) Rheumatoid arthritis: Immunohistochemistry and in situ hybridization studies on tissues from the joints of patients suffering from rheumatoid arthritis show an increased level of VEGF and its receptors (Fava et al., 1994 J. Exp. Med. 180, 341). Additionally, Koch et al., 1994 J. Immunol. 152, 4149, found that VEGF-specific antibodies were able to significantly reduce the mitogenic activity of synovial tissues from patients suffering from rheumatoid arthritis. These observations support a direct role for VEGF in rheumatoid arthritis. Other angiogenic factors including those of the present invention may also be involved in arthritis.

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5) Endometriosis: Various studies indicate that VEGF is directly implicated in endometriosis. In one study, VEGF concentrations measured by ELISA in peritoneal fluid were found to be significantly higher in women with endometriosis than in women without endometriosis (24.1 ± 15 ng/ml vs 13.3 ± 7.2 ng/ml in normals). In patients with endometriosis, higher concentrations of VEGF were detected in the proliferative phase of the menstrual cycle (33 ± 13 ng/ml) compared to the secretory phase (10.7 ± 5 ng/ml). The cyclic variation was not noted in fluid from normal patients (McLaren et al., 1996, Human Reprod. 11, 220-223). In another study, women with moderate to severe endometriosis had significantly higher concentrations of peritoneal fluid VEGF than women without endometriosis. There was a positive correlation between the severity of endometriosis and the concentration of VEGF in peritoneal fluid. In human endometrial biopsies, VEGF expression increased relative to the early proliferative phase approximately 1.6-, 2-, and 3.6-fold in midproliferative, late proliferative, and secretory endometrium (Shifren et al., 1996, J. Clin. Endocrinol. Metab. 81, 3112-3118).

In a third study, VEGF-positive staining of human ectopic endometrium was shown to be localized to macrophages (double immunofluorescent staining with CD14 marker). Peritoneal fluid macrophages demonstrated VEGF staining in women with and without endometriosis. However, increased activation of macrophages (acid phosphatatse activity) was demonstrated in fluid from women with endometriosis compared with controls. Peritoneal fluid macrophage conditioned media from patients with endometriosis resulted in significantly increased cell proliferation ([<sup>3</sup>H] thymidine incorporation) in HUVEC cells compared to controls. The percentage of peritoneal fluid macrophages with VEGFR2 mRNA was higher during the secretory phase, and significantly higher in fluid from women with endometriosis (80 ± 15%) compared with controls (32 ± 20%). Flt-mRNA was detected in

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peritoneal fluid macrophages from women with and without endometriosis, but there was no difference between the groups or any evidence of cyclic dependence (McLaren et al., 1996, J. Clin. Invest. 98, 482-489).

In the early proliferative phase of the menstrual cycle, VEGF has been found to be expressed in secretory columnar epithelium (estrogen-responsive) lining both the oviducts and the uterus in female mice. During the secretory phase, VEGF expression was shown to have shifted to the underlying stroma composing the functional endometrium. In addition to examining the endometrium, neovascularization of ovarian follicles and the corpus luteum, as well as angiogenesis in embryonic implantation sites have been analyzed. For these processes, VEGF was expressed in spatial and temporal proximity to forming vasculature (Shweiki et al., 1993, J. Clin. Invest. 91, 2235-2243).

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The present body of knowledge in VEGFR1 and/or VEGFR2 research indicates the need for methods to assay VEGFR1 and/or VEGFR2 activity and for compounds that can regulate VEGFR1 and/or VEGFR2 expression for research, diagnostic, and therapeutic use. As described herein, the nucleic acid molecules of the present invention can be used in assays to diagnose disease state related of VEGF, VEGFR1 and/or VEGFR2 levels. In addition, the nucleic acid molecules can be used to treat disease state related to VEGF and/or VEGFR, such as VEGFR1 and/or VEGFR2 levels.

Particular processes, diseases, or conditions that can be associated with VEGFR1 and/or VEGFR2 levels include, but are not limited to, gynecologic neovascularization, such as endometriosis, endometrial carcinoma, gynecologic bleeding disorders, irregular menstrual cycles, ovulation, premenstrual syndrome (PMS), menopausal dysfunction, other diseases and conditions discussed herein, and other diseases or conditions that are related to or respond to the levels of VEGF and/or VEGFr, such as VEGFR1 and/or VEGFR2, in a cell or tissue, alone or in combination with other therapies

The use of GnRH (gonadotropin releasing hormone) agonists, Lupron Depot (Leuprolide Acetate), Synarel (naferalin acetate), Zolodex (goserelin acetate), Suprefact (buserelin acetate), Danazol, or oral contraceptives including, but not limited to, Depo-Provera or Provera (medroxyprogesterone acetate), or any other estrogen/progesterone contraceptive, are all non-limiting examples of compounds and methods that can be combined with or used in conjunction with the nucleic acid molecules of the instant invention. Various chemotherapies can be readily combined with nucleic acid molecules of the invention for the treatment of endometrial carcinoma. Common chemotherapies that can be combined with nucleic acid molecules of the instant invention include various combinations of cytotoxic drugs to kill the

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cancer cells. These drugs include but are not limited to paclitaxel (Taxol), docetaxel, cisplatin, methotrexate, cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate, gemcitabine, vinorelbine etc. Those skilled in the art will recognize that other drug compounds and therapies can be readily combined with the nucleic acid molecules of the instant invention and are hence within the scope of the instant invention.

### **Animal Models**

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There are several animal models in which the anti-angiogenesis effect of nucleic acids of the present invention, such as ribozymes, directed against VEGF-R mRNAs can be tested. Typically, a corneal model has been used to study angiogenesis in rat and rabbit since recruitment of vessels can easily be followed in this normally avascular tissue (Pandey et al., 1995 Science 268: 567-569). In these models, a small Teflon or Hydron disk pretreated with an angiogenesis factor (e.g. bFGF or VEGF) is inserted into a pocket surgically created in the cornea. Angiogenesis is monitored 3 to 5 days later. Ribozymes directed against VEGF-R mRNAs would be delivered in the disk as well, or dropwise to the eye over the time course of the experiment. In another eye model, hypoxia has been shown to cause both increased expression of VEGF and neovascularization in the retina (Pierce et al., 1995 Proc. Natl. Acad. Sci. USA. 92: 905-909; Shweiki et al., 1992 J. Clin. Invest. 91: 2235-2243).

In human glioblastomas, it has been shown that VEGF is at least partially responsible for tumor angiogenesis (Plate et al., 1992 Nature 359, 845). Animal models have been developed in which glioblastoma cells are implanted subcutaneously into nude mice and the progress of tumor growth and angiogenesism is studied (Kim et al., 1993 supra, Millauer et al., 1994 supra).

Another animal model that addresses neovascularization involves Matrigel, an extract of basement membrane that becomes a solid gel when injected subcutaneously (Passaniti et al., 1992 Lab. Invest. 67: 519-528). When the Matrigel is supplemented with angiogenesis factors such as VEGF, vessels grow into the Matrigel over a period of 3 to 5 days and angiogenesis can be assessed. Ribozymes directed against VEGF-R mRNAs can be delivered in the Matrigel to assess anti-angiogesis effect.

Several animal models exist for screening of anti-angiogenic agents. These include corneal vessel formation following comeal injury (Burger et al., 1985 Cornea 4: 35-41; Lepri, et al., 1994 J. Ocular Pharmacol. 10: 273-280; Ormerod et al., 1990 Am. J. Pathol. 137: 1243-1252) or intracorneal growth factor implant (Grant et al., 1993 Diabetologia 36: 282-291; Pandey et al. 1995 supra; Zieche et al., 1992 Lab. Invest. 67: 711-715), vessel

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growth into Matrigel matrix containing growth factors (Passaniti et al., 1992 supra), female reproductive organ neovascularization following hormonal manipulation (Shweiki et al., 1993 Clin. Invest. 91: 2235-2243), several models involving inhibition of tumor growth in highly vascularized solid tumors (O'Reilly et al., 1994 Cell 79: 315-328; Senger et al., 1993 Cancer and Metas. Rev. 12: 303-324; Takahasi et al., 1994 Cancer Res. 54: 4233-4237; Kim et al., 1993 supra), and transient hypoxia-induced neovascularization in the mouse retina (Pierce et al., 1995 Proc. Natl. Acad. Sci. USA. 92: 905-909).

The cornea model, described in Pandey et al. supra, is the most common and well characterized anti-angiogenic agent efficacy screening model. This model involves an avascular tissue into which vessels are recruited by a stimulating agent (growth factor, thermal or alkalai burn, endotoxin). The corneal model utilizes the intrastromal corneal implantation of a Teflon pellet soaked in a VEGF-Hydron solution to recruit blood vessels toward the pellet which can be quantitated using standard microscopic and image analysis techniques. To evaluate their anti-angiogenic efficacy, ribozymes are applied topically to the eye or bound within Hydron on the Teflon pellet itself. This avascular cornea as well as the Matrigel (see below) provide for low background assays. While the corneal model has been performed extensively in the rabbit, studies in the rat have also been conducted.

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The mouse model (Passaniti et al., supra) is a non-tissue model which utilizes Matrigel, an extract of basement membrane (Kleinman et al., 1986) or Millipore<sup>®</sup> filter disk, which can be impregnated with growth factors and anti-angiogenic agents in a liquid form prior to injection. Upon subcutaneous administration at body temperature, the Matrigel or Millipore<sup>®</sup> filter disk forms a solid implant. VEGF embedded in the Matrigel or Millipore<sup>®</sup> filter disk would be used to recruit vessels within the matrix of the Matrigel or Millipore<sup>®</sup> filter disk which can be processed histologically for endothelial cell specific vWF (factor VIII antigen) immunohistochemistry, Trichrome-Masson stain, or hemoglobin content. Like the cornea, the Matrigel or Millipore<sup>®</sup> filter disk are avascular; however, it is not tissue. In the Matrigel or Millipore<sup>®</sup> filter disk model, ribozymes are administered within the matrix of the Matrigel or Millipore<sup>®</sup> filter disk to test their anti-angiogenic efficacy. Thus, delivery issues in this model, as with delivery of ribozymes by Hydron- coated Teflon pellets in the rat cornea model, are minimized due to the homogeneous presence of the ribozyme within the respective matrix.

These models offer a distinct advantage over several other angiogenic models listed previously. The ability to use VEGF as a pro-angiogenic stimulus in both models is highly desirable since ribozymes target only VEGFr mRNA. In other words, the involvement of

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other non-specific types of stimuli in the cornea and Matrigel models is not advantageous from the standpoint of understanding the pharmacologic mechanism by which the anti-VEGFr mRNA ribozymes produce their effects. In addition, the models allow for testing the specificity of the anti-VEGFr mRNA ribozymes by using either aFGF or bFGF as a proangiogenic factor. Vessel recruitment using FGF should not be affected in either model by anti-VEGFr mRNA ribozymes. Other models of angiogenesis, including vessel formation in the female reproductive system using hormonal manipulation (Shweiki et al., 1993 supra); a variety of vascular solid tumor models which involve indirect correlations with angiogenesis (O'Reilly et al., 1994 supra; Senger et al., 1993 supra; Takahasi et al., 1994 supra; Kim et al., 1993 supra); and retinal neovascularization following transient hypoxia (Pierce et al., 1995 supra), were not selected for efficacy screening due to their non-specific nature, although they can be useful models due to a demonstrated correlation between VEGF and angiogenesis.

Other model systems to study tumor angiogenesis is reviewed by Folkman, 1985 Adv. 15 Cancer. Res., 43, 175.

### Use of murine models

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For a typical systemic study involving 10 mice (20 g each) per dose group, 5 doses (1, 3, 10, 30 and 100 mg/kg daily over 14 days continuous administration), approximately 400 mg of ribozyme, formulated in saline would be used. A similar study in young adult rats (200 g) would require over 4 g. Parallel pharmacokinetic studies involve the use of similar quantities of ribozymes further justifying the use of murine models.

Ribozymes and Lewis lung carcinoma and B-16 melanoma murine models

Identifying a common animal model for systemic efficacy testing of ribozymes is an efficient way of screening ribozymes for systemic efficacy.

The Lewis lung carcinoma and B-16 murine melanoma models are well accepted models of primary and metastatic cancer and are used for initial screening of anti-cancer agents. These murine models are not dependent upon the use of immunodeficient mice, are relatively inexpensive, and minimize housing concerns. Both the Lewis lung and B-16 melanoma models involve subcutaneous implantation of approximately 106 tumor cells from metastatically aggressive tumor cell lines (Lewis lung lines 3LL or D122, LLc-LN7; B-16-BL6 melanoma) in C57BL/6J mice. Alternatively, the Lewis lung model can be produced by the surgical implantation of tumor spheres (approximately 0.8 mm in diameter). Metastasis

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also can be modeled by injecting the tumor cells directly intraveneously. In the Lewis lung model, microscopic metastases can be observed approximately 14 days following implantation with quantifiable macroscopic metastatic tumors developing within 21-25 days. The B-16 melanoma exhibits a similar time course with tumor neovascularization beginning 4 days following implantation. Since both primary and metastatic tumors exist in these models after 21-25 days in the same animal, multiple measurements can be taken as indices of efficacy. Primary tumor volume and growth latency as well as the number of micro- and macroscopic metastatic lung foci or number of animals exhibiting metastases can be quantitated. The percent increase in lifespan can also be measured. Thus, these models provide suitable primary efficacy assays for screening systemically administered ribozymes/ribozyme formulations.

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In the Lewis lung and B-16 melanoma models, systemic pharmacotherapy with a wide variety of agents usually begins 1-7 days following tumor implantation/inoculation with either continuous or multiple administration regimens. Concurrent pharmacokinetic studies can be performed to determine whether sufficient tissue levels of ribozymes can be achieved for pharmacodynamic effect to be expected. Furthermore, primary tumors and secondary lung metastases can be removed and subjected to a variety of *in vitro* studies (*i.e.* target RNA reduction).

Flt-1, KDR and/or flk-1 protein levels can be measured clinically or experimentally by FACS analysis. Flt-1, KDR and/or flk-1 encoded mRNA levels can be assessed by Northern analysis, RNase-protection, primer extension analysis and/or quantitative RT-PCR. Ribozymes that block flt-1, KDR and/or flk-1 protein encoding mRNAs and therefore result in decreased levels of flt-1, KDR and/or flk-1 activity by more than 20% in vitro can be identified.

Ribozymes and/or genes encoding them are delivered by either free delivery, liposome delivery, cationic lipid delivery, adeno-associated virus vector delivery, adenovirus vector delivery, retrovirus vector delivery or plasmid vector delivery in these animal model experiments (see above).

Subjects can be treated by locally administering nucleic acids targeted against VEGF-R by direct injection. Routes of administration include, but are not limited to, intravascular, intramuscular, subcutaneous, intraarticular, aerosol inhalation, oral (tablet, capsule or pill form), topical, systemic, ocular, intraperitoneal and/or intrathecal delivery.

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Surgically induced models of endometriosis have been developed in rats, mice, and rabbits. Non-human primates demonstrate spontaneous endometriosis, but surgical induction can also be used. In addition to the surgical technique, cycle monitoring can be performed by daily vaginal cytology in primates. For all of the surgically induced models of endometriosis, the following general procedure is used. An initial laparotomy is performed to implant tissue from a donor animal. A portion of one uterine horn (or one complete horn in the case of mice) is removed. The endometrium of this piece of uterus is separated from the myometrium and cut into small segments (4-10 mm2). Segments (approximately 3) are sutured to various locations within the abdominal cavity (peritoneum, intestinal mesentery vessels, uterus, broad ligament). Cummings and Metcalf (1996) attached whole segments of mouse uterus without separating the endometrium from the myometrium. Implants are allowed to grow for 3-6 A second laparotomy is sometimes performed to verify development of endometriosis-like foci (vascularization and cysts filled with clear fluid). This second laparotomy was done in the studies by Ouereda et al., (1996) and Stoeckemann et al., (1995). After 3-6 weeks post-surgery and/or following visualization of endometriosis, drug treatment is initiated and continued for a prescribed period of time. At the termination of these studies, animals are euthanized. Endpoints include, but are not limited to, changes in the surface area of the implants and tissue mass of the ectopic endometrial implants (see for example Brogniez et al., 1995, Human Reprod. 10, 927-931; Cummings et al., 1996, Tox. Appl. Pharm. 138, 131-139; Cummings and Metcalf, 1996, Proc. Soc. Exp. Biol. Med. 212, 332-337; D'Hooghe et al., 1996, Fertility and Sterility. 66, 809-813; Quereda et al., 1996, Eur. J. Obstet. Gynecol. Rep. Biol. 67, 35-40; and Stoeckemann et al., 1995, Human Reprod. 10, 3264-3271).

#### Combination therapies

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Gemcytabine and cyclophosphamide are non-limiting examples of chemotherapeutic agents that can be combined with or used in conjunction with the nucleic acid molecules (e.g. ribozymes and antisense molecules) of the instant invention. Those skilled in the art will recognize that other anti-angiogenic and/or anti-cancer compounds and therapies can be similarly be readily combined with the nucleic acid molecules of the instant invention (e.g. 30 ribozymes and antisense molecules) and are hence within the scope of the instant invention. Such compounds and therapies are well known in the art (see for example Cancer: Principles

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and Pranctice of Oncology, Volumes 1 and 2, eds Devita, V.T., Hellman, S., and Rosenberg, S.A., J.B. Lippincott Company, Philadelphia, USA; incorporated herein by reference) and include, without limitations, folates, antifolates, pyrimidine analogs, fluoropyrimidines, purine analogs, adenosine analogs, topoisomerase I inhibitors, anthrapyrazoles, retinoids, antibiotics, anthacyclins, platinum analogs, alkylating agents, nitrosoureas, plant derived compounds such as vinca alkaloids, epipodophyllotoxins, tyrosine kinase inhibitors, taxols, radiation therapy, surgery, nutritional supplements, gene therapy, radiotherapy, for example 3D-CRT, immunotoxin therapy, for example ricin, and monoclonal antibodies. Specific examples of chemotherapeutic compounds than can be combined with or used in conjuction with the nucleic acid molecules of the invention include but are not limited to Paclitaxel; Docetaxel; Methotrexate; Doxorubin; Edatrexate; Vinorelbine; Tomaxifen; Leucovorin; 5fluoro uridine (5-FU); Irinotecan (CAMPTOSAR® or CPT-11 or Camptothecin-11 or Campto); Cisplatin; Carboplatin; Amsacrine; Cytarabine; Bleomycin; Mitomycin C; Dactinomycin; Mithramycin; Hexamethylmelamine; Dacarbazine; L-asperginase; Nitrogen mustard; Melphalan, Chlorambucil; Busulfan; Ifosfamide; 4-hydroperoxycyclophosphamide, Thiotepa; Tamoxifen, Herceptin; IMC C225; ABX-EGF: and combinations thereof.

### Diagnostic uses

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The nucleic acid molecules of this invention (e.g., enzymatic nucleic acid molecules) can be used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of VEGF and/or VEGFr, such as VEGFR1 and/or VEGFR2 RNA in a cell. The close relationship between enzymatic nucleic acid molecule activity and the structure of the target RNA allows the detection of mutations in any region of the molecule which alters the base-pairing and three-dimensional structure of the target RNA. By using multiple enzymatic nucleic acid molecules described in this invention, one can map nucleotide changes which are important to RNA structure and function in vitro, as well as in cells and tissues. Cleavage of target RNAs with enzymatic nucleic acid molecules can be used to inhibit gene expression and define the role (essentially) of specified gene products in the progression of disease. In this manner, other genetic targets can be defined as important mediators of the disease. These experiments can lead to better treatment of the disease progression by affording the possibility of combinational therapies (e.g., multiple enzymatic nucleic acid molecules targeted to different genes, enzymatic nucleic acid molecules coupled with known small molecule inhibitors, or intermittent treatment with combinations of enzymatic nucleic acid molecules and/or other chemical or biological molecules). Other in

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vitro uses of enzymatic nucleic acid molecules of this invention are well known in the art, and include detection of the presence of mRNAs associated with VEGF, VEGFR1 and/or VEGFR2-related condition. Such RNA is detected by determining the presence of a cleavage product after treatment with an enzymatic nucleic acid molecule using standard methodology.

In a specific example, enzymatic nucleic acid molecules which cleave only wild-type or mutant forms of the target RNA are used for the assay. The first enzymatic nucleic acid molecule is used to identify wild-type RNA present in the sample and the second enzymatic nucleic acid molecule is used to identify mutant RNA in the sample. As reaction controls, synthetic substrates of both wild-type and mutant RNA are cleaved by both enzymatic nucleic acid molecules to demonstrate the relative enzymatic nucleic acid molecule efficiencies in the reactions and the absence of cleavage of the "non-targeted" RNA species. The cleavage products from the synthetic substrates also serve to generate size markers for the analysis of wild-type and mutant RNAs in the sample population. Thus each analysis requires two enzymatic nucleic acid molecules, two substrates and one unknown sample which is combined into six reactions. The presence of cleavage products is determined using an RNAse protection assay so that full-length and cleavage fragments of each RNA can be analyzed in one lane of a polyacrylamide gel. It is not absolutely required to quantify the results to gain insight into the expression of mutant RNAs and putative risk of the desired phenotypic changes in target cells. The expression of mRNA whose protein product is implicated in the development of the phenotype (i.e., VEGFR1 and/or VEGFR2) is adequate to establish risk. If probes of comparable specific activity are used for both transcripts, then a qualitative comparison of RNA levels will be adequate and will decrease the cost of the initial diagnosis. Higher mutant form to wild-type ratios are correlated with higher risk whether RNA levels are compared qualitatively or quantitatively. The use of enzymatic nucleic acid molecules in diagnostic applications contemplated by the instant invention is described, for example, in Usman et al., US Patent Application No. 09/877,526, George et al., US Patent Nos. 5,834,186 and 5,741,679, Shih et al., US Patent No. 5,589,332, Nathan et al., US Patent No 5,871,914, Nathan and Ellington, International PCT publication No. WO 00/24931, Breaker et al., International PCT Publication Nos. WO 00/26226 and 98/27104, and Sullenger et al., US Patent Application Serial No. 09/205,520.

#### Additional Uses

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Uses of sequence-specific enzymatic nucleic acid molecules of the instant invention can have many of the same applications for the study of RNA that DNA restriction endonucleases have for the study of DNA (Nathans et al., 1975 Ann. Rev. Biochem. 44:273). For example,

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the pattern of restriction fragments can be used to establish sequence relationships between two related RNAs, and large RNAs can be specifically cleaved to fragments of a size more useful for study. The ability to engineer sequence specificity of the enzymatic nucleic acid molecule is ideal for cleavage of RNAs of unknown sequence. Applicant has described the use of nucleic acid molecules to down-regulate gene expression of target genes in bacterial, microbial, fungal, viral, and eukaryotic systems including plant, or mammalian cells.

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All patents and publications mentioned in the specification are indicative of the levels of skill of those skilled in the art to which the invention pertains. All references cited in this disclosure are incorporated by reference to the same extent as if each reference had been incorporated by reference in its entirety individually.

One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The methods and compositions described herein as presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art, which are encompassed within the spirit of the invention, are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention. Thus, such additional embodiments are within the scope of the present invention and the following claims.

The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations which is not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of" and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by preferred embodiments, optional features, modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention as defined by the description and the appended claims.

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In addition, where features or aspects of the invention are described in terms of Markush groups or other grouping of alternatives, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group or other group.

5 Other embodiments are within the following claims.

### TABLE I

#### Characteristics of Ribozymes

#### **Group I Introns**

Size: ~200 to >1000 nucleotides.

Requires a U in the target sequence immediately 5' of the cleavage site.

Binds 4-6 nucleotides at 5' side of cleavage site.

Over 75 known members of this class. Found in *Tetrahymena* thermophila rRNA, fungal mitochondria, chloroplasts, phage T4, blue-green algae, and others.

## RNAseP RNA (M1 RNA)

Size: ~290 to 400 nucleotides.

RNA portion of a ribonucleoprotein enzyme. Cleaves tRNA precursors to form mature tRNA.

Roughly 10 known members of this group all are bacterial in origin.

#### Hammerhead Ribozyme

Size: ~13 to 40 nucleotides.

Requires the target sequence UH immediately 5' of the cleavage site.

Binds a variable number of nucleotides on both sides of the cleavage site.

14 known members of this class. Found in a number of plant pathogens (virusoids) that use RNA as the infectious agent (Figure 1 and 2)

#### Hairpin Ribozyme

Size: ~50 nucleotides.

Requires the target sequence GUC immediately 3' of the cleavage site.

Binds 4-6 nucleotides at 5' side of the cleavage site and a variable number to the 3' side of the cleavage site.

Only 3 known member of this class. Found in three plant pathogen (satellite RNAs of the tobacco ringspot virus, arabis mosaic virus and chicory yellow mottle virus) which uses RNA as the infectious agent (Figure 3).

# Hepatitis Delta Virus (HDV) Ribozyme

Size: 50 - 60 nucleotides (at present).

Sequence requirements not fully determined.

Binding sites and structural requirements not fully determined, although no sequences 5' of cleavage site are required.

Only 1 known member of this class. Found in human HDV (Figure 4).

# Neurospora VS RNA Ribozyme

Size: ~144 nucleotides (at present)

Cleavage of target RNAs recently demonstrated. Sequence requirements not fully determined. Binding sites and structural requirements not fully determined. Only 1 known member of this class. Found in *Neurospora* VS RNA (Figure 5).

Table II:

A. 2.5 µmol Synthesis Cycle ABI 394 Instrument

Reagent	Equivalents	Amount	Wait Time* DNA	Wait Time* 2'- O-methyl	Wait Time* RNA
Phosphoramidites	6.5	163 µL	45 sec	2.5 min	7.5 min
S-Ethyl Tetrazole	. 23.8	238 µL	45 sec	2.5 min	7.5 min
Acetic Anhydride	100	233 µL	5 sec	5 sec	5 sec
N-Methyl Imidazole	186	233 µL	5 sec	5 sec	5 sec
TCA	176	2.3 mL	21 sec	21 sec	21 sec
lodine	11.2	1.7 mL	45 sec	45 sec	45 sec
Beaucage	12.9	645 µL	100 sec	300 sec	300 sec
Acetonitrile	NA	6.67 mL	AN	NA AN	AN A
				_	
Reagent	Equivalents	Amount	Walt Time* DNA Wait Time* 2'- O-methyl	Wait Time⁺ 2'- O-methyl	Wait Time* RNA
Phosphoramidites	15	31 µL	45 sec	233 sec	465 sec
S-Ethyl Tetrazole	38.7	31 µL	45 sec	233 min	465 sec
Acetic Anhydride	655	124 µL	5 sec	5 sec	. 5 sec
N-Methyl Imidazofe	1245	124 pL	5 sec	5 sec	5 sec
TCA	200	732 µL	10 sec	10 sec	10 sec
lodine	20.6	244 pL	15 sec	15 sec	15 sec

300 sec	NA		Wait Time* 2'-O- Wait Time* Ribo methyl	180 sec 360sec	180 min 360 sec	10 sec 10 sec	10 sec 10 sec	15 sec 15 sec		200 sec 200 sec	AN N
300 sec	N N	rument	Time*								NA
100 sec	A A	96 well Inst		60 sec	60 sec	10 sec	10 sec	15 sec	30 sec	100 sec	¥
232 µL	2.64 mL	C. 0.2 µmol Synthesis Cycle 96 well Instrument	Amount DNA/2'-O-methyl/Ribo	40/60/120 µL	40/60/120 µL	50/50/50 µL	50/50/50 µL	250/500/500 µL	80/80/80 µL	80/120/120	1150/1150/1150 uL
7.7	NA	G G	Equivalents DNA/2'-O-methyl/Ribo	22/33/66	70/105/210	265/265/265	502/502/502	238/475/475	6.8/6.8/6.8	34/51/51	NA
Beaucage	Acetonitrile		Reagent	Phosphoramidites	S-Ethyl Tetrazole	Acetic Anhydride	N-Methyl Imidazole	TCA	lodine	Beancage	Acetonitrile

\* Walt time does not include contact time during delivery.

Table III: Patient Demographics

Dose cohort	· · · ·		T	1	
(mg/m²)	Pt#	Age	Sex:	Diagnosis	Doses
10	1001	49	F	NSC Lung	29
10	1002	65	F	liposarcoma	120
10	1003	49	M	nasopharyngeal CA	109
30	1004	35	M	non-small cell lung	1
30	1005	45	F	melanoma (ocular)	113
30	1006	57	M	colon	199
30	1007	39	F	epitheliod hemangioendothelioma	198
100	1008	52	M	adrenal CA	57
100	1009	44	F	breast	35
100	1010	62	F	renal	134
300	1011	24	F	melanoma	31
300	1012	57	M	renal cell	178
300	1013	53	M	nasopharyngeal SCCA	29
300	1014	64	F	peritoneal mesothelioma	324
500	1011			pertender meconional	327
100	1015	65	M	melanoma	140
100	1015	65	M	melanoma	140
100 100	1015 1016	65 77 26	M F	melanoma breast	140 265
100 100 100	1015 1016 1017	65 77	M F F	melanoma breast melanoma	140 265 35
100 100 100 100	1015 1016 1017 1018	65 77 26 69 65	M F F	melanoma breast melanoma melanoma	140 265 35 7
100 100 100 100 100 100 100	1015 1016 1017 1018 1019 1020 1021	65 77 26 69 65 59	M F F F	melanoma breast melanoma melanoma endometrial sarcoma	140 265 35 7 500
100 100 100 100 100 100 100 100	1015 1016 1017 1018 1019 1020 1021 1022	65 77 26 69 65 59	M F F F M	melanoma breast melanoma melanoma endometrial sarcoma carcinoid	140 265 35 7 500 124
100 100 100 100 100 100 100 100	1015 1016 1017 1018 1019 1020 1021 1022 1023	65 77 26 69 65 59 43 78	M F F F M M M F	melanoma breast melanoma melanoma endometrial sarcoma carcinoid gallbladder adeno carcinoma	140 265 35 7 500 124 34
100 100 100 100 100 100 100 100 100	1015 1016 1017 1018 1019 1020 1021 1022 1023 1024	65 77 26 69 65 59 43 78 40	M F F F M M M F F F F F F F F F F F F F	melanoma breast melanoma melanoma endometrial sarcoma carcinoid gallbladder adeno carcinoma colorectal	140 265 35 7 500 124 34 8
100 100 100 100 100 100 100 100 100 100	1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025	65 77 26 69 65 59 43 78 40 52	M F F F M M M F F F F F F F F F F F F F	melanoma breast melanoma melanoma endometrial sarcoma carcinoid gallbladder adeno carcinoma colorectal breast	140 265 35 7 500 124 34 8 50
100 100 100 100 100 100 100 100 100 100	1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026	65 77 26 69 65 59 43 78 40 52 39	M F F F M M M F F F F F F F F F F F F	melanoma breast melanoma melanoma endometrial sarcoma carcinoid gallbladder adeno carcinoma colorectal breast parotid adenocarcinoma	140 265 35 7 500 124 34 8 50 285
100 100 100 100 100 100 100 100 100 100	1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027	65 77 26 69 65 59 43 78 40 52 39	M F F F M M M F F F F F F F F F F	melanoma breast melanoma melanoma endometrial sarcoma carcinoid gallbladder adeno carcinoma colorectal breast parotid adenocarcinoma breast	140 265 35 7 500 124 34 8 50 285
100 100 100 100 100 100 100 100 100 100	1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028	65 77 26 69 65 59 43 78 40 52 39 55	M F F F M M M F F F F F M M M M M F F F F M	melanoma breast melanoma melanoma endometrial sarcoma carcinoid gallbladder adeno carcinoma colorectal breast parotid adenocarcinoma breast breast breast breast breast melanoma	140 265 35 7 500 124 34 8 50 285 71
100 100 100 100 100 100 100 100 100 100	1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028	65 77 26 69 65 59 43 78 40 52 39 55 52 38	M F F F M M F F F F F M M M M M M M M M	melanoma breast melanoma melanoma endometrial sarcoma carcinoid gallbladder adeno carcinoma colorectal breast parotid adenocarcinoma breast breast breast breast melanoma pancreatic	140 265 35 7 500 124 34 8 50 285 71 34
100 100 100 100 100 100 100 100 100 100	1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028	65 77 26 69 65 59 43 78 40 52 39 55	M F F F M M M F F F F F M M M M M F F F F M	melanoma breast melanoma melanoma endometrial sarcoma carcinoid gallbladder adeno carcinoma colorectal breast parotid adenocarcinoma breast breast breast breast breast melanoma	140 265 35 7 500 124 34 8 50 285 71 34 36

One patient taken off study due to progressive disease. Allowed to resume ANGIOZYME on a compassionate basis.

As of September 1, 2001, all patients were off study. (Although one patient resumed treatment per above note)

Table IV Pharmacokinetic parameters of ANGIOZYME after bolus subcutaneous administration.

		g/m²	30 m	g/m²	100 m	0 mg/m	300 ше/ш	ıg/m²
	Mean	SD	Mean	SD	Mean	SD	Mean	SD
Day I Cmax (ug/mL)	0.43	0.07	0.62	0.28	3.17	69.0	8.91	2.93
AUCt (ug*hr/mL)	2.60	1.43	6.04	2.70	34.14	2.28	89.87	21.68
AUCinf (ug*hr/mL)	4.40	90.0	7.99	1.66	37.51	1.91	101.57	13.47
t(1/2) (hr)	3.62	0.79	7.32	6.94	4.58	0.02	9.26	6.20
$CL/F(L/hr/m^2)$	2.24	0.08	3.73	0.92	2.96	0.61	2.99	0.43
Day 29 Cmax (ug/mL)	0.35	0.19	1.17	0.53	3.23	0.35	8.93	6.71
AUCt (ug*hr/mL)	2.11	1.31	7.29	1.16	31.87	1.91	119.42	65.84
AUCinf (ug*hr/mL)	3.38	1.31	8.54	2.46	33.61	2.16	132.73	67.82
t(1/2) (hr)	4.49	1.60	3.26	1.01	4.66	0.35	7.24	0.70
CL/F (L/hr/m²)	2.49	1.48	3.69	0.94	3.21	0.56	2.72	1.40

Table V: Human FLT DNAzyme and Substrate Sequence

Pos	Substrate	Seq ID No	DNAzyme	Seq ID No
17	ncancace e caccacce	1	GGGAGGAG GGCTAGCTACAACGA CGAGAGGA	1703
28	CCUCCCCG G CAGCGGCG	2	CGCCGCTG GGCTAGCTACAACGA CGGGGAGG	1704
31	CCCCGGCA G CGGCGGCG	3	CGCCGCCG GGCTAGCTACAACGA TGCCGGGG	1705
34	CGGCAGCG G CGGCGGCU	4	AGCCGCCG GGCTAGCTACAACGA CGCTGCCG	1706
37	CAGCGGCG G CGGCUCGG	5	CCGAGCCG GGCTAGCTACAACGA CGCCGCTG	1707
40	CGGCGGCG G CUCGGAGC	6	GCTCCGAG GGCTAGCTACAACGA CGCCGCCG	1708
47	GGCUCGGA G CGGGCUCC	7	GGAGCCCG GGCTAGCTACAACGA TCCGAGCC	1709
51	CGGAGCGG G CUCCGGGG	8	CCCCGGAG GGCTAGCTACAACGA CCGCTCCG	1710
59	GCUCCGGG G CUCGGGUG	9	CACCCGAG GGCTAGCTACAACGA CCCGGAGC	1711
65	GGGCUCGG G UGCAGCGG	10	CCGCTGCA GGCTAGCTACAACGA CCGAGCCC	1712
67	GCUCGGGU G CAGCGGCC	11	GGCCGCTG GGCTAGCTACAACGA ACCCGAGC	1713
70	CGGGUGCA G CGGCCAGC	12	GCTGGCCG GGCTAGCTACAACGA TGCACCCG	1714
73	GUGCAGCG G CCAGCGGG	13	CCCGCTGG GGCTAGCTACAACGA CGCTGCAC	1715
77	AGCGGCCA G CGGGCCUG	14	CAGGCCCG GGCTAGCTACAACGA TGGCCGCT	1716
81	GCCAGCGG G CCUGGCGG	15	CCGCCAGG GGCTAGCTACAACGA CCGCTGGC	1717
86	CGGGCCUG G CGGCGAGG	16	CCTCGCCG GGCTAGCTACAACGA CAGGCCCG	1718
89	GCCUGGCG G CGAGGAUU	17	AATCCTCG GGCTAGCTACAACGA CGCCAGGC	1719
95	CGGCGAGG A UUACCCGG	18	CCGGGTAA GGCTAGCTACAACGA CCTCGCCG	1720
98	CGAGGAUU A CCCGGGGA	19	TCCCCGGG GGCTAGCTACAACGA AATCCTCG	1721
108	CCGGGGAA G UGGUUGUC	20	GACAACCA GGCTAGCTACAACGA TTCCCCGG	1722
111	GGGAAGUG G UUGUCUCC	21	GGAGACAA GGCTAGCTACAACGA CACTTCCC	1723
114	AAGUGGUU G UCUCCUGG	22	CCAGGAGA GGCTAGCTACAACGA AACCACTT	1724
122	GUCUCCUG G CUGGAGCC	23	GGCTCCAG GGCTAGCTACAACGA CAGGAGAC	1725
128	UGGCUGGA G CCGCGAGA	24	TCTCGCGG GGCTAGCTACAACGA TCCAGCCA	1726
131	CUGGAGCC G CGAGACGG	25	CCGTCTCG GGCTAGCTACAACGA GGCTCCAG	1727
136	GCCGCGAG A CGGGCGCU	26	AGCGCCCG GGCTAGCTACAACGA CTCGCGGC	1728
140	CGAGACGG G CGCUCAGG	27	CCTGAGCG GGCTAGCTACAACGA CCGTCTCG	1729
142	AGACGGGC G CUCAGGGC	28	GCCCTGAG GGCTAGCTACAACGA GCCCGTCT	1730
149	CGCUCAGG G CGCGGGGC	29	GCCCCGCG GGCTAGCTACAACGA CCTGAGCG	1731
151	CUCAGGGC G CGGGGCCG	30	CGGCCCCG GGCTAGCTACAACGA GCCCTGAG	1732
156	GCCCCGC G CCGCCGCC	31	GCCGCCGG GGCTAGCTACAACGA CCCGCGCC	1733
160	CGGGGCCG G CGGCGGCG	32	CGCCGCCG GGCTAGCTACAACGA CGGCCCCG	1734
163	GGCCGGCG G CGGCGAAC	33	GTTCGCCG GGCTAGCTACAACGA CGCCGGCC	1735
166	CGGCGGCG G CGAACGAG	34	CTCGTTCG GGCTAGCTACAACGA CGCCGCCG	1736
170	GGCGGCGA A CGAGAGGA	35	TCCTCTCG GGCTAGCTACAACGA TCGCCGCC	1737
178	- ACGAGAGG A CGGACUCU	36	AGAGTCCG GGCTAGCTACAACGA CCTCTCGT	1738
182	GAGGACGG A CUCUGGCG	37	CGCCAGAG GGCTAGCTACAACGA CCGTCCTC	1739
188	GGACUCUG G CGGCCGGG	38	CCCGGCCG GGCTAGCTACAACGA CAGAGTCC	1740
191	cucuadea e caaeanca	39	CGACCCGG GGCTAGCTACAACGA CGCCAGAG	1741
196	GCGGCCGG G UCGUUGGC	40	GCCAACGA GGCTAGCTACAACGA CCGGCCGC	1742
199	GCCGGGUC G UUGGCCGG	41	CCGGCCAA GGCTAGCTACAACGA GACCCGGC	1743
203	GGUCGUUG G CCGGGGGA	42	TCCCCCGG GGCTAGCTACAACGA CAACGACC	1744
212	CCGGGGGA G CGCGGGCA	43	TGCCCGCG GGCTAGCTACAACGA TCCCCCGG	1745
214	GGGGGAGC G CGGGCACC	44	GGTGCCCG GGCTAGCTACAACGA GCTCCCCC	1746
218	GAGCGCGG G CACCGGGC	45	GCCCGGTG GGCTAGCTACAACGA CCGCGCTC	1747
220	GCGCGGC A CCGGGCGA	46	TCGCCCGG GGCTAGCTACAACGA GCCCGCGC	
225	GGCACCGG G CGAGCAGG	47	CCTGCTCG GGCTAGCTACAACGA CCGGTGCC	1749
229	CCGGGCGA G CAGGCCGC	48	GCGGCCTG GGCTAGCTACAACGA TCGCCCGG	1750

222	GOGAGGAG C GOGGGTGG	40	CONCOCC COUTACOTACA ACCA CONCOCCO	1761
233	GCGAGCAG G CCGCGUCG AGCAGGCC G CGUCGCGC	50	CGACGCGG GGCTAGCTACAACGA CTGCTCGC GCGCGACG GGCTAGCTACAACGA GGCCTGCT	1751
238	CAGGCCGC G UCGCGCUC	51	GAGCGCGA GGCTAGCTACAACGA GCGCCTG	1753
241	GCCGCGUC G CGCUCACC	52	GGTGAGCG GGCTAGCTACAACGA GACGCGGC	1754
243	CGCGUCGC G CUCACCAU	53	ATGGTGAG GGCTAGCTACAACGA GCGACGCG	1755
247	UCGCGCUC A CCAUGGUC	54	GACCATGG GGCTAGCTACAACGA GCGACGCG	
250	CGCUCACC A UGGUCAGC	55	GCTGACCA GGCTAGCTACAACGA GGTGAGCG	1756 1757
253	UCACCAUG G UCAGCUAC	56	GTAGCTGA GGCTAGCTACAACGA CATGGTGA	1758
257	CAUGGUCA G CUACUGGG	57	CCCAGTAG GGCTAGCTACAACGA CATGGTGA	
260	GGUCAGCU A CUGGGACA	58	TGTCCCAG GGCTAGCTACAACGA AGCTGACC	1760
266	CUACUGGG A CACCGGGG	59	CCCCGGTG GGCTAGCTACAACGA CCCAGTAG	1761
268	ACUGGGAC A CCGGGGUC	60	GACCCGG GGCTAGCTACAACGA GTCCCAGT	1762
274	ACACCGGG G UCCUGCUG	61	CAGCAGGA GGCTAGCTACAACGA CCCGGTGT	1763
279	GGGGUCCU G CUGUGCGC	62	GCGCACAG GGCTAGCTACAACGA AGGACCCC	1764
282	GUCCUGCU G UGCGCGCU	63	AGCGCGCA GGCTAGCTACAACGA AGCAGGAC	1765
284	CCUGCUGU G CGCGCUGC	64	GCAGCGCG GGCTAGCTACAACGA ACAGCAGG	1766
286	UGCUGUGC G CGCUGCUC	65	GAGCAGCG GGCTAGCTACAACGA GCACAGCA	1767
288	CUGUGCGC G CUGCUCAG	66	CTGAGCAG GGCTAGCTACAACGA GCGCACAG	1768
291	UGCGCGCU G CUCAGCUG	67	CAGCTGAG GGCTAGCTACAACGA AGCGCGCA	1769
296	GCUGCUCA G CUGUCUGC	68	GCAGACAG GGCTAGCTACAACGA TGAGCAGC	1770
299	GCUCAGCU G UCUGCUUC	69	GAAGCAGA GGCTAGCTACAACGA AGCTGAGC	1771
303	AGCUGUCU G CUUCUCAC	70	GTGAGAAG GGCTAGCTACAACGA AGACAGCT	1772
310	UGCUUCUC A CAGGAUCU	71	AGATCCTG GGCTAGCTACAACGA GAGAAGCA	1773
315	CUCACAGG A UCUAGUUC	72	GAACTAGA GGCTAGCTACAACGA CCTGTGAG	1774
320	AGGAUCUA G UUCAGGUU	73	AACCTGAA GGCTAGCTACAACGA TAGATCCT	1775
326	UAGUUCAG G UUCAAAAU	74	ATTTTGAA GGCTAGCTACAACGA CTGAACTA	1776
333	GGUUCAAA A UUAAAAGA	75	TCTTTTAA GGCTAGCTACAACGA TTTGAACC	1777
341	AUUAAAAG A UCCUGAAC	76	GTTCAGGA GGCTAGCTACAACGA CTTTTAAT	1778
348	GAUCCUGA A CUGAGUUU	77	AAACTCAG GGCTAGCTACAACGA TCAGGATC	1779
353	UGAACUGA G UUUAAAAG	78	CTTTTAAA GGCTAGCTACAACGA TCAGTTCA	1780
362	UUUAAAAG G CACCCAGC	79	GCTGGGTG GGCTAGCTACAACGA CTTTTAAA	1781
364	UAAAAGGC A CCCAGCAC	80	GTGCTGGG GGCTAGCTACAACGA GCCTTTTA	1782
369	GGCACCCA G CACAUCAU	81	ATGATGTG GGCTAGCTACAACGA TGGGTGCC	1783
371	CACCCAGC A CAUCAUGC	82	GCATGATG GGCTAGCTACAACGA GCTGGGTG	1784
373	CCCAGCAC A UCAUGCAA	83	TTGCATGA GGCTAGCTACAACGA GTGCTGGG	1785
376	AGCACAUC A UGCAAGCA	84	TGCTTGCA GGCTAGCTACAACGA GATGTGCT	1786
378	CACAUCAU G CAAGCAGG	85	CCTGCTTG GGCTAGCTACAACGA ATGATGTG	1787
382	UCAUGCAA G CAGGCCAG	86	CTGGCCTG GGCTAGCTACAACGA TTGCATGA	1788
386	GCAAGCAG G CCAGACAC	87	GTGTCTGG GGCTAGCTACAACGA CTGCTTGC	1789
391	CAGGCCAG A CACUGCAU	88	ATGCAGTG GGCTAGCTACAACGA CTGGCCTG	1790
393	GGCCAGAC A CUGCAUCU	89	AGATGCAG GGCTAGCTACAACGA GTCTGGCC	1791
396	CAGACACU G CAUCUCCA	90	TGGAGATG GGCTAGCTACAACGA AGTGTCTG	1792
398	GACACUGC A UCUCCAAU	91	ATTGGAGA GGCTAGCTACAACGA GCAGTGTC	1793
405	CAUCUCCA A UGCAGGGG	92	CCCCTGCA GGCTAGCTACAACGA TGGAGATG	1794
407	UCUCCAAU G CAGGGGG	93	CCCCCTG GGCTAGCTACAACGA ATTGGAGA	1795
418	GGGGGAA G CAGCCCAU	94	ATGGGCTG GGCTAGCTACAACGA TTCCCCCC	1796
421	GGGAAGCA G CCCAUAAA	95	TTTATGGG GGCTAGCTACAACGA TGCTTCCC	1797
425	AGCAGCCC A UAAAUGGU	96	ACCATTTA GGCTAGCTACAACGA GGGCTGCT	1798
429	GCCCAUAA A UGGUCUUU	97	AAAGACCA GGCTAGCTACAACGA TTATGGGC	1799
432	CAUAAAUG G UCUUUGCC	98	GGCAAAGA GGCTAGCTACAACGA CATTTATG	1800
438	UGGUCUUU G CCUGAAAU	99	ATTTCAGG GGCTAGCTACAACGA AAAGACCA	1801
445	UGCCUGAA A UGGUGAGU	100	ACTCACCA GGCTAGCTACAACGA TTCAGGCA	1802

452 ANDGUIGA G UARGGANA 461 UANGGANA G CONANGOC 103 GCCTTTCG GGCTAGCTACAGGA TCACCATT 1804 468 AOGCANAG G CUGAGCAU 104 ATGCTTCG GGCTAGCTACAAGGA TTTCGTT 1805 473 ANGGCUGA G CAURACUA 105 TAGTTAG GGCTAGCTACAAGGA TTTCGTT 1807 475 GGCUGAGC A UAACUAA 105 TTAGTTAG GGCTAGCTACAACGA TCAGCCTT 1807 476 UGAGCAUA A CUBACUA 107 AGATTAG GGCTAGCTACAACGA TCAGCCTT 1807 4776 UGAGCAUA A CUBACUG 108 CAGGCAGA GGCTAGCTACAACGA TATGCTCA 1808 483 AURACUAA A UCUGCCUG 108 CAGGCAGA GGCTAGCTACAACGA TATGCTCA 1804 481 AUCUGCCU G UGGAGGA 109 TCCACAGG GGCTAGCTACAACGA TATGTTAT 1810 481 AUCUGCCU G UGGAGGA 109 TCCACAGG GGCTAGCTACAACGA TATGTTAT 1810 481 AUCUGCCU G UGGAGGA 110 TCTTCCCA GGCTAGCTACAACGA TATGTTAT 1810 481 AUCUGCCU G UGGAGGA 111 GTTTCCCA GGCTAGCTACAACGA AGACTATTAG 1811 500 UGGAGGAA A UGCCACAG 112 GTTTCCCA GGCTAGCTACAACGA AGACGAAT 1812 501 AAGAAUGU G CAAACCAA 111 GTTTCCCA GGCTAGCTACAACGA AGGCAGAT 1812 502 AAGAAAUG G CAAACCAA 112 ATTGTTT GGCTAGCTACAACGA ATTTCTT 1815 503 AAGAAAUG G CAAACCAA 111 CAGAATTG GGCTAGCTACAACGA TATTCTT 1815 515 ACAAUUCU G CAGGUACU 113 CAGAATTG GGCTAGCTACAACGA TATTCTT 1815 515 ACAAUUCU G CAGGUACU 115 AAGTACTG GGCTAGCTACAACGA TATTCTC 1816 518 AUUCUGCAGU A CUUUAAC 116 GGTTAAGTG GGCTAGCTACAACGA TATTCTC 1816 520 UCUGCAGU A CUUUAAC 117 GGTTAAG GGCTAGCTACAACGA TACAACAT 1818 521 CUUCACA G UACUUUAA 116 GTTAAGTG GGCTAGCTACAACGA TACAACAT 1818 523 AACCUUGA A CACAGCUC 119 GAGCTGTG GGCTAGCTACAACGA TACAAGTT 1820 533 AACCUUGA A CACAGCUC 119 GAGCTGTG GGCTAGCTACAACGA TACAAGTT 1820 534 UGAACCA G CUCAAGCA 118 GTTCAAGG GGCTAGCTACAACGA TACAGGT 1821 535 CUUCAGAC A CACAGCUC 120 TTCAAGG GGCTAGCTACAACGA TCAAGGT 1821 536 GUACUUUA A CCUUGAAC 121 TGCTTGA GGCTAGCTACAACGA TCAAGGT 1821 537 CACACCAC G CUCAAGCA 121 TGCTTGA GGCTAGCTACAACGA TCAAGGT 1821 538 UGAACCAC G CUCAAGCA 121 TGCTTGA GGCTAGCTACAACGA TCAAGGT 1821 544 CAGCUCAA G CAAACCAU 122 GTTAGCTG GGCTAGCTACAACGA TCAAGGT 1821 551 CACAACCAC A CUGCCUC 122 GTTAGCTG GGCTAGCTACAACGA TGCAGAG 1821 552 CACACCUC A CUUCACA 122 GTTAGCTG GGCTAGCTACAACGA TGCAGTA 1825 553 CAAACCAC A CUGCCC 123 AAGCAGA 123 AACC	440	CIVOLANICO O LICACITARO	107	COMPACTOR COCCERCON CARCON CARONICA	1002
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491 AUCUGCCU G UGGAAGAA 110 TTCTTCCA GGCTAGCTACAACGA AGGCAGAT 500 UGGAAGAA A UGGCAAAC 111 GTTTGCCA GGCTAGCTACAACGA TTCTTCCA 1813 503 AAGAAUG G CAAACAAU 112 ATTGTTTG GGCTAGCTACAACGA TTCTTCA 1814 507 AAUGGCAA A CAAUUCUG 113 CAGAATTG GGCTAGCTACAACGA CATTCTT 1815 510 GGCAAACA A UUCUGCAG 114 CTGCAGAA GGCTAGCTACAACGA TTGCCTT 1815 510 GGCAAACA A UUCUGCAG 114 CTGCAGAA GGCTAGCTACAACGA TGTTTGCC 1816 515 ACAAUUCU G CAGUACUU 115 AAGTACTG GGCTAGCTACAACGA TGTTTGCC 1816 516 AUCUGCA G UACUUUAA 116 TTAAAGTA GGCTAGCTACAACGA AGAATTGT 1817 518 AUUCUGCA G UACUUUAA 116 TTAAAGTA GGCTAGCTACAACGA AGAATTGT 1818 520 UCUGCAGU A CUUUAACC 117 GGTAAAAG GGCTAGCTACAACGA ACTGCAGA 1819 526 GUACUUUA A CCUUGAAC 118 GTTCAAGG GGCTAGCTACAACGA ACTGCAGA 1819 526 GUACUUUA A CCUUGAAC 119 GAGCTGTG GGCTAGCTACAACGA ACTGCAGA 1820 533 AACCUUGA A CACACCUC 119 GAGCTGTG GGCTAGCTACAACGA TAAAGTAC 533 AACCUUGAA C ACAACCAC 120 TTGAGCTG GGCTAGCTACAACGA TAAAGTAC 544 CAGCUCAA G CUCAAGCA 121 TGCTTGAG GGCTAGCTACAACGA TTGCTTGA 1822 545 UGAACACA G CUCAAGCA 122 GTGGTTTG GGCTAGCTACAACGA TTGCTTGA 1823 544 CAGCUCAA G CAAACCAC 123 CAGTTTGG GGCTAGCTACAACGA TTGCTTGA 1825 551 AGCAAACCA C ACUGGCU 124 AGCCAGTG GGCTAGCTACAACGA TTGCTTGA 1825 551 AGCAAACCA C ACUGGCU 124 AGCCAGTG GGCTAGCTACAACGA TTGCTTGA 1825 553 CAAACCAC A CUGGCUUC 125 GAAGCCAC G GGTAGCTACAACGA TTGCTTGC 1826 553 UGGCUUCU A CAGCUGGCU 127 TGCAGCTG GGCTAGCTACAACGA AGGACCACGA 1829 556 CUUCUACA G CUGCAAUUC 129 GATATTTG GGCTAGCTACAACGA AGGACCACGA 1829 557 CCACACUUG C CUGCACU 129 GATATTTG GGCTAGCTACAACGA AGGACCA 1829 558 CUACAGCU G CAAAUAUC 129 GATATTTG GGCTAGCTACAACGA AGGACCA 1820 559 CUACAGCU G CAAAUAUC 129 GATATTTG GGCTAGCTACAACGA AGGACCA 1830 569 CUACAGCU G CAAAUAUC 129 GATATTTG GGCTAGCTACAACGA AGGACCA 1831 573 AGCUGCAA U AUCUACUA 132 AGGTAGCTA GGCTAGCTACAACGA ATTGCAGC 1831 580 AAUAUCUA G CUGCAAUU 129 GATATTTG GGCTAGCTACAACGA AGGACCAA TTGCAGC 1831 580 AAUAUCUA G CUGCAAU 129 GATATTTG GGCTAGCTACAACGA AGGACCA 1831 580 AAUAUCUA G CUGCAAU 129 GATATTTG GGCTAGCTACAACGA AGGACCA 1831 580 AAUAUCUA G CUGCAAU 133 AGCACCAG GGCTAGCTACA		<del></del>			
SOO					1811
503   AAGAANUG G CAAACAAU   112   ATTGTTTG GGCTAGCTACAACGA CATTTCTT   1814     507   AAUGGCAA A CAAUUCUG   113   CAGAATTG GGCTAGCTACAACGA TTGCCATT   1815     510   GGCAAACA A UUCUGCAG   114   CTGCAGAA GGCTAGCTACAACGA TGTTTGCC   1816     515   ACAAUUCU   G CAGUACUU   115   AAGTACTG GGCTAGCTACAACGA AGAATTGT   1817     518   AUUCUGCA G UACUUUAA   116   TTAAAGTA GGCTAGCTACAACGA AGAATTGT   1817     520   UCUGCAGU A CUUUAAAC   117   GGGTAAAAG GGCTAGCTACAACGA AGAATTGT   1819     521   GUACUUUA A CCUUGAAC   118   GTTCAAAG GGCTAGCTACAACGA ACGAATGCAGA   1819     522   GUACUUUA A CCUUGAAC   118   GTTCAAAG GGCTAGCTACAACGA ACGAATGCAGA   1819     523   AACCUUGA A CACAGCUC   119   GAGCTGTG GGCTAGCTACAACGA TAAAGTAC   1820     533   AACCUUGA C CACAGCAC   120   TTGAGCTG GGCTAGCTACAACGA TCAAGGTT   1821     535   CUUGAAC A CAGCCUCA   121   TGCTTGAG GGCTAGCTACAACGA TTCATGG   1822     538   UGAACACA G CUCAAGCA   122   TTGATGTG GGCTAGCTACAACGA TTGGTTCA   1823     544   CAGCUCAA G CACACCUG   123   CAGTGTG GGCTAGCTACAACGA TTGCTTGA   1825     545   UCAAGCAA C ACACACUG   123   CAGTGTG GGCTAGCTACAACGA TTGCTTGA   1825     551   AGCAAACCA C ACUGGCUC   124   AGCCAGTG GGCTAGCTACAACGA TTGCTTGA   1825     552   CAAACCAA C ACUGGCU   125   GAGCACG GGCTAGCTACAACGA CAGTGTGC   1826     553   CAAACCAA C ACUGGCUC   126   TGTAGAAG GGCTAGCTACAACGA CAGTGTGC   1827     557   CCACACUG G CUUCUACA   126   TGTAGAAG GGCTAGCTACAACGA CAGTGTGC   1827     558   CUUCUACA G CUGCAAAU   128   ATTTGCAG GGCTAGCTACAACGA AGAAGCA   1829     566   CUUCUACA G CUGCAAAU   128   ATTTGCAG GGCTAGCTACAACGA AGAAGCA   1829     557   CUGCAAAU A UCUACCUC   125   GAGTATTG GGCTAGCTACAACGA AGTTGTGA   1831     557   CUGCAAAU A UCUACCUC   134   AGATTAGA GGCTAGCTACAACGA AGTTGAGA   1832     558   CUAGCUGU A CUUCACA   132   AGATTAGA GGCTAGCTACAACGA AGTTGAGA   1832     559   CUAGACCU G CAAAUAUC   136   AGATTAGA GGCTAGCTACAACGA AGTTGAGA   1835     560   AAUAUCUA G CUGUACCU   134   AGATTAG GGCTAGCTACAACGA AGTTGAGA   1835     561   CUGACCUU A CUUCAAAG   135   ATTGAGA GGCTAGCTACAACGA AGTTGATA					1812
507   ANUGGCAA A CAAUUCUG					
S10			112	ATTGTTTG GGCTAGCTACAACGA CATTTCTT	1814
515         ACAAUUCU G CAGUACUU         115         AAGTACTG GGCTAGCTACAACGA AGAATTGT         1817           518         AUUCUGCA G UACUULAA         116         TTAAAGTA GGCTAGCTACAACGA ACTGCAGAT         1818           520         UCUGCAGU A CUUUAACC         117         GGTTAAAG GGCTAGCTACAACGA ACTGCAGAT         1818           526         GUACUULA A CCUUGAAC         118         GTTCAAGG GGCTAGCTACAACGA TCAAGGT         1821           533         AACCUUGA A CACGUCAA         120         TTGAGGT GGCTAGCTACAACGA TTCAAGGT         1821           535         CUQUAACA G CUCAAGCA         121         TGCTTGAG GGCTAGCTACAACGA TTGTCTA         1822           544         CAGCUCAA G CAAACCAC         122         GTGGTTTG GGCTAGCTACAACGA TTGTCTA         1823           548         UCAAGCAA A CCACCUG         123         CAGTGTG GGCTAGCTACAACGA TTGCTTGA         1825           551         AGCAAACC A CACUGGCU         124         AGCCAGTG GGCTAGCTACAACGA GTGTTTG         1826           557         CCACACUG G CUUCUACA         126         TGTGAGAG GGCTAGCTACAACGA AGTGTTG         1828           563         UGGCUCU A CAGCUGCA         127         TGCAGCTG GGCTAGCTACAACGA AGTGTTGC         1829           564         CUUCACA G CUGCAAU         128         ATTTGCAG GGCTAGCTACAACGA AGAGCA AGATCAGA AGAGCAACAA         183			<del></del>	CAGAATTG GGCTAGCTACAACGA TTGCCATT	1815
S18		<del></del>		CTGCAGAA GGCTAGCTACAACGA TGTTTGCC	1816
520         UCUGCAGU A CUJUAACC         117         GGTTAAAG GGCTAGCTACAACGA ACTGCACA         1819           526         GUACUJUA A CCUJUGAAC         118         GTTCAAGG GGCTAGCTACAACGA TAAAGTAC         1820           533         AACCUJGA A CACAGCUC         119         GAGCTGT GGCTAGCTACAACGA TAAAGGT TB21           535         CCUJUGAAC A CACAGCUGA         121         TTGTTGAG GGCTAGCTACAACGA GTTCATAGG         1822           538         UGAACACA G CUCAAGCA         121         TGCTTGAG GGCTAGCTACAACGA TTGAGCTG         1824           544         CAGGUCA G CAAACCAC         122         GTGTTTG GGCTAGCTACAACGA TTGAGCTG         1824           548         UCAAGCA A CACUGGU         124         AGCCAGTG GGCTAGCTACAACGA TTGCTTGA         1825           551         AGCAAACCA C CUUCUACA         126         TGTAGAGG GGCTAGCTACAACGA GTGGTTTG         1826           553         CAAACCAC A CUUGUACA         126         TGTAGAGG GGCTAGCTACAACGA AGAAGCA         1829           557         CCACACUG G CUUCUACA         126         TGTAGAGG GGCTAGCTACAACGA AGAAGCA         1828           566         CUUCUACA G CUGCAAAU         128         ATTTGCAG GGCTAGCTACAACGA AGAAGAACA         1830           575         CUGACAGU G CAAAUAUC         129         GATAGTTA GGCTAGCTACAACGA ATTGCAGCA         1832	515	ACAAUUCU G CAGUACUU	115	AAGTACTG GGCTAGCTACAACGA AGAATTGT	1817
526         GUACUUUA A CCUUGAAC         118         GTTCAAGG GGCTAGCTACAACGA TAAAGTAC         1820           533         AACCUUGA A CACAGCUC         119         GAGCTGTG GGCTAGCTACAACGA TCAAGGTT         1821           535         CUUUAAC A CAGCUCAA         120         TTGAGCTG GGCTAGCTACAACGA TCAAGGT         1821           538         UGAACACA G CUCAAGCA         121         TGCTTGAG GGCTAGCTACAACGA TTGAGCTG         1823           544         CAGCUCAA G CAAACCAC         122         GTGGTTTG GGCTAGCTACAACGA TTGCTTGA         1825           548         UCAAGCAA A CCACCUG         123         CAGTGTGG GGCTAGCTACAACGA GTTTGCT         1825           551         AGCAAACC A CACUGGCU         124         AGCCAGTG GGCTAGCTACAACGA GTTGTTTG         1826           553         CAAACCAC A CUUGCUAC         125         GAAGCCAG GCTAGCTACAACGA CAGTGTTG         1826           553         UGGCUUCU A CAGCUGCA         127         TGCAGCTG GGCTAGCTACAACGA CAGTGTGTG         1828           563         UGGCUUCU A CAGCUGCA         127         TGCAGCTG GGCTAGCTACAACGA TGTAGAGG         1830           566         CUUCUACA G CUGCAAU         128         ATTTGCAG GGCTAGCTACAACGA TTCAGACGA         1831           573         AGCUGCAA UAUCACCU         130         GCTAGATA         GGCTAGCTACAACGA TTCTGACCT		····		TTAAAGTA GGCTAGCTACAACGA TGCAGAAT	1818
533   AACCUUGA A CACAGCUC   119   GAGCTGTG GGCTAGCTACAACGA TCAAGGTT   1821		UCUGCAGU A CUUUAACC	117	GGTTAAAG GGCTAGCTACAACGA ACTGCAGA	1819
S35	526		118	GTTCAAGG GGCTAGCTACAACGA TAAAGTAC	1820
538         UGAACACA G CUCAAGCA         121         TGCTTGAG GGCTAGCTACAACGA TGTGTTCA         1823           544         CAGCUCAA G CAAACCAC         122         GTGGTTTG GGCTAGCTACAACGA TTGAGTG         1824           548         UCAAGCAA A CACACUG         132         CAGTGTGG GGCTAGCAACGA TTGGTTGA         1825           551         AGCAAACC A CACUGGCU         124         AGCCAGTG GGCTACCAACGA GTGGTTGCT         1826           553         CAAACCAC A CUGGCUUC         125         GAAGCCAG GGCTAGCTACAACGA GTGGTTTG         1827           557         CCACACUG G CUUCUACA         126         TGTAGAAG GGCTAGCTACAACGA AGAAGCCA         1829           563         UGGCUUCU A CAGCUGCA         127         TGCAGCTG GGCTACCAACGA AGAAGCCA         1829           566         CUUCUACA G CUGCAAAU         128         ATTTGCAG GGCTACCAACGA AGAAGCCA         1830           573         AGCUGCAA A UAUCUAGC         130         GCTAGATACAACGA AGCTACAACGA AGCTAGA         1831           575         CUGCAAAU A UCUAGCUG         131         CAGCTAGA GGCTAGCTACAACGA ATTTGCAGCT         1832           575         CUGCAAAU A UCUAGCU         132         AGGTACAG GGCTAGCTACAACGA ATTTGCAGT         1833           575         CUGCAAUA         UCUAGCUG         131         CAGCTAGG         GCTAGCTACAACGA ATGATATT	533	AACCUUGA A CACAGCUC	119	GAGCTGTG GGCTAGCTACAACGA TCAAGGTT	1821
544         CAGCUCAA G CAAACCAC         122         GTGGTTTG GGCTACAACGA TTGAGTG         1824           548         UCAAGCAA A CCACACUG         123         CAGTGTGG GGCTACAACGA TTGCTTGA         1825           551         AGCAAACC A CACUGGCU         124         AGCCAGTG GCTTACAACGA GTTTTGCT         1826           553         CAAACCAC A CUGGCUUC         125         GAAGCCAG GGCTAGCTACAACGA AGGTTTGCTT         1827           557         CCACACUG G CUUCUACA         126         TGTAGAAG GGCTAGCTACAACGA AGAAGCCA         1829           563         UGGCUUCU A CAGCUGCA         127         TGCAGCTG GGCTACAACGA AGAAGCCA         1829           566         CUUCUACA G CUGCAAAU         128         ATTTGCAG GGCTAGCTACAACGA AGAAGCA         1830           569         CUACAGCU G CAAAUAUC         129         GATATTTG GGCTACAACGA AGCTTGAA         1831           573         AGCUGCAA U AUCUAGCU         130         GCTAGATA GGCTACAACGA ATTTGCAGT         1832           580         AAUAUCUA G CUGCACU         131         CAGCTAGA GGCTAGCTACAACGA TAGATATT         1835           583         AUCUAGCU G UACCUACU         133         AGTAGGG GGCTAGCTACAACGA AGCTAGAT         1836           585         CUAGCUGU A CUUCAAAG         135         CTTTGAAG GGCTACAACGA ACAGCAACAGA TACACTAGA GAACAGAACA	535	CCUUGAAC A CAGCUCAA	120	TTGAGCTG GGCTAGCTACAACGA GTTCAAGG	1822
548         UCAAGCAA A CCACACUG         123         CAGTGTGG GGCTAGCAACGA TTGCTTGA 1825           551         AGCAAACC A CACUGGCU         124         AGCCAGTG GGCTACAACGA GGTTTGCT 1826           553         CAAACCAC A CUGGCUUC         125         GAAGCAG GGCTAGCTACAACGA GTGGTTTG 1827           557         CCACACUG G CUUCUACA         126         TGTAGAAG GGCTAGCTACAACGA CAGTGTGGG 1828           563         UGGCUUCU A CAGCUGCA         127         TGCAGCTG GGCTAGCTACAACGA AGAAGCCA 1829           566         CUUCUACA G CUGCAAAU         128         ATTTGCAG GGCTAGCTACAACGA TGAGAG         1830           569         CUACAGCU G CAAAUAUC         129         GATATTTG GGCTAGCTACAACGA ACTGTAGA         1831           573         AGCUGCAA A UAUCUAGC         130         GCTAGATA GGCTAGCTACAACGA ACTTGCAGCT         1832           575         CUGCAAAU A UCUAGCU         131         CAGCTAGAG GGCTAGCTACAACGA ACTGAGTAGTAGA         1833           580         AAUAUCUA G CUGUACCU         132         AGGTACAG GGCTAGCTACAACGA ACAGCAAGTAGAGA         1836           583         AUCUAGCU G UACCUACU         133         AGTAGATA GGCTAGCTACAACGA ACAGCAAGTAGAGA         1836           589         CUGGACUA A UCUCAAAG         135         CTTTTGAAG GGCTAGCTACAACGA ACAGCAAGTAGAGA         1836           612         GAAACAGA A UCUGCAA	538	UGAACACA G CUCAAGCA	121	TGCTTGAG GGCTAGCTACAACGA TGTGTTCA	1823
S51	544	CAGCUCAA G CAAACCAC	122	GTGGTTTG GGCTAGCTACAACGA TTGAGCTG	1824
553         CAAACCAC A CUGGCUUC         125         GAAGCCAG GGCTAGCTACAACGA GTGGTTTG         1827           557         CCACACUG G CUUCUACA         126         TGTAGAAG GGCTAGCTACAACGA CAGTGTGG         1828           563         UGGCUUCU A CAGCUGCA         127         TGCAGCTG GGCTAGCTACAACGA AGAAGCCA         1829           566         CUUCUACA G CUGCAAAU         128         ATTTGCAG GGCTAGCTACAACGA AGAAGCCA         1830           569         CUACAGCU G CAAAUAUC         129         GATATTTG GGCTAGCTACAACGA AGCTGTAG         1831           573         AGCUGCAA A UAUCUAGCU         130         GCTAGATA GGCTAGCTACAACGA ATTGCAG         1832           575         CUGCAAAU A UCUAGCU         131         CAGCTAGA GGCTAGCTACAACGA ATTTGCAG         1833           580         AAUAUCUA G CUGUACCU         132         AGGTACAG GGCTAGCTACAACGA ATTTGCAG         1836           583         AUCUAGCU G UACCUACU         133         AGTAGGTA GGCTAGCTACAACGA AGCTAGAT         1836           585         CUAGCUGU A CCUACAU         133         AGTACGA GGCTAGCTACAACGA ACGCTAGA         1837           607         AGAACGA A CAGAAUCU         136         AGATCTG GGCTAGCTACAACGA ACGATCTTCT         1838           612         GAAACCAGA A UCUAUAUA         138         ATTGCAGA GGCTAGCTACAACGA TCTGTTC         1840     <	548	UCAAGCAA A CCACACUG	123	CAGTGTGG GGCTAGCTACAACGA TTGCTTGA	1825
557         CCACACUG G CUUCUACA         126         TGTAGAAG GGCTAGCTACAACGA CAGTGTGG 1828           563         UGGCUUCU A CAGCUGCA         127         TGCAGCTG GGCTAGCTACAACGA AGAAGCCA         1829           566         CUUCUACA G CUGCAAAU         128         ATTTGCAG GGCTAGCTACAACGA AGAAGCCA         1829           569         CUACAGCU G CAAAUAUC         129         GATATTTG GGCTAGCTACAACGA AGCTGTAG         1831           573         AGCUGCAA A UAUCUAGC         130         GCTAGATA GGCTAGCTACAACGA ATTGCAGCTA         1832           575         CUGCAAAU A UCUAGCU         131         CAGCTAGA GGCTAGCTACAACGA ATTGCAG 1833           580         AAUAUCUA G CUGUACCU         132         AGGTACAG GGCTAGCTACAACGA ATGATATT         1834           583         AUCUAGCU G UACCUACU         133         AGTAGGTA GGCTACCAACGA AGACTAGTA         1835           585         CUAGCUGU A CUUCAAAG         135         CTTTGAAG GGCTAGCTACAACGA AGACTAG 1837           607         AGAAGGAA A UCUGCAAU         136         AGATTCTG GGCTAGCTACAACGA TCCTTTCT         1838           612         GAAACAGA A UCUGCAAU         137         ATTGCAGA GGCTAGCTACAACGA TCCTTTCT         1839           616         CAGAAUCU G CAAUCUAU         138         ATAGATTG GGCTACCAACGA AGATTCTT         1840           619         AAUCUGC	551	AGCAAACC A CACUGGCU	124	AGCCAGTG GGCTAGCTACAACGA GGTTTGCT	1826
563         UGGCUUCU A CAGCUGCA         127         TGCAGCTG GGCTAGCTACAACGA AGAAGCCA         1829           566         CUUCUACA G CUGCAAAU         128         ATTTGCAG GGCTAGCTACAACGA TGTAGAAG         1830           569         CUACAGCU G CAAAUAUC         129         GATATTG GGCTAGCTACAACGA AGCTGTAG         1831           573         AGCUGCAA A UAUCUAGC         130         GCTAGATA GGCTAGCTACAACGA ATTGCAGCT         1832           575         CUGCAAAU A UCUAGCUG         131         CAGCTAGA GGCTAGCTACAACGA ATTGCAGCT         1833           580         AAUAUCUA G CUGUACCU         132         AGTAGGTA GGCTAGCTACAACGA AGCTAGAT         1835           583         AUCUAGCU G UACCUACU         133         AGTAGGTA GGCTAGCTACAACGA AGCTAGAT         1835           589         CUAGCUGU A CUUCAAAG         135         CTTTGAAG GGCTAGCTACAACGA AGGTACAG         1836           607         AGAAGGAA A UCUGCAAU         136         AGATTCTG GGCTACAACGA TCTGTTC         1838           612         GAAACAGA A UCUGCAAU         137         ATTGCAGA GGCTAGCTACAACGA TCTGTTC         1839           616         CAGAAUCU G CAAUCUAU         138         ATAGATTG GGCTACCAACGA AGATTCTG         1840           619         AAUCUACA A UCUAUAUA         139         TATATAGA GGCTAGCTACAACGA AGATTCTG         1841	553	CAAACCAC A CUGGCUUC	125	GAAGCCAG GGCTAGCTACAACGA GTGGTTTG	1827
566         CUUCUACA G CUGCAAAU         128         ATTTGCAG GGCTAGCTACAACGA TGTAGAAG         1830           569         CUACAGCU G CAAAUAUC         129         GATATTTG GGCTAGCTACAACGA AGCTGTAG         1831           573         AGCUGCAA A UAUCUAGC         130         GCTAGATA GGCTAGCTACAACGA TTGCAGCT         1832           575         CUGCAAAU A UCUAGCUG         131         CAGCTAGA GGCTAGCACACGA ATTTGCAG         1833           580         AAUAUCUA G CUGUACCU         132         AGGTACAG GGCTAGCACACGA AGCTAGAT         1835           583         AUCUAGCU G UACCUACU         133         AGTAGGTA GGCTAGCACACGA AGCTAGAT         1835           585         CUAGCUGU A CCUACUUC         134         GAAGTAGG GGCTAGCACACGA ACGCTAGATCA         1836           589         CUGUACCU A CUUCAAAG         135         CTTTGAAG GGCTACCACACGA AGGTACCA         1837           607         AGAAGGA A UCUCAAAU         136         AGATTCTG GGCTACCACACGA TCCTTCTT         1838           612         GAAACAGA A UCUGCAAU         137         ATTGCAGA GGCTACCACACGA TCCTTCTT         1849           616         CAGAAUCU G CAAUCUAU         138         ATAGATTG GGCTACCACACGA TGCAGTTCTTCT         1840           619         AAUCUAGA         140         TAAATATAG GGCTAGCTACACGA AGATTGCA         1841	557	CCACACUG G CUUCUACA	126	TGTAGAAG GGCTAGCTACAACGA CAGTGTGG	1828
569         CUACAGCU G CAAAUAUC         129         GATATTTG GGCTAGCTACAACGA AGCTGTAG         1831           573         AGCUGCAA A UAUCUAGC         130         GCTAGATA GGCTAGCTACAACGA TTGCAGCT         1832           575         CUGCAAAU A UCUAGCUG         131         CAGCTAGA GGCTAGCTACAACGA ATTTGCAG         1833           580         AAUAUCUA G CUGUACCU         132         AGGTACAG GGCTAGCTACAACGA TAGATATT         1834           583         AUCUAGCU G UACCUACU         133         AGTAGGTA GGCTAGCACACGA AGCTAGAT         1835           585         CUAGCUGU A CCUACUUC         134         GAAGTAGG GGCTAGCAACGA ACGCTAGACAG ACGTAGA         1836           589         CUGUACCU A CUUCAAAG         135         CTTTGAAG GGCTACCAACGA AGGTACAG         1837           607         AGAAGGA A UCUGCAAU         136         AGATTCTG GGCTACCAACGA TCCTTCTT         1838           612         GAAACAGA A UCUGCAAU         137         ATTGCAGA GGCTACCAACGA TCTGTTTCT         1840           619         AAUCUGCA A UCUAUAU         139         TATATAGA GGCTAGCAACGA TGCAACGA TGAATTCT         1841           623         UGCAAUCU A UAUAUUUA         140         TAAAAATA GGCTAGCTACAACGA ATAGATTGA         1842           625         CAAUCUAU A UUUUAUUG         141         AATAAATA GGCTAGCTACAACGA ATAATAATT         1843 <td>563</td> <td>UGGCUUCU A CAGCUGCA</td> <td>127</td> <td>TGCAGCTG GGCTAGCTACAACGA AGAAGCCA</td> <td>1829</td>	563	UGGCUUCU A CAGCUGCA	127	TGCAGCTG GGCTAGCTACAACGA AGAAGCCA	1829
573         AGCUGCAA A UAUCUAGC         130         GCTAGATA GGCTAGCTACAACGA TTGCAGCT         1832           575         CUGCAAAU A UCUAGCUG         131         CAGCTAGA GGCTAGCTACAACGA ATTTGCAG         1833           580         AAUAUCUA G CUGUACCU         132         AGGTACAG GGCTAGCTACAACGA AGCTAGAT         1834           583         AUCUAGCU G UACCUACU         134         GAAGTAGG GGCTAGCTACAACGA AGCTAGAT         1835           585         CUAGCUGU A CUUCAAAG         135         CTTTGAAG GGCTAGCTACAACGA ACGCTACAG         1837           607         AGAAGGAA A CAGAAUCU         136         AGATTCTG GGCTAGCTACAACGA TCCTTCT         1838           612         GAAACAGA A UCUGCAAU         137         ATTGCAGA GGCTAGCTACAACGA TCTGTTTC         1839           616         CAGAAUCU G CAAUCUAU         138         ATAGATTG GGCTAGCTACAACGA TCTGCTTC         1840           619         AAUCUGCA A UCUAUAUA         139         TATATAGA GGCTAGCTACAACGA TGCAGATT         1841           623         UGCAAUCU A UAUAUAUA         140         TAAATATA GGCTAGCTACAACGA AGATTGCA         1842           625         CAAUCUAU A UAUUUUAU         141         AATAAATA GGCTAGCTACAACGA ATATAGAT         1844           627         AUCUAUAU A UUUAUUAG         142         CTAATAAA GGCTAGCTACAACGA ATATAATAT         1845	566	CUUCUACA G CUGCAAAU	128	ATTTGCAG GGCTAGCTACAACGA TGTAGAAG	1830
575         CUGCAAAU A UCUAGCUG         131         CAGCTAGA GCTAGCTACAACGA ATTTGCAG         1833           580         AAUAUCUA G CUGUACCU         132         AGGTACAG GGCTAGCTACAACGA TAGATATT         1834           583         AUCUAGCU G UACCUACU         133         AGTAGGTA GGCTAGCTACAACGA AGCTAGAT         1835           585         CUAGCUGU A CCUACUUC         134         GAAGTAGG GGCTAGCTACAACGA ACAGCTAG         1836           589         CUGUACCU A CUUCAAAG         135         CTTTGAAG GGCTAGCTACAACGA AGGTACAG         1837           607         AGAAGGAA A CAGAAUCU         136         AGATTCTG GGCTAGCTACAACGA TCCTTCT         1838           612         GAAACAGA A UCUGCAAU         137         ATTGCAGA GGCTAGCTACAACGA TCTGTTTC         1839           616         CAGAAUCU G CAAUCUAU         138         ATAGATTG GGCTAGCTACAACGA AGATTCTG         1840           619         AAUCUGCA A UCUAUAUA         139         TATATAGA GGCTAGCTACAACGA AGATTCTG         1841           623         UGCAAUCU A UAUAUUUA         140         TAAATATA GGCTAGCTACAACGA AGATTGCA         1842           625         CAAUCUAU A UAUUUUAU         141         AATAAATA GGCTACCAACGA ATATAGAT         1844           631         AUUAUAU A UUUAUUAG         142         CTAATAAA GGCTACCAACGA AATATAT         1845	569	CUACAGCU G CAAAUAUC	129	GATATTTG GGCTAGCTACAACGA AGCTGTAG	1831
AUGUAGU G CUGUACCU 132 AGGTACAG GGCTAGCTACAACGA TAGATATT 1834  583 AUCUAGCU G UACCUACU 133 AGTAGGTA GGCTAGCTACAACGA AGCTAGAT 1835  585 CUAGCUGU A CCUACUUC 134 GAAGTAGG GGCTAGCTACAACGA ACAGCTAG 1836  589 CUGUACCU A CUUCAAAG 135 CTTTGAAG GGCTAGCTACAACGA ACAGCTAG 1837  607 AGAAGGAA A CAGAAUCU 136 AGATTCTG GGCTAGCTACAACGA AGGTACAG 1837  612 GAAACAGA A UCUGCAAU 137 ATTGCAGA GGCTAGCTACAACGA TCTCTTCT 1839  616 CAGAAUCU G CAAUCUAU 138 ATAGATTG GGCTAGCTACAACGA TCTGTTTC 1840  619 AAUCUGCA A UCUAUAUA 139 TATATAGA GGCTAGCTACAACGA AGATTCCT 1841  623 UGCAAUCU A UAUAUUUA 140 TAAATATA GGCTAGCTACAACGA AGATTGCA 1842  625 CAAUCUAU A UAUUUAUU 141 AATAAATA GGCTAGCTACAACGA ATAGATTG 1843  627 AUCUAUAU A UUUAUUAG 142 CTAATAAA GGCTAGCTACAACGA ATATAGAT 1844  631 AUAUAUUU A UUAGUGAU 143 ATCACTAA GGCTAGCTACAACGA AAATATAT 1845  635 AUUUAUUA G UGAUACAG 144 CTGTATCA GGCTAGCTACAACGA TAATAAAT 1846  638 UAUUAGUG A UACAGGUA 145 TACCTGTA GGCTAGCTACAACGA ATATAAAT 1847  640 UUAGUGAU A CAGGUAGA 146 TCTACCTG GGCTAGCTACAACGA ATCACTAA 1847  641 UGAUACAG G UAGACCUU 147 AAGGTCTA GGCTAGCTACAACGA ATCACTAA 1848  642 ACAGGUAG A CCUUUCGU 148 ACGAAAGG GGCTAGCTACAACGA CTCTACTA 1849  648 ACAGGUAG A CCUUUCGU 148 ACGAAAGG GGCTAGCTACAACGA CTCTACCTA 1850  661 UCGUAGAG A UGUACAGU 150 ACTGTACA GGCTAGCTACAACGA ATCTCAC 1851  662 GUAGAGAU G UACAGUGA 151 TCACTGTA GGCTAGCTACAACGA ATCTCAC 1852  663 GUAGAGAU G UACAGUGA 151 TCACTGTA GGCTAGCTACAACGA ATCTCACA 1852  663 GUAGAGAU G UACAGUGA 151 TCACTGTA GGCTAGCTACAACGA ATCTCACA 1852	573	AGCUGCAA A UAUCUAGC	130	GCTAGATA GGCTAGCTACAACGA TTGCAGCT	1832
AUCUAGCU G UACCUACU 133 AGTAGGTA GGCTAGCTACAACGA AGCTAGAT 1835  585 CUAGCUGU A CCUACUUC 134 GAAGTAGG GGCTAGCTACAACGA ACAGCTAG 1836  589 CUGUACCU A CUUCAAAG 135 CTTTGAAG GGCTAGCTACAACGA ACAGCTAG 1837  607 AGAAGGAA A CAGAAUCU 136 AGATTCTG GGCTAGCTACAACGA ATCCTTCT 1838  612 GAAACAGA A UCUGCAAU 137 ATTGCAGA GGCTAGCTACAACGA TCTGTTTC 1839  616 CAGAAUCU G CAAUCUAU 138 ATAGATTG GGCTAGCTACAACGA TCTGTTTC 1840  619 AAUCUGCA A UCUAUAUA 139 TATATAGA GGCTAGCTACAACGA AGATTCTG 1841  623 UGCAAUCU A UAUAUUUA 140 TAAATATA GGCTAGCTACAACGA AGATTGCA 1842  625 CAAUCUAU A UAUUUAUU 141 AATAAATA GGCTAGCTACAACGA ATAGATTG 1843  627 AUCUAUAU A UUUAUUAG 142 CTAATAAA GGCTAGCTACAACGA ATATAGAT 1844  631 AUAUAUUU A UUAGUGAU 143 ATCACTAA GGCTAGCTACAACGA AAATATAT 1845  635 AUUUAUUA G UGAUACAG 144 CTGTATCA GGCTAGCTACAACGA TAATAAAT 1846  638 UAUUAGUG A UACAGGUA 145 TACCTGTA GGCTAGCTACAACGA ATATAAAT 1847  640 UUAGUGAU A CAGGUAGA 146 TCTACCTG GGCTAGCTACAACGA ATCACTAA 1848  644 UGAUACAG G UAGACCUU 147 AAGGTCTA GGCTAGCTACAACGA ATCACTAA 1848  648 ACAGGUAG A CCUUUCGU 148 ACGAAAGG GGCTAGCTACAACGA CTACTACA 1849  648 ACAGGUAG A CCUUUCGU 148 ACGAAAGG GGCTAGCTACAACGA CTACCTAC 1850  655 GACCUUUC G UAGAGAUG 149 CATCTCTA GGCTAGCTACAACGA CTCACCTG 1850  661 UCGUAGAG A UGUACAGU 150 ACTGTACA GGCTAGCTACAACGA ATCTCAC 1852  663 GUAGAGAU G UACAGGUA 151 TCACTGTA GGCTAGCTACAACGA ATCTCAC 1852	575	CUGCAAAU A UCUAGCUG	131	CAGCTAGA GGCTAGCTACAACGA ATTTGCAG	1833
CUAGCUGU A CCUACUUC 134 GAAGTAGG GGCTAGCTACAACGA ACAGCTAG 1836  589 CUGUACCU A CUUCAAAG 135 CTTTGAAG GGCTAGCTACAACGA AGGTACAG 1837  607 AGAAGGAA A CAGAAUCU 136 AGATTCTG GGCTAGCTACAACGA TTCCTTCT 1838  612 GAAACAGA A UCUGCAAU 137 ATTGCAGA GGCTAGCTACAACGA TTCCTTCT 1839  616 CAGAAUCU G CAAUCUAU 138 ATAGATTG GGCTAGCTACAACGA TCTGTTTC 1840  619 AAUCUGCA A UCUAUAUA 139 TATATAGA GGCTAGCTACAACGA TGCAGATT 1841  623 UGCAAUCU A UAUAUUUA 140 TAAATATA GGCTAGCTACAACGA AGATTGCA 1842  625 CAAUCUAU A UAUUUAUU 141 AATAAATA GGCTAGCTACAACGA ATAGATTG 1843  627 AUCUAUAU A UUUAUUAG 142 CTAATAAA GGCTAGCTACAACGA ATATAGAT 1844  631 AUAUAUUU A UUAGUGAU 143 ATCACTAA GGCTAGCTACAACGA AAATATAT 1845  635 AUUUAUUA G UGAUACAG 144 CTGTATCA GGCTAGCTACAACGA TAATAAAT 1846  638 UAUUAGUG A UACAGGUA 145 TACCTGTA GGCTAGCTACAACGA ATCACTAA 1847  640 UUAGUGAU A CAGGUAGA 146 TCTACCTG GGCTAGCTACAACGA ATCACTAA 1848  644 UGAUACAG G UAGACCUU 147 AAGGTCTA GGCTAGCTACAACGA CTGATACA 1849  648 ACAGGUAG A CCUUUCGU 148 ACGAAAGG GGCTAGCTACAACGA CTACATCA 1850  655 GACCUUUC G UAGAGAUG 149 CATCTCTA GGCTAGCTACAACGA CTACCTGT 1850  661 UCGUAGAG A UGUACAGU 150 ACTGTACA GGCTAGCTACAACGA CTCTACGA 1852  663 GUAGAGAU G UACAGUGA 151 TCACTGTA GGCTAGCTACAACGA CTCTACGA 1852	580	AAUAUCUA G CUGUACCU	132	AGGTACAG GGCTAGCTACAACGA TAGATATT	1834
CUGUACCU A CUUCAAAG  135 CTTTGAAG GGCTAGCTACAACGA AGGTACAG  607 AGAAGGAA A CAGAAUCU  136 AGATTCTG GGCTAGCTACAACGA TTCCTTCT  1838  612 GAAACAGA A UCUGCAAU  137 ATTGCAGA GGCTAGCTACAACGA TCTGTTTC  1839  616 CAGAAUCU G CAAUCUAU  138 ATAGATTG GGCTAGCTACAACGA TCTGTTTC  1840  619 AAUCUGCA A UCUAUAUA  139 TATATAGA GGCTAGCTACAACGA TGCAGATT  1841  623 UGCAAUCU A UAUAUUUA  140 TAAATATA GGCTAGCTACAACGA AGATTGCA  625 CAAUCUAU A UAUUUAUU  141 AATAAATA GGCTAGCTACAACGA ATAGATTG  1843  627 AUCUAUAU A UUUAUUAG  142 CTAATAAA GGCTAGCTACAACGA ATATAGAT  1844  631 AUAUAUUU A UUAGUGAU  143 ATCACTAA GGCTAGCTACAACGA AAATATAT  1845  635 AUUUAUUA G UGAUACAG  144 CTGTATCA GGCTAGCTACAACGA TAATAAAT  1846  638 UAUUAGUG A UACAGGUA  145 TACCTGTA GGCTAGCTACAACGA CACTAATA  1847  640 UUAGUGAU A CAGGUAGA  145 TACCTGTA GGCTAGCTACAACGA ATCACTAA  1848  644 UGAUACAG G UAGACCUU  147 AAGGTCTA GGCTAGCTACAACGA CTGTATCA  1849  648 ACAGGUAG A CCUUUCGU  148 ACGAAAGG GGCTAGCTACAACGA CTGTATCA  1850  655 GACCUUUC G UAGAGAUG  149 CATCTCTA GGCTAGCTACAACGA GAAAGGTC  1851  661 UCGUAGAG A UGUACAGU  150 ACTGTACA GGCTAGCTACAACGA CTCTACGA  1852  663 GUAGAGAU G UACAGUGA  151 TCACTGTA GGCTAGCTACAACGA ATCTCTAC  1853	583	AUCUAGCU G UACCUACU	133	AGTAGGTA GGCTAGCTACAACGA AGCTAGAT	1835
607 AGAAGGAA A CAGAAUCU 136 AGATTCTG GGCTAGCTACAACGA TTCCTTCT 1838 612 GAAACAGA A UCUGCAAU 137 ATTGCAGA GGCTAGCTACAACGA TCTGTTTC 1839 616 CAGAAUCU G CAAUCUAU 138 ATAGATTG GGCTAGCTACAACGA AGATTCTG 1840 619 AAUCUGCA A UCUAUAUA 139 TATATAGA GGCTAGCTACAACGA TGCAGATT 1841 623 UGCAAUCU A UAUAUUUA 140 TAAATATA GGCTAGCTACAACGA AGATTGCA 1842 625 CAAUCUAU A UAUUUAUU 141 AATAAATA GGCTAGCTACAACGA ATAGATTG 1843 627 AUCUAUAU A UUUAUUAG 142 CTAATAAA GGCTAGCTACAACGA ATATAGAT 1844 631 AUAUAUUU A UUAGUGAU 143 ATCACTAA GGCTAGCTACAACGA AAATATAT 1845 635 AUUUAUUA G UGAUACAG 144 CTGTATCA GGCTAGCTACAACGA TAATAAAT 1846 638 UAUUAGUG A UACAGGUA 145 TACCTGTA GGCTAGCTACAACGA CACTAATA 1847 640 UUAGUGAU A CAGGUAGA 146 TCTACCTG GGCTAGCTACAACGA ATCACTAA 1848 644 UGAUACAG G UAGACCUU 147 AAGGTCTA GGCTAGCTACAACGA CTGTATCA 1849 648 ACAGGUAG A CCUUUCGU 148 ACGAAAGG GGCTAGCTACAACGA CTGTATCA 1849 648 ACAGGUAG A CCUUUCGU 148 ACGAAAGG GGCTAGCTACAACGA GAAAGGTC 1850 655 GACCUUUC G UAGAGAUU 149 CATCTCTA GGCTAGCTACAACGA GAAAGGTC 1851 661 UCGUAGAG A UGUACAGU 150 ACTGTACA GGCTAGCTACAACGA ATCTCTAC 1852 663 GUAGAGAU G UACAGGUA 151 TCACTGTA GGCTAGCTACAACGA ATCTCTAC 1853	585	CUAGCUGU A CCUACUUC	134	GAAGTAGG GGCTAGCTACAACGA ACAGCTAG	1836
612 GAAACAGA A UCUGCAAU 137 ATTGCAGA GGCTAGCTACAACGA TCTGTTTC 1839 616 CAGAAUCU G CAAUCUAU 138 ATAGATTG GGCTAGCTACAACGA AGATTCTG 1840 619 AAUCUGCA A UCUAUAUA 139 TATATAGA GGCTAGCTACAACGA TGCAGATT 1841 623 UGCAAUCU A UAUAUUUA 140 TAAATATA GGCTAGCTACAACGA AGATTGCA 1842 625 CAAUCUAU A UAUUUAUU 141 AATAAATA GGCTAGCTACAACGA ATAGATTG 1843 627 AUCUAUAU A UUUAUUAG 142 CTAATAAA GGCTAGCTACAACGA ATATAGAT 1844 631 AUAUAUUU A UUAGUGAU 143 ATCACTAA GGCTAGCTACAACGA AAATATAT 1845 635 AUUUAUUA G UGAUACAG 144 CTGTATCA GGCTAGCTACAACGA TAATAAAT 1846 638 UAUUAGUG A UACAGGUA 145 TACCTGTA GGCTAGCTACAACGA CACTAATA 1847 640 UUAGUGAU A CAGGUAGA 146 TCTACCTG GGCTAGCTACAACGA ATCACTAA 1848 644 UGAUACAG G UAGACCUU 147 AAGGTCTA GGCTAGCTACAACGA CTGTATCA 1849 648 ACAGGUAG A CCUUUCGU 148 ACGAAAGG GGCTAGCTACAACGA CTACCTGT 1850 655 GACCUUUC G UAGAGAUG 149 CATCTCTA GGCTAGCTACAACGA GAAAGGTC 1851 661 UCGUAGAG A UGUACAGU 150 ACTGTACA GGCTAGCTACAACGA ATCTCTAC 1852 663 GUAGAGAU G UACAGGUA 151 TCACTGTA GGCTAGCTACAACGA ATCTCTAC 1853	589	CUGUACCU A CUUCAAAG	135	CTTTGAAG GGCTAGCTACAACGA AGGTACAG	1837
616 CAGAAUCU G CAAUCUAU 138 ATAGATTG GGCTAGCTACAACGA AGATTCTG 1840 619 AAUCUGCA A UCUAUAUA 139 TATATAGA GGCTAGCTACAACGA TGCAGATT 1841 623 UGCAAUCU A UAUAUUUA 140 TAAATATA GGCTAGCTACAACGA AGATTGCA 1842 625 CAAUCUAU A UAUUUAUU 141 AATAAATA GGCTAGCTACAACGA ATAGATTG 1843 627 AUCUAUAU A UUUAUUAG 142 CTAATAAA GGCTAGCTACAACGA ATATAGAT 1844 631 AUAUAUUU A UUAGUGAU 143 ATCACTAA GGCTAGCTACAACGA AAATATAT 1845 635 AUUUAUUA G UGAUACAG 144 CTGTATCA GGCTAGCTACAACGA TAATAAAT 1846 638 UAUUAGUG A UACAGGUA 145 TACCTGTA GGCTAGCTACAACGA CACTAATA 1847 640 UUAGUGAU A CAGGUAGA 146 TCTACCTG GGCTAGCTACAACGA ATCACTAA 1848 644 UGAUACAG G UAGACCUU 147 AAGGTCTA GGCTAGCTACAACGA CTGTATCA 1849 648 ACAGGUAG A CCUUUCGU 148 ACGAAAGG GGCTAGCTACAACGA CTACCTGT 1850 655 GACCUUUC G UAGAGAUG 149 CATCTCTA GGCTAGCTACAACGA CTACCTGT 1851 661 UCGUAGAG A UGUACAGU 150 ACTGTACA GGCTAGCTACAACGA CTCTACGA 1852 663 GUAGAGAU G UACAGUGA 151 TCACTGTA GGCTAGCTACAACGA ATCTCTAC 1853	607	AGAAGGAA A CAGAAUCU	136	AGATTCTG GGCTAGCTACAACGA TTCCTTCT	1838
AUCUGCA A UCUAUAUA 139 TATATAGA GGCTAGCTACAACGA TGCAGATT 1841 623 UGCAAUCU A UAUAUUUA 140 TAAATATA GGCTAGCTACAACGA AGATTGCA 1842 625 CAAUCUAU A UAUUUAUU 141 AATAAATA GGCTAGCTACAACGA ATAGATTG 1843 627 AUCUAUAU A UUUAUUAG 142 CTAATAAA GGCTAGCTACAACGA ATATAGAT 1844 631 AUAUAUUU A UUAGUGAU 143 ATCACTAA GGCTAGCTACAACGA AAATATAT 1845 635 AUUUAUUA G UGAUACAG 144 CTGTATCA GGCTAGCTACAACGA TAATAAAT 1846 638 UAUUAGUG A UACAGGUA 145 TACCTGTA GGCTAGCTACAACGA CACTAATA 1847 640 UUAGUGAU A CAGGUAGA 146 TCTACCTG GGCTAGCTACAACGA ATCACTAA 1848 644 UGAUACAG G UAGACCUU 147 AAGGTCTA GGCTAGCTACAACGA CTGTATCA 1849 648 ACAGGUAG A CCUUUCGU 148 ACGAAAGG GGCTAGCTACAACGA CTACCTGT 1850 655 GACCUUUC G UAGAGAUG 149 CATCTCTA GGCTAGCTACAACGA CTACCTGT 1850 661 UCGUAGAG A UGUACAGU 150 ACTGTACA GGCTAGCTACAACGA CTCTACGA 1852 663 GUAGAGAU G UACAGUGA 151 TCACTGTA GGCTAGCTACAACGA ATCTCTAC 1853	612	GAAACAGA A UCUGCAAU	137	ATTGCAGA GGCTAGCTACAACGA TCTGTTTC	1839
G23 UGCAAUCU A UAUAUUUA 140 TAAATATA GGCTAGCTACAACGA AGATTGCA 1842 625 CAAUCUAU A UAUUUAUU 141 AATAAATA GGCTAGCTACAACGA ATAGATTG 1843 627 AUCUAUAU A UUUAUUAG 142 CTAATAAA GGCTAGCTACAACGA ATATAGAT 1844 631 AUAUAUUU A UUAGUGAU 143 ATCACTAA GGCTAGCTACAACGA AAATATAT 1845 635 AUUUAUUA G UGAUACAG 144 CTGTATCA GGCTAGCTACAACGA TAATAAAT 1846 638 UAUUAGUG A UACAGGUA 145 TACCTGTA GGCTAGCTACAACGA CACTAATA 1847 640 UUAGUGAU A CAGGUAGA 146 TCTACCTG GGCTAGCTACAACGA ATCACTAA 1848 644 UGAUACAG G UAGACCUU 147 AAGGTCTA GGCTAGCTACAACGA CTGTATCA 1849 648 ACAGGUAG A CCUUUCGU 148 ACGAAAGG GGCTAGCTACAACGA CTACCTGT 1850 655 GACCUUUC G UAGAGAUG 149 CATCTCTA GGCTAGCTACAACGA CTACCTGT 1850 661 UCGUAGAG A UGUACAGU 150 ACTGTACA GGCTAGCTACAACGA CTCTACGA 1852 663 GUAGAGAU G UACAGUGA 151 TCACTGTA GGCTAGCTACAACGA ATCTCTAC 1853	616	CAGAAUCU G CAAUCUAU	138	ATAGATTG GGCTAGCTACAACGA AGATTCTG	1840
625 CAAUCUAU A UAUUUAUU 141 AATAAATA GGCTAGCTACAACGA ATAGATTG 1843 627 AUCUAUAU A UUUAUUAG 142 CTAATAAA GGCTAGCTACAACGA ATATAGAT 1844 631 AUAUAUUU A UUAGUGAU 143 ATCACTAA GGCTAGCTACAACGA AAATATAT 1845 635 AUUUAUUA G UGAUACAG 144 CTGTATCA GGCTAGCTACAACGA TAATAAAT 1846 638 UAUUAGUG A UACAGGUA 145 TACCTGTA GGCTAGCTACAACGA CACTAATA 1847 640 UUAGUGAU A CAGGUAGA 146 TCTACCTG GGCTAGCTACAACGA ATCACTAA 1848 644 UGAUACAG G UAGACCUU 147 AAGGTCTA GGCTAGCTACAACGA CTGTATCA 1849 648 ACAGGUAG A CCUUUCGU 148 ACGAAAGG GGCTAGCTACAACGA CTACCTGT 1850 655 GACCUUUC G UAGAGAUG 149 CATCTCTA GGCTAGCTACAACGA GAAAGGTC 1851 661 UCGUAGAG A UGUACAGU 150 ACTGTACA GGCTAGCTACAACGA CTCTACGA 1852	619	AAUCUGCA A UCUAUAUA	139	TATATAGA GGCTAGCTACAACGA TGCAGATT	1841
AUCUAUAU A UUUAUUAG 142 CTAATAAA GGCTAGCTACAACGA ATATAGAT 1844 631 AUAUAUUU A UUAGUGAU 143 ATCACTAA GGCTAGCTACAACGA AAATATAT 1845 635 AUUUAUUA G UGAUACAG 144 CTGTATCA GGCTAGCTACAACGA TAATAAAT 1846 638 UAUUAGUG A UACAGGUA 145 TACCTGTA GGCTAGCTACAACGA CACTAATA 1847 640 UUAGUGAU A CAGGUAGA 146 TCTACCTG GGCTAGCTACAACGA ATCACTAA 1848 644 UGAUACAG G UAGACCUU 147 AAGGTCTA GGCTAGCTACAACGA CTGTATCA 1849 648 ACAGGUAG A CCUUUCGU 148 ACGAAAGG GGCTAGCTACAACGA CTACCTGT 1850 655 GACCUUUC G UAGAGAUG 149 CATCTCTA GGCTAGCTACAACGA GAAAGGTC 1851 661 UCGUAGAG A UGUACAGU 150 ACTGTACA GGCTAGCTACAACGA CTCTACGA 1852 663 GUAGAGAU G UACAGUGA 151 TCACTGTA GGCTAGCTACAACGA ATCTCTAC 1853	623	UGCAAUCU A UAUAUUUA	140	TAAATATA GGCTAGCTACAACGA AGATTGCA	1842
AUAUAUUU A UUAGUGAU 143 ATCACTAA GGCTAGCTACAACGA AAATATAT 1845 635 AUUUAUUA G UGAUACAG 144 CTGTATCA GGCTAGCTACAACGA TAATAAAT 1846 638 UAUUAGUG A UACAGGUA 145 TACCTGTA GGCTAGCTACAACGA CACTAATA 1847 640 UUAGUGAU A CAGGUAGA 146 TCTACCTG GGCTAGCTACAACGA ATCACTAA 1848 644 UGAUACAG G UAGACCUU 147 AAGGTCTA GGCTAGCTACAACGA CTGTATCA 1849 648 ACAGGUAG A CCUUUCGU 148 ACGAAAGG GGCTAGCTACAACGA CTACCTGT 1850 655 GACCUUUC G UAGAGAUG 149 CATCTCTA GGCTAGCTACAACGA GAAAGGTC 1851 661 UCGUAGAG A UGUACAGU 150 ACTGTACA GGCTAGCTACAACGA CTCTACGA 1852 663 GUAGAGAU G UACAGUGA 151 TCACTGTA GGCTAGCTACAACGA ATCTCTAC 1853	625	CAAUCUAU A UAUUUAUU	141	AATAAATA GGCTAGCTACAACGA ATAGATTG	1843
635 AUUUAUUA G UGAUACAG 144 CTGTATCA GGCTAGCTACAACGA TAATAAAT 1846 638 UAUUAGUG A UACAGGUA 145 TACCTGTA GGCTAGCTACAACGA CACTAATA 1847 640 UUAGUGAU A CAGGUAGA 146 TCTACCTG GGCTAGCTACAACGA ATCACTAA 1848 644 UGAUACAG G UAGACCUU 147 AAGGTCTA GGCTAGCTACAACGA CTGTATCA 1849 648 ACAGGUAG A CCUUUCGU 148 ACGAAAGG GGCTAGCTACAACGA CTACCTGT 1850 655 GACCUUUC G UAGAGAUG 149 CATCTCTA GGCTAGCTACAACGA GAAAGGTC 1851 661 UCGUAGAG A UGUACAGU 150 ACTGTACA GGCTAGCTACAACGA CTCTACGA 1852	627	AUCUAUAU A UUUAUUAG	142	CTAATAAA GGCTAGCTACAACGA ATATAGAT	1844
638 UAUUAGUG A UACAGGUA 145 TACCTGTA GGCTAGCTACAACGA CACTAATA 1847 640 UUAGUGAU A CAGGUAGA 146 TCTACCTG GGCTAGCTACAACGA ATCACTAA 1848 644 UGAUACAG G UAGACCUU 147 AAGGTCTA GGCTAGCTACAACGA CTGTATCA 1849 648 ACAGGUAG A CCUUUCGU 148 ACGAAAGG GGCTAGCTACAACGA CTACCTGT 1850 655 GACCUUUC G UAGAGAUG 149 CATCTCTA GGCTAGCTACAACGA GAAAGGTC 1851 661 UCGUAGAG A UGUACAGU 150 ACTGTACA GGCTAGCTACAACGA CTCTACGA 1852 663 GUAGAGAU G UACAGUGA 151 TCACTGTA GGCTAGCTACAACGA ATCTCTAC 1853	631	AUAUAUUU A UUAGUGAU	143	ATCACTAA GGCTAGCTACAACGA AAATATAT	1845
640 UUAGUGAU A CAGGUAGA 146 TCTACCTG GGCTAGCTACAACGA ATCACTAA 1848 644 UGAUACAG G UAGACCUU 147 AAGGTCTA GGCTAGCTACAACGA CTGTATCA 1849 648 ACAGGUAG A CCUUUCGU 148 ACGAAAGG GGCTAGCTACAACGA CTACCTGT 1850 655 GACCUUUC G UAGAGAUG 149 CATCTCTA GGCTAGCTACAACGA GAAAGGTC 1851 661 UCGUAGAG A UGUACAGU 150 ACTGTACA GGCTAGCTACAACGA CTCTACGA 1852 663 GUAGAGAU G UACAGUGA 151 TCACTGTA GGCTAGCTACAACGA ATCTCTAC 1853	635	AUUUAUUA G UGAUACAG	144	CTGTATCA GGCTAGCTACAACGA TAATAAAT	1846
644 UGAUACAG G UAGACCUU 147 AAGGTCTA GGCTAGCTACAACGA CTGTATCA 1849 648 ACAGGUAG A CCUUUCGU 148 ACGAAAGG GGCTAGCTACAACGA CTACCTGT 1850 655 GACCUUUC G UAGAGAUG 149 CATCTCTA GGCTAGCTACAACGA GAAAGGTC 1851 661 UCGUAGAG A UGUACAGU 150 ACTGTACA GGCTAGCTACAACGA CTCTACGA 1852 663 GUAGAGAU G UACAGUGA 151 TCACTGTA GGCTAGCTACAACGA ATCTCTAC 1853	638	UAUUAGUG A UACAGGUA	145	TACCTGTA GGCTAGCTACAACGA CACTAATA	1847
648 ACAGGUAG A CCUUUCGU 148 ACGAAAGG GGCTAGCTACAACGA CTACCTGT 1850 655 GACCUUUC G UAGAGAUG 149 CATCTCTA GGCTAGCTACAACGA GAAAGGTC 1851 661 UCGUAGAG A UGUACAGU 150 ACTGTACA GGCTAGCTACAACGA CTCTACGA 1852 663 GUAGAGAU G UACAGUGA 151 TCACTGTA GGCTAGCTACAACGA ATCTCTAC 1853	640	UUAGUGAU A CAGGUAGA	146	TCTACCTG GGCTAGCTACAACGA ATCACTAA	1848
655 GACCUUUC G UAGAGAUG 149 CATCTCTA GGCTAGCTACAACGA GAAAGGTC 1851 661 UCGUAGAG A UGUACAGU 150 ACTGTACA GGCTAGCTACAACGA CTCTACGA 1852 663 GUAGAGAU G UACAGUGA 151 TCACTGTA GGCTAGCTACAACGA ATCTCTAC 1853	644	UGAUACAG G UAGACCUU	147	AAGGTCTA GGCTAGCTACAACGA CTGTATCA	1849
661 UCGUAGAG A UGUACAGU 150 ACTGTACA GGCTAGCTACAACGA CTCTACGA 1852 663 GUAGAGAU G UACAGUGA 151 TCACTGTA GGCTAGCTACAACGA ATCTCTAC 1853	648	ACAGGUAG A CCUUUCGU	148	ACGAAAGG GGCTAGCTACAACGA CTACCTGT	1850
663 GUAGAGAU G UACAGUGA 151 TCACTGTA GGCTAGCTACAACGA ATCTCTAC 1853	655	GACCUUUC G UAGAGAUG	149	CATCTCTA GGCTAGCTACAACGA GAAAGGTC	1851
663 GUAGAGAU G UACAGUGA 151 TCACTGTA GGCTAGCTACAACGA ATCTCTAC 1853	661	UCGUAGAG A UGUACAGU	150	ACTGTACA GGCTAGCTACAACGA CTCTACGA	
	663	GUAGAGAU G UACAGUGA	151	TCACTGTA GGCTAGCTACAACGA ATCTCTAC	1853
995   MGAGAUGU A CAGUGAAA   152  TTTCACTG GGCTAGGTACAACGA ACATCTCT  1854	665	AGAGAUGU A CAGUGAAA	152	TTTCACTG GGCTAGCTACAACGA ACATCTCT	1854

692 UCCCCGAR À UUNDICACC 692 UCCCCGAR À UUNDICACC 695 COGANUU A UNDICACAU 696 UCCCCGAR À UUNDICACC 695 COGANUU A UNDICACAU 697 GANAUURU À CACAUGAC 697 GANAUURU À CACAUGAC 698 COGANUU A UACACAUG 699 ANUURIDACA C AUGACUG 699 ANUURIDACA C AUGACUG 699 ANUURIDACA C AUGACUG 691 UUNDICACA 691 UUNDICACA C AUGACUG 691 UUNDICACA 691 UUNDICACA 691 UUNDICACA 691 UUNDICACA 692 GORAGGAR 693 C CUCCUCAU 694 UUCACAUG 695 COMBRIG 694 UUCACAUG 695 CUCAUCAC 696 GORAGGAR 697 GORAGGAR 697 GORAGGAR 698 CUCAUCAC 698 GORAGGAR 698 CUCAUCAC 698 GORAGGAR 699 CUCAUCAC 699 GORAGGAR 699 COCCOGGU 699 CUCAUCAC 699 GORAGGAR 699 COCCOGGU 699 CUCAUCAC 699 GORAGGAR 699 GORAGGAR 699 COCCOGGU 699 CUCAUCAC 699 COCCOGGU 699 CUCAUCAC 699 COCCOGGU 699 CUCACUC 699 CUCACUC 699 COCCOGGU 699 CUCACUC 699 COCCOGGU 699 COCCOGGU 699 CUCACUC 699 COCCOGGU 699 COCCO	668	GAUGUACA G UGAAAUCC	153	GGATTTCA GGCTAGCTACAACGA TGTACATC	1855
CCCCCARA A UUAUACAC					
GEORGANGE   GEORGANGE   GEOTGETACACAGE ANTTICGO   1858   GEOTGETACACAGE ANTTICGO   1858   GEOTGETACACAGE ANTTICGO   1858   GEOTGETACACAGE ANTTICGO   1859   GEOTGETACACAGE ANTATITIT   1859   GEOTGETACACAGE ANTATITIT   1859   GEOTGETACACACAGE ANTATITIT   1850   GEOTGETACACACAGE ANTATATIT   1852   GEOTGETACACACAGE ANTATATIT   1852   GEOTGETACACAGE ANTATATIT   1852   GEOTGETACACACAGE ANTATATIT   1852   GEOTGETACACACAGE ANTATATIT   1852   GEOTGETACACACAGE ANTATATIT   1852   GEOTGETACACACAGE ANTATATICACACACACACACACACACACACACACACACACA	<del> </del>				
987 GARAUURU A CACAUGAC 157 OTCATGTG GGCTAGCTACAACGA ATAATTTC 1859 869 ARUURURCA C AUGACUGA 158 CAGTCATG GGCTAGCTACAACGA GTATAATT 1860 961 UURURCACA C UGACUGAA 159 TECATCA GGCTAGCTACAACGA GTATAATT 1860 964 UACACAUG A CUGACUGA 159 TECATCA GGCTAGCTACAACGA GTATAATT 1860 978 GGAAGGGA C CUCGUCAU 161 ATGACGAG GGCTAGCTACAACGA CATGTGTA 1862 979 GAGAGGGA G CUCGUCAU 161 ATGACGAG GGCTAGCTACAACGA CATGTGTA 1862 9712 GGGAGCUC G UCCUCCUC 163 GCAGGGAA GGCTACACACGA GACTCCC 1863 9712 GGGAGCUC G UCCUCCUC 163 GCAGGGAA GGCTACCACACGA GACGCCC 1865 9712 CAUUCCCU G CCGGGUUA 164 TAACCCCG GCTAGCTACAACGA GACGCAC 1865 9722 CAUUCCCU G CCGGGUUA 165 TACCCTGA GGCTAGCTACAACGA GACGCAC 1866 9730 GCCGGGUU A CGUCACCU 166 AGGTGAC GGCTAGCTACAACGA CAGCGCAG 1866 9731 GCCCGGGU A CCUCACAU 167 TAGGTGA GGCTAGCTACAACGA CAGCGCAG 1867 9732 CGGGUUAC G UCACCUAA 167 TAGGTGA GGCTAGCTACAACGA CAGCGCAG 1869 9732 CGGGUUAC G UCACCUAA 167 TAGGTGA GGCTAGCTACAACGA CAGCGCAG 1869 9734 GUUACGUC A CAUCACUU 168 AGGTTAGG GGCTAGCTACAACGA CAGCGCAG 1867 9740 GUCACCUA A CAUCACUU 169 CAGTGATG GGCTAGCTACAACGA CAGCTAAC 1871 9742 CACCUAAC A UCACUGUU 170 AACAGTGA GGCTAGCTACAACGA AGGTGAC 1871 9745 CUBACAUC A CUGUUACU 171 AACAGTGA GGCTAGCTACAACGA GACGTTAC 1872 9746 CUBACAUC A CUUUCAAUA 172 TAAAACAG GGCTAGCTACAACGA AGGTGAT 1872 9751 UCCACUU A CUUUAANA 173 TATAAAG GGCTAGCTACAACGA ACAGTGA 1875 9762 UURAAAAA G UUCCCUGU 174 AGTGGAA GGCTAGCTACAACGA ACAGTGA 1875 9773 UCCACUUGA C CUUUGAUC 175 GTGTCAAG GGCTAGCTACAACGA ACAGTGA 1877 9786 GAUCCUC A CUUUGAUC 176 CAAAGTG GGCTAGCTACAACGA ACAGTGA 1877 9787 CACCUUGA C CUUUGAUC 177 GTCAAG GGCTAGCTACAACGA GATGTATTA 1876 9788 GAUCCUC A CUUUGAUC 177 GTCAAG GGCTAGCTACAACGA GATGTATTA 1877 979 GAAGAACG C AUGUUGA 176 GTCAAGAG GGCTAGCTACAACGA GATGTATTA 1877 979 GAAGAACG A CUUUGAUC 177 GTCAAG GGCTAGCTACAACGA GATAGTGA 1877 979 GAAGAACG A CUUUGAUC 178 ATTGGGA GGCTAGCTACAACGA GATAGTGA 1877 979 GAAGAACG A CUUUGAUC 179 GTTCAAG GGCTAGCTACAACGA GATAGTGA 1881 979 GAAGAACG A CUUUGAAC 179 GTTCAAG GGCTAGCTACAACGA GTAAGTG 1881 980 AAUCUGG A CUUUGAA 1880 ATTGCAG GGCTAGCTACAACG	<b></b>				
### ANUMAINAC A CAUGACUGA   158   CAGTCATG GGCTAGCTACAACGA GTATATT   1860   ### 1861   UUADACAC A UGACUGAA   159   TTCAGTCA GGCTAGCTACAACGA GTGTATAA   1861   ### 1862   GGAAGGGA   GCUCGUCAU   161   ATGACGAG GGCTAGCTACAACGA GTGTATAA   1861   ### 1863   GGAAGGGA G CUCGUCAU   161   ATGACGAG GGCTAGCTACAACGA TCCCTTCC   1863   ### 1864   GGAAGCUC G UCADUCCO   162   GGGAATCA GGCTAGCTACAACGA TCCCTTCC   1865   ### 1865   GGAAGCUC G UCADUCCO   162   GGGAATCA GGCTAGCTACAACGA GAGCTACC   1864   ### 1866   GGAAGCUC G UCADUCCO   163   GCAGGGA GGCTAGCTACAACGA GAGGGACT   1865   ### 1867   GCAUCCCU G CCGGGUUA   164   TAACCCGG GGCTAGCTACAACGA AGGGAATT   1866   ### 1866   TAACCCGG GCCTAGCTACAACGA AGGGAATT   1866   ### 1866   TAACCCGG GGCTAGCTACAACGA AGGGAATT   1866   ### 1867   TAAGGTAA GGCTAGCTACAACGA AGCGGACG   1867   ### 1867   GCACGCGU A   165   TAAGGTAA GGCTAACGACA ACCCGGC   1869   ### 1867   GCACGCU A   166   AGGTGAG GGCTAAGCTACAACGA ACCCGGC   1869   ### 1867   GCACGCGU A   167   TAAGGTGA GGCTAACTACAACGA GACGTAAC   1870   ### 1868   ACUCACCU A CUACACU A   169   CAGTGAG GGCTAACTACAACGA GACGTAAC   1871   ### 1869   ACUCACGU A CUACACU A CUACAUG AGCTAACACGA GACGTAAC   1871   ### 1869   ACUCACGU A CUACAUG AGCTAACACGA GACGTAAC   1871   ### 1860   ACUCACGU A CUACAUG AGCTAACACGA GACGTAAC   1872   ### 1860   ACUCACGU A CUACAUG AGCTAACACGA GACTAACACGA GACTAACACGA GACCTAACACGA CACCCAGA CACCACCAGA CACCCAGA CACCCAGA CACCCAGA CACCCAGA CACCCAGA CACCCAGA CAC					
S91					
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727 CCUGCOGG G UUACGUCA 165 TGACGTAA GGCTAGCTACAACGA CCGGCAGG 1867 730 GCCGGGUU A CGUCACCU 166 AGGTGAGC GGCTAGCTACAACGA ACCCGGC 1867 731 GCCGGGUU A CGUCACCU 166 AGGTGAGC GGCTAGCTACAACGA ACCCGGC 1867 732 CGGGUUAC G UCACCUAA 167 TTAGGTGA GGCTAGCTACAACGA GTAACCGG 1869 733 GUUACGUC A CCUAACAU 168 ATGTTAGG GGCTAGCTACAACGA GTAACCGG 1869 734 GUCACCUA A CAUCACUG 169 CAGTGATG GGCTAGCTACAACGA TAGGTGAC 1870 740 GUCACCUA A CAUCACUGU 170 AACAGTGA GGCTAGCTACAACGA TAGGTGAC 1871 742 CACCUAAC A UCACUGUU 171 AGTAACAG GGCTAGCTACAACGA GTAGGTTAG 1873 748 ACAUCACU G UUACUUUA 172 TAAAGTAA GGCTAGCTACAACGA GATGTTAG 1873 748 ACAUCACU G UUACUUUA 172 TAAAGTAA GGCTAGCTACAACGA AGCAGTGA 1875 751 UCACUGUU A CUUUAAAA 173 TTTTAAAG GGCTAGCTACAACGA AGCAGTGA 1875 762 UUAAAAAA G UUUCCACU 174 AGTGGAAA GGCTAGCTACAACGA AGCAGTGA 1876 763 AAGUUUCC A CUUGACC 175 GTGCAAG GGCTAGCTACAACGA AGCAGTGA 1876 764 AAGUUUCC A CUUGACC 175 GTGCAAG GGCTAGCTACAACGA GGAAACTT 1877 773 UCCACUUG A CACUUUGA 176 CTAAAGTG GGCTAGCTACAACGA CGAAGTGA 1876 775 CACUUGA A CACUUUGA 176 TCAAAGTG GGCTAGCTACAACGA CAAGTGGA 1879 7761 ACACUUUG A UCCCUGAU 178 ATCAGGGA GGCTAGCTACAACGA CAAGTGGA 1879 7781 ACACUUUG A UCCCUGAU 178 ATCAGGGA GGCTAGCTACAACGA CAAGTGGT 1880 788 GAUCCCUG A UGGAAAC 179 GTTTTCCA GGCTAGCTACAACGA CAAGTGGT 1880 789 GAAAACGC A UAAUCUGG 181 AGTTATG GGCTAGCTACAACGA CAAGTGT 1880 799 GAAAACGC A UAAUCUGG 182 CCAGATTA GGCTAGCTACAACGA CAAGTGT 1880 802 AACGCAUA A UCUGGGAC 183 GTCCCAGA GGCTAGCTACAACGA CTTTCCAT 1884 802 AACGCAUA A UCUGGGAC 183 GTCCCAGA GGCTAGCTACAACGA CTTTCCAT 1884 803 AAUCUGG A CAGUUAGA 184 TTCTACTG GGCTAGCTACAACGA CCAGTTT 1886 804 AGCACUA A UCUAACA 186 TGATGGA GGCTAGCTACAACGA CCAGTTT 1886 805 AAUCUGG A CAGUAGAA 184 TTCTACTG GGCTAGCTACAACGA CCTTTCTA 1886 806 AAGGCUU A UCAAAUCA 186 TGATGGAG GGCTAGCTACAACGA CCTTTCTA 1886 807 AAUCUGG A CAGUAGAA 187 TTCTATG GGCTAGCTACAACGA CCTTTCTA 1886 808 AAUCUGAAC A UCAAAGAA 189 TTCTATG GGCTAGCTACAACGA CCTTTCTA 1886 809 AAUCUGGA C UAAAAGAA 199 TTCTATG GGCTAGCTACAACGA ATGATTGA 1891 841 UACAACUG A CAAAGAA 199 TTCTATG GGCTAGCTACAACGA ATG	$\vdash$				
730 GCC9GGUU A CGUCACU  166 AGGT9ACG GGCTAGCTACAACGA AACCCGGC 1868  732 CGGGUUAC G UCACCUAA  167 TTAGGTGA GGCTAGCTACAACGA GTAACCG 1869  735 GUUACGUC A CCUAACAU  168 ATGTTAGG GGCTAGCTACAACGA GACGTAAC  1870  740 GUCACCUA A CAUCACUG  169 CAGTGATG GGCTAGCTACAACGA AACGTAAC  1870  742 CACCUAAC A UCACUGUU  170 AACAGTGA GGCTAGCTACAACGA TTAGGTG 1871  742 CACCUAAC A UCACUGUU  171 AGTAACAG GGCTAGCTACAACGA GATGTGAC  748 ACAUCACU G UUACUUAU  171 ATTAAACGA GGCTAGCTACAACGA GATGTTAG  748 ACAUCACU G UUACUUAU  172 TAAAGTAA GGCTAGCTACAACGA ATGGTTGT  749 UCACUGUU A CUUUAANA  173 TTTTAAAG GGCTAGCTACAACGA AGCAGTGT  751 UCACUGUU A CUUUAANA  173 TTTTAAAG GGCTAGCTACAACGA AACAGTGA  768 AAGUUCC A CUUGACC  174 AGTGGAAA GGCTAGCTACAACGA AACAGTGA  768 AAGUUCC A CUUGACC  175 GTGTCAAG GGCTAGCTACAACGA AACAGTGA  7773 UCCACUUG A CACUUGGA  176 TCAAAGTG GGCTAGCTACAACGA CAAAGTGG  1877  778 CACUUGA A CACUUGAU  177 GATCAAAG GGCTAGCTACAACGA CAAAGTGG  1879  7781 ACACUUUG A UCGACU  178 ATCAGGGA GGCTAGCTACAACGA CAAAGTGG  1879  7781 ACACUUGA A UCGAACA  179 GTTTCCA GGCTAGCTACAACGA CAAGTGGA  1879  788 GAUCCCUG A UGGAAAAC  179 GTTTCCA GGCTAGCTACAACGA CAAGTGGA  1880  799 GAAAACC A UAAUCUU  181 AGATTATG GGCTAGCTACAACGA CAAGTGT  1881  802 AACCGAUA A UCUGGGA  182 CCCAGATTA GGCTAGCTACAACGA CAGGATTTCCATC  1882  802 AACCGAUA A UCUGGGA  184 TTCTACTG GGCTAGCTACAACGA CAGGATTTCCATC  1884  802 AACCGAUA A UCUGGGAC  183 GTCCCAG GGCTAGCTACAACGA CAGGATTTCCATC  1884  802 AACCGAUA A UCUGACA  1886  802 AACCGAUA A UCUGACA  1886  803 AAUCUGG A CAGUAGAA  184 TTCTACTG GGCTAGCTACAACGA TTTCCATC  1886  804 AUCUGAC  805 AGGCCUC  806 AGGACUC  807 AGGACAC  807 AGGACAC  807 AGGACAC  808 AGGACAC  808 AGGACAC  809 AAUCUGGA  809 AAUCUGGA  800 AAUCUGAAC  800 AACCGAUA  800 AAUCUGAA  800 AACCGAUA  800 AACCGACACGA  800 A					
732         CGGGUUAC G UCACCUAA         167         TTAGGTGA GGCTAGCTACAAGA GTAACCG         1869           735         GUUACGUC A CCUAACAU         168         ATGTTAGG GGCTAGCTACAACGA GACGTAAC         1870           740         GUCACCUA A CAUCACUG         169         CAGTGATG GGCTAGCTACAACGA TAGGTGAC         1871           742         CACCUAACA A UACUGUU         170         AACAGTGA GGCTAGCTACAACGA GTTAGGTG         1872           745         CUAACAUC A CUGUUACU         171         AGTAACAG GGCTAGCTACAACGA AGTGTATG         1873           748         ACAUCACU G UUACAUUAANA         173         TTTAAAG GGCTAGCTACAACGA AACAGTG         1874           751         UCACUGUU A CUUUAANA         173         TTTAAAG GGCTAGCTACAACGA AACAGTG         1876           762         UUAAAAAA G UUUCCACU         174         AGTGAAA GGCTAGCTACAACGA ACAGTGA         1877           763         AAGUUUC A CUUGACAC         175         GTGTCAAG         GGCTAGCTACAACGA CAAGTGA         1877           773         UCCACUUGA A CUUGACAC         175         GTGTCAAG         GCTAGCTACAACGA CAAGTGA         1877           781         ACACUUGA A CUUGAUCA         177         GTTCAAG GGCTAGCTACAACGA CAAGTGT         1880           795         GAUGAAAA         160         ATTATGCG GCTAGCTACAACGA CAAGGTTTCCAACGA					
735   GUUACGUC A CCUAACAU   168   ATGTTAGG GGCTAGCTACAACGA GACGTAAC   1870     740   GUCACCUA A CAUCACUG   169   CAGTGATG GGCTAGCTACAACGA TAGGTGAC   1871     742   CACCUAAC A UCACUGUU   170   AACAGTGA GGCTAGCTACAACGA GTTAGGTG   1872     745   CUAACAUC A CUGUUACU   171   AGTAACAG GGCTAGCTACAACGA GATGTTAG   1873     748   ACAUCACU G UUACUUUA   172   TAAAGTAA GGCTAGCTACAACGA AGTGTATAG   1873     751   UCACUGUU A CUUUAANA   173   TTTTAAAG GGCTAGCTACAACGA AACAGTGA   1875     762   UUAAAAAA G UUUCCACU   174   AGTGGAAA GGCTAGCTACAACGA ACAGTGA   1875     763   AAGUUUCC A CUUUGACC   175   GTGTCAAG GGCTAGCTACAACGA ACAGTGA   1877     773   UCCACUUG A CACUUUGA   176   TCAAAGTG GGCTAGCTACAACGA CAAGTGGA   1877     775   CACUUGAC A CUUUGAUC   177   ATCAGAGA GGCTAGCTACAACGA CAAGTGGA   1878     775   CACUUGAC A CUUUGAUC   177   ATCAGAGA GGCTAGCTACAACGA CAAGTGGA   1879     778   ACACUUUGA UCCCUGAU   178   ATCAGGGA GGCTAGCTACAACGA CAAAGTG   1880     788   GAUCCCUG A UGGAAAAC   179   GTTTTCCA GGCTAGCTACAACGA CAAGGATC   1881     795   GAUGGAAA A CGCAUAAU   180   ATTATGCG GGCTAGCTACAACGA CAAGGATC   1881     797   UGGAAAAC G CAUAAUU   181   AGATTATG GGCTAGCTACAACGA CATGTTTCCA   1882     802   AACGCAUA A UCUUGGGAC   183   GTCCCAGA GGCTAGCTACAACGA CATGTTTC   1884     802   AACGCAUA A UCUUGGGAC   183   GTCCCAGA GGCTAGCTACAACGA CCCACATT   1886     803   AAUCUGGG A CAGUAGAA   184   TTCTACTG GGCTAGCTACAACGA CCCACATT   1886     804   AUGAAACG G UAGAAAGA   184   TTCTACTG GGCTAGCTACAACGA CCCACATT   1886     805   AAUCUGG A UACUACA   186   TGATGATG GGCTAGCTACAACGA CCCACATT   1886     806   AGGCUUC A UCAUACA   187   TGATATGA GGCTAGCTACAACGA CCCACATT   1886     807   AUGAAACG U AUGAAAU   188   ATTTGAT GGCTAGCTACAACGA CCCACATT   1889     808   AUUCAAAU G CAACGUC   191   GTACGTTG GGCTAGCTACAACGA CTCTTCTA   1889     809   AAUCUGA A UGAAAAGA   193   TTGTTAG GGCTAGCTACAACGA CTGTACTACA     800   ACAGUACA A UGACAAAGA   193   TTGTTAG GGCTAGCTACAACGA CTGTACTT   1894     801   AUGAACGU A CAAAGAA   194   TTCTTTG GGCTAGCTACAACGA TTGTATT   1894     803   A					
740         GUCACCUA A CAUCACUG         169         CAGTGATG GCTAGCTACAACGA TAGGTGAC         1871           742         CACCUARC A UCACUGUU         170         AACAGTGA GGCTAGCTACAACGA GTTAGGTG         1872           745         CUAACAUC A CUGUUACU         171         AGTAACGA GGCTAGCTACAACGA GATGTTAG         1873           748         ACAUCACU G UUACUUA         172         TARAGTAA GGCTAGCTACAACGA AGCAGTGA         1875           751         UCACUGUU A CUUUAAAA         173         TTTTAAAG GGCTAGCTACAACGA AACAGTGA         1875           762         UUAAAAAA G UUUCCACU         174         AGTGGAAA GGCTAGCTACAACGA GAAGTGA         1876           768         AAGUUUCC A CUUUGACAC         175         GTGTCAAG GGCTAGCTACAACGA GAAGTGA         1876           773         UCCACUUGA C ACUUUGA         176         ATCAGGGA GGCTAGCTACAACGA CAAGTGAT         1878           775         CACCUUGA A CCUUGAU         177         GATCAAAG GGCTAGCTACAACGA CAAGTGT         1880           781         ACACCUUGA A UCCCUGAU         178         ATCAGGGA GGCTAGCTACAACGA CAAGGTT         1880           785         GAUGAAAA A CGCAUAAU         180         ATTATGCG GGCTAGCTACAACGA CTTTCCATC         1882           797         UGGAAACC G UAAUCUGG         181         ACATTATGCGGCTAGCTACAACGA GTTTCCATC         1883     <					
742         CACCUAAC A UCACUGUU         170         AACAGTGA GGCTAGCTACAACGA GTTAGGTG         1872           745         CUAACAUC A CUGUUACU         171         AGTAACAG GGCTAGCTACAACGA GATGTTAG         1873           748         ACAUCACU A CUGUUACA         172         TAAAGTAA GGCTAGCTACAACGA AGTGATGT         1874           751         UCACUGUU A CUGUAANA         173         TTTTAAAG GGCTAGCTACAACGA AGAGTGA         1875           762         UUAAAAAA G UUUCCACU         174         AGTGGAAA GGCTAGCTACAACGA GGAAACTT         1877           768         AAGUUUCC A CUGACAC         175         GTGTCAAG GGCTAGCTACAACGA GGAAACTT         1877           773         UCCACUUGA C A CUGUAGAC         176         TCAAAGTG GGCTAGCTACAACGA GAAACTT         1879           781         ACACUUGA C A CUGUAGAC         177         GATCAAAG GGCTAGCTACAACGA GTCAACTGT         1879           788         GAUCCUG A UGGAAAC         179         GTTTCCA GGCTAGCTACAACGA GTAGTTCAACTGA CAAGATCT         1881           795         GAUGGAAA A UGCUGG         181         AGATTATG GGCTAGCTACAACGA GTTTTCA         1882           797         UGGAAAAC G UAAUCUGG         182         CCAGATTA GGCTAGCTACAACGA GTTTTCA         1884           802         AACGCAU A UCUGACA         181         GTCCCAGA GGCTAGCTACAACGA GCCTTTTC         1886					
745         CUAACAUC A CUGUUACU         171         AGTAACAG GGCTAGCTACAACGA GATGTTAG         1873           748         ACAUCACU G UUACUUA         172         TAAAGTAA GGCTAGCTACAACGA AGTGATGT         1874           751         UCACUGUU A CUUUAAAA         173         TTTAAAG GGCTAGCTACAACGA AACAGTGA         1875           762         UUAAAAAA G UUUCCACU         174         AGTGGAAA GGCTAGCTACAACGA TTTTTTAA         1876           768         AAGUUUC A CUUUGAC         175         GTCTCAAG GGCTAGCTACAACGA CTAAGTGA         1877           773         UCCACUUG A CACUUUGAU         176         TCAAAGTG GGCTAGCTACAACGA CAAAGTGT         1877           775         CACUUGA UCCCUGAU         177         GATCAAGG GGCTAGCTACAACGA CAAAGTGT         1880           781         ACACUUUG A UCCCUGAU         178         ATCAGGGA GGCTAGCTACAACGA CAAAGTGT         1880           788         GAUCCCUG A UGGAAAAC         179         GTTTTCCA         GGCTAGCTACAACGA CAAAGTGT         1880           795         GAUGGAAA         160         ATTATGCG GGCTAGCTACAACGA CTTTCCAT         1882           797         UGGAAAAC G AUAAUCUG         181         AGTTACTA GGCTAGCTACAACGA GCTTTCCA         1883           802         AACGCAUA A UCUGGGAC         183         GTCCCAGA GCTAGCTACAACGA TATGCCTT         1886					
748         ACAUCACU G UUACUUUA         172         TAAAGTAA GGCTAGCTACAACGA AGTGATGT 1874           751         UCACUGUU A CUUUAAAA         173         TTTTAAAG GGCTAGCTACAACGA AACAGTGA 1875           762         UUAAAAAA G UUUCCACU         174         AGTGGAAA GGCTAGCTACAACGA TTTTTTAA 1876           768         AAGUUUCC A CUUGACAC         175         GTGTCAAG GGCTAGCTACAACGA GAAACTT 1877           773         UCCACUUG A CACUUUGA         176         TCAAAAG GGCTAGCTACAACGA GTAAAGTG 1878           775         CACUUGA C A CUUUGAUC         177         GATCAAAG GGCTAGCTACAACGA CAAAGTGT 1880           781         ACACUUG A UCCCUGAU         178         ATCAGGGA GGCTAGCTACAACGA CAAAGTGT 1880           788         GAUCGCUG A UGGAAAAC         179         GTTTTCCA GGCTAGCTACAACGA CAAGGATC 1881           795         GAAAACGA A CGCAUAAU         180         ATTATGCG GGCTAGCTACAACGA GTTTTCCAT 1882           797         UGGAAAAC G CAUAAUCU         181         AGATTATG GGCTAGCTACAACGA GTTTTCCAT 1883           799         GAAAACGA A UCUGGGAC         183         GTCCCAGA GGCTAGCTACAACGA GCTTTTCT 1884           802         AACGCAUA A UCUGGGAC         183         GTCCCAGA GGCTAGCTACAACGA CCCAGATT 1886           812         CUGGGACA G UAGAAGG         185         CCTTTCTA GGCTACACACGA CTTTCTA 1886           812         UAGAA					
TITTANAG GGCTAGCTACAACGA AACAGTGA 1875					
762         UUAAAAAA G UUUCCACU         174         AGTGGAAA GGCTAGCTACAACGA TTTTTTAA 1876           768         AAGUUUCC A CUUGACAC         175         GTGTCAAG GGCTAGCTACAACGA GGAAACTT 1877           773         UCCACUUG A CACUUGAA         176         TCAAAGTG GGCTAGCTACAACGA CAAGTGGA 1878           775         CACUUGAC A CUUUGAUC         177         GATCAAGG GGCTAGCTACAACGA CAAGTGG 1880           781         ACACUUGA A UCCCUGAU         178         ATCAGGGA GGCTAGCTACAACGA CAAGTGG 1880           788         GAUCCCUG A UGGAAAAC         179         GTTTTCCA GGCTAGCTACAACGA CAGGGATC 1881           795         GAUGGAAA A CGCAUAAU         180         ATTATGCG GGCTAGCTACAACGA GTTTTCCA 1883           797         UGGAAACC A UAAUCUGG         182         CCAGATTA GGCTAGCTACAACGA GTTTTCCA 1883           802         AACGCAUA A UCUGGGAC         183         CCCAGAT GGCTAGCTACAACGA GTTTTCCA 1885           809         AAUCUGGG A CAGUAGA         184         TTCTACTG GGCTAGCTACAACGA CCCAGATT 1886           812         CUGGGACA G UAGAAAGG         185         CCTTTCTA GGCTAGCTACAACGA CCCAGATT 1886           821         UAGAAAGG         186         TGATGAAG         GCTTTCTA 1888           826         AGGCUCU A UAUCAA         187         TGATGAAG GGCTAGCTACAACGA ATGAAGCA 1890           829         GCUUCAUC A UAUCAA					
768 AAGUUUCC A CUUGACAC 175 GTGTCAAG GGCTAGCTACAACGA GGAAACTT 1877 773 UCCACUUG A CACUUUGA 176 TCAAAGTG GGCTAGCTACAACGA CAAGTGGA 1878 775 CACUUGAC A CUUUGAUC 177 GATCAAAG GGCTAGCTACAACGA GTCAAGTG 1887 781 ACACUUUG A UCCCUGAU 178 ATCAGGGA GGCTAGCTACAACGA CAAACTGT 1880 788 GAUCCCUG A UGGAAAAC 179 GTTTTCCA GGCTAGCTACAACGA CAAACTGT 1881 795 GAUGGAAA A CGCAUAAU 180 ATTATGCG GGCTAGCTACAACGA TTTCCATC 1882 797 UGGAAAAC G CAUAAUCU 181 AGATTATG GGCTAGCTACAACGA TTTCCCATC 1883 799 GAAAACGC A UAAUCUGG 182 CCAGATTA GGCTAGCTACAACGA GTTTTCCA 1883 802 AACGCAUA A UCUGGGAC 183 GTCCCAGA GGCTAGCTACAACGA GTTTTCCA 1885 809 AAUCUGGG A CAGUAGAA 184 TTCTACTG GGCTAGCTACAACGA TATGCGTT 1886 812 CUGGGACA G UAGAAAGG 185 CCTTTCTA GGCTAGCTACAACGA TATGCGTT 1886 812 CUGGGACA G UAGAAAGG 185 CCTTTCTA GGCTAGCTACAACGA TCCCCAGATT 1886 826 AGGGCUUC A UCUCAUCA 186 TGATGAAG GGCTAGCTACAACGA TGTCCCAG 1889 829 GCUUCAUC A UAUCAAAU 188 ATTTGATA GGCTAGCTACAACGA TGTCCCAG 1889 829 GCUUCAUC A UAUCACA 187 TGATATGA GGCTAGCTACAACGA CCTTTCTA 1886 820 AGGCCUUC A UAUCAAAU 188 ATTTGATA GGCTAGCTACAACGA ATGAAGG 1890 831 UUCAUCAU A UCAAAUGC 189 GCATTTGA GGCTAGCTACAACGA ATGATGA 1891 836 CAUAUCAA A UGCAACGU 190 ACGTTTGA GGCTAGCTACAACGA ATGATGA 1891 837 AUCAACG A CAACGUAC 191 GTACGTTG GGCTAGCTACAACGA ATGATGA 1891 838 UAUCAAAU G CAACGUAC 191 GTACGTTG GGCTAGCTACAACGA ATGATGA 1892 841 CAAAUGCA A CGUACAAA 192 TTTTTTGA GGCTAGCTACAACGA ATGATGA 1893 842 TTTTTTTT GGCTAGCTACAACGA ATGATTGA 1893 843 AAUCCAAC G UACAAAA 192 TTTTTTTGA GGCTAGCTACAACGA ATGATTGA 1893 844 CAAAUGCA A CGUACAAA 192 TTTTTTTGA GGCTAGCTACAACGA ATGATTGA 1894 845 AGCAACG UACAAAA 192 TTTTTTTGA GGCTAGCTACAACGA ATGATTGA 1895 846 GUCAACGU A CAAGAAA 192 TTTTTTTGA GGCTAGCTACAACGA ATGATTTCT 1894 847 ACAGAGA A CAGUCC 196 GTCAGAGA GGCTAGCTACAACGA ATGATTGA 1896 848 AAUCAGAC G UCAAAGAA 199 TTTCTTTGA GGCTAGCTACAACGA ATGATTTC 1898 849 GAAAUAGG G CUUCUGAC 196 GTCAGAGA GGCTAGCAACGA CGTATTTC 1898 840 AACAGUCA A CAGGUCU 199 ACCTTTGA GGCTAGCTACAACGA AGGTTGCA 1900 841 CCUGUGAA G CAACGUC 196 GTCAGAGA GGCTAGCAACGA TTCTTTGT 1903 842 ACCAG	<del></del>				
773         UCCACUUG A CACUUGA         176         TCAAAGTG GCTAGCTACAACGA CAAGTGGA 1878           775         CACUUGAC A CUUUGAUC         177         GATCAAAG GCTAGCTACAACGA GTCAAGTG 1879           781         ACACUUG A UGCCUGAU         178         ATCAGGA GCTAGCTACAACGA CAAAGTGT 1880           788         GAUCCUG A UGGAAAAC         179         GTTTTCCA GGCTAGCTACAACGA CAGGATC 1881           795         GAUGGAAA         A CGCAUAAUU         180         ATTATGCG GGCTAGCTACAACGA TTTCCAT 1882           797         UGGAAAAC G CAUAAUCU         181         AGATTATG GGCTAGCTACAACGA GTTTTCCA 1883           799         GAAAACGC A UAAUCUGG         182         CCCAGATTA GGCTAGCTACAACGA GTTTTCCA 1883           802         AACGCAUA A UCUGGGAC         183         GTCCCAGA GGCTAGCTACAACGA TATGCGTT         1885           809         AAUCUGG A CAGUAGAA         184         TCTCATCTA GGCTAGCTACAACGA CCCAGATT         1886           812         CUGGACA G UAGAAAGA         185         CCTTTCTA GGCTAGCTACAACGA CTTCTCTA 1888           821         UAGAAAGG C CUUCAUCA         186         TGATTAGA GGCTAGCTACAACGA CTTCTACA         1887           822         GCUUCAUC A UAUCAAAU         188         ATTTGATA GGCTAGCTACAACGA GATGAACGA CTTAGAAGA         1890           831         UUCAUCAU A UCAAAUGC         189         GCATTTGA					
775         CACUUGAC A CUUUGAUC         177         GATCAAAG GGCTAGCTACAACGA GTCAAGTG         1879           781         ACACUUUG A UCCCUGAU         178         ATCAGGGA GGCTAGCTACAACGA CAAAGTGT         1880           788         GAUCCCUG A UGGAAAAC         179         GTTTTCCA GGCTAGCTACAACGA CAAGGATC         1881           795         GAUGGAAA A CGCAUAAU         180         ATTATGGG GGCTAGCTACAACGA TTTCCATC         1882           797         UGGAAACG C AUAAUCUG         181         AGATTATG GGCTAGCTACAACGA GTTTTCCAT         1883           799         GAAAACGCA A UAAUCUGG         182         CCCAGATTA GGCTAGCTACAACGA GTTTTCCAT         1884           802         AACGCAUA A UCUGGGAC         183         GTCCCAGA GGCTAGCTACAACGA ATGCGTT         1886           809         AAUCUGGG A CAGUAGAA         184         TTCTACTG GGCTAGCTACAACGA ATGCGCTT         1886           812         CUGGGACA G UAGAAAGG         185         CCTTTCTA GGCTAGCTACAACGA TCCCCAG 1887           821         UAGAAAGG G CUUCAUCA         186         TGATGAGG         GCTAGCTACAACGA CCTTTCTA 1888           826         AGGCUUC A UCAUAUCA         187         TGATATGA GGCTAGCTACAACGA ATGAGA 1891           831         UUCALCAU A UCAAAUGC         189         GCATTTGA GGCTAGCTACAACGA ATGATATTG         1892           832 <td></td> <td></td> <td></td> <td></td> <td></td>					
781         ACACUUUG A UCCCUGAU         178         ATCAGGGA GGCTAGCTACAACGA CAAAGTCT         1880           788         GAUCCCUG A UGGAAAAC         179         GTTTTCCA GGCTAGCTACAACGA CAGGGATC         1881           795         GAUGGAAA A CGCAUAAU         180         ATTATGCG GGCTAGCTACAACGA CTTTCCATC         1882           797         UGGAAAACG C A UAAUCUG         181         AGATTATG GGCTAGCTACAACGA GTTTTCCA         1883           799         GAAAACGC A UAAUCUGG         182         CCAGATTA GGCTAGCTACAACGA GCGTTTTC         1884           802         AACGCAUA A UCUGGGAC         183         GTCCCAGA GCCTAGCTACAACGA CCCAGATT         1885           809         AAUCUGG A CAGUAGAA         184         TTCTACTG GGCTAGCTACAACGA TATGCCTT         1886           812         CUGGGACA G UAGAAAGG         185         CCTTTCTA GGCTAGCTACAACGA TATGCCTAG         1887           821         UAGAAAGG G CUUCAUCA         186         TGATATGA GGCTAGCTACAACGA TATGACGA TAGACCAT         1889           822         GCUUCAUC A UAUCAAAU         188         ATTGATA GGCTAGCTACAACGA GATGATACA         1890           831         UUCADCAU A UCAAAUGC         189         GCATTTGA GGCTAGCTACAACGA ATGATATATG         1891           838         UAUCAAAU         180         GTACGTTG GGCTAGCTACAACGA ATTGATATG         1893 <td></td> <td></td> <td></td> <td></td> <td></td>					
788         GAUCCCUG A UGGAAAAC         179         GTTTTCCA GGCTAGCTACAACGA CAGGGATC         1881           795         GAUGGAAA A CGCAUAAU         180         ATTATGCG GGCTAGCTACAACGA TTTCCATC         1882           797         UGGAAAAC G CAUAAUCU         181         AGATTATG GGCTAGCTACAACGA GTTTTCCA         1883           799         GAAAACGC A UAAUCUGG         182         CCAGATTA GGCTAGCTACAACGA GCTTTTC         1884           802         AACGCAUA A UCUGGGAC         183         GTCCCAGA GGCTAGCTACAACGA TATGCGTT         1885           809         AAUCUGGG A CAGUAGAA         184         TTCTACTG GGCTAGCTACAACGA CCCAGATT         1886           812         CUGGGACA G UAGAAAGG         185         CCTTTCTA GGCTAGCTACAACGA CCTTTCTA         1887           821         UAGAAAGG G CUUCAUCA         186         TGATGAG GGCTAGCTACAACGA CCTTTCTA         1888           826         AGGGCUCA U CAUAUCA         187         TGATATGA GGCTACAACGA GAAGACCT         1889           829         GCUUCAUC A UCAUAUCA         188         ATTTGATA GGCTACAACGA GAAGAACCA         1891           831         UUCADCAU A UCAAAUGC         189         GCATTGA GGCTACCAACGA ATGATGAA         1891           838         UAUCAAAU G CAACGUA         191         GTACGTTG GGCTACCAACGA ATTTGATA         1892					
795         GAUGGAAA         CGCAUAAU         180         ATTATGCG         GGCTAGCTACAACGA         TTTCCATC         1882           797         UGGAAAAC         G CAUAAUCU         181         AGATTATG         GGCTAGCTACAACGA         GTTTTCCA         1883           799         GAAAACGC         A UAUCUGG         182         CCAGATTA         GGCTAGCTACAACGA         GCGTTTTC         1884           802         AACGCAUA         A UCUGGGAC         183         GTCCCAGA         GGCTAGCTACAACGA         CCCAGATT         1885           809         AAUCUGGG         A CAGUAGAA         184         TTCTACTG         GGCTAGCTACAACGA         CCCAGATT         1886           812         CUGGGACA         GUAGAAAGG         185         CCTTTCTA         GGCTAGCTACAACGA         CCCAGATT         1886           821         UAGAAAGG         G UAGAAAGG         187         TGATATTGA         GGCTAGCTACAACGA         CCTTTCTA         1888           826         AGGGCUUC         A UAUCAAAU         188         ATTTGATA         GGCTAGCTACAACGA         GAAGCCCT         1889           829         GCUUCAU         A UAUCAAAU         189         GCATTTGA         GGCTAGCTACAACGA         ATTGATATG         1891           831         UUCAUCA					
797         UGGAAAAC G CAUAAUCU         181         AGATTATG GGCTAGCTACAACGA GTTTTCCA         1883           799         GAAAACGC A UAAUCUGG         182         CCAGATTA GGCTAGCTACAACGA GCGTTTCC         1884           802         AACGCAUA A UCUGGGAC         183         GTCCCAGA GGCTAGCTACAACGA TATGCGTT         1885           809         AAUCUGGG A CAGUAGAA         184         TTCTACTG GGCTAGCTACAACGA CCCAGATT         1886           812         CUGGGACA G UAGAAAGG         185         CCTTTCTA GGCTAGCTACAACGA TGTCCCAG         1887           821         UAGAAAGG G CUUCAUCA         186         TGATGAG GGCTAGCACACGA CCTTCTA         1888           826         AGGGCUUC A UCAUAUCA         187         TGATATGA GGCTAGCACACGA GAGCCCT         1889           829         GCUUCAUC A UAUCAAAU         188         ATTTGATA GGCTAGCACACA ATGATGAA         1891           831         UUCAUCAU A UCAAAUCC         189         GCATTTGA GGCTAGCACACAA ATGATGAA         1891           836         CAUAUCAA A UGCAACGU         190         ACGTTGCA GGCTAGCACACAA ATGATGAA         1892           831         UAUCAAAU G CAACGUA         191         GTACGTG GGCTAGCACACAA ATTTGATA         1892           834         UAUCAAAU G CAACGUA         191         TTTGTACG GGCTAGCTACAACGA ATTTGCATTTGA         1893 <tr< td=""><td></td><td></td><td></td><td></td><td></td></tr<>					
799         GAAAACGC A UAAUCUGG         182         CCAGATTA GGCTAGCTACAACGA GCGTTTC         1884           802         AACGCAUA A UCUGGGAC         183         GTCCCAGA GGCTAGCTACAACGA TATGCGTT         1885           809         AAUCUGGG A CAGUAGAA         184         TTCTACTG GGCTAGCTACAACGA CCCAGATT         1886           812         CUGGGACA G UAGAAAGG         185         CCTTTCTA GGCTAGCTACAACGA TGTCCCAG         1887           821         UAGAAAGG G CUUCAUCA         186         TGATATGA GGCTAGCTACAACGA CCTTCTTA         1888           826         AGGGCUUC A UCAUAUCA         187         TGATATGA GGCTAGCTACAACGA GAAGCCCT         1889           829         GCUUCAUC A UAUCAAAU         188         ATTTGATA GGCTAGCTACAACGA GATGAAGC         1890           831         UUCAUCAU A UCAAAUGC         189         GCATTTGA GGCTAGCTACAACGA ATGATGAA         1891           836         CAUAUCAA A UGCAACGU         190         ACGTTGCA GGCTAGCTACAACGA ATGATATA         1892           838         UAUCAAAUG G CAACGUAC         191         GTACGTTG GGCTAGCTACAACGA ATTTGATA         1893           841         CAAAUGCA A CGUACAAA         192         TTTGTAC GGCTAGCTACAACGA TGCATTG         1894           843         AAUGCAACGU A CAAAGAAA         193         TCTTTGTA GGCTAGCTACAACGA ACGTTGCA         1896					
802         AACGCAUA A UCUGGGAC         183         GTCCCAGA GGCTAGCTACAACGA TATGCGTT         1885           809         AAUCUGGG A CAGUAGAA         184         TTCTACTG GGCTAGCTACAACGA CCCAGATT         1886           812         CUGGGACA G UAGAAAGG         185         CCTTTCTA GGCTAGCTACAACGA TGTCCCAG         1887           821         UAGAAAGG G CUUCAUCA         186         TGATATGA GGCTAGCTACAACGA CTTTCTA         1888           826         AGGGCUUC A UCAUAUCA         187         TGATATGA GGCTAGCTACAACGA GAAGCCCT         1889           829         GCUUCAUC A UAUCAAAU         188         ATTTGATA GGCTAGCTACAACGA GATGAAGC         1890           831         UUCAUCAU A UCAAAUGC         189         GCATTTGA GGCTAGCTACAACGA ATGATGAA         1891           836         CAUAUCAA A UGCAACGU         190         ACGTTGCA GGCTAGCTACAACGA ATGATTATG         1892           838         UAUCAAAU G CAACGUAC         191         GTACGTTG GGCTAGCTACAACGA ATTTGATA         1893           841         CAAAUGCA A CGUACAAA         192         TTTGTACG GGCTAGCTACAACGA TGCATTG         1894           843         AAUGCAAC G UACAAAGA         193         TCTTTGTA GGCTACCAACGA ACGTTGCAT         1895           845         UGCAACGU A CAAAGAAA         194         TTTCTTG GGCTAGCTACAACGA ACGTTGCA         1896 </td <td></td> <td></td> <td></td> <td></td> <td></td>					
809 AAUCUGGG A CAGUAGAA 184 TTCTACTG GGCTAGCTACAACGA CCCAGATT 1886 812 CUGGGACA G UAGAAAGG 185 CCTTTCTA GGCTAGCTACAACGA TGTCCCAG 1887 821 UAGAAAGG G CUUCAUCA 186 TGATGAAG GGCTAGCTACAACGA CCTTTCTA 1888 826 AGGGCUUC A UCAUAUCA 187 TGATATGA GGCTAGCTACAACGA CCTTTCTA 1888 829 GCUUCAUC A UAUCAAAU 188 ATTTGATA GGCTAGCTACAACGA GAAGCCCT 1889 831 UUCAUCAU A UCAAAUGC 189 GCATTTGA GGCTAGCTACAACGA ATGATGAA 1891 836 CAUAUCAA A UGCAACGU 190 ACGTTGCA GGCTAGCTACAACGA ATGATGAA 1891 838 UAUCAAAU G CAACGUAC 191 GTACGTTG GGCTAGCAACGA ATTTGATAT 1893 841 CAAAUGCA A CGUACAAA 192 TTTGTACG GGCTAGCAACGA ATTTGATAT 1894 843 AAUGCAAC G UACAAAGA 193 TCTTTGTA GGCTAGCTACAACGA ATGTTGCAT 1895 845 UGCAACGU A CAAAGAAA 194 TTTCTTTG GGCTAGCTACAACGA ACGTTGCA 1896 853 ACAAAGAA A UAGGGCUU 195 AAGCCCTA GGCTAGCTACAACGA TCTTTGT 1897 858 GAAAUAGG G CUUCUGAC 196 GTCAGAAG GGCTAGCTACAACGA CCTATTTC 1898 865 GGCUUCUG A CCUGUGAA 197 TTCACAGG GGCTAGCTACAACGA CCTATTTC 1898 865 GGCUUCUG A CCUGUGAA 197 TTCACAGG GGCTAGCTACAACGA CAGAAGCC 1899 869 UCUGACCU G UGAAGCAA 198 TTGCTTCA GGCTAGCTACAACGA AGGTCAGA 1900 874 CCUGUGAA G CAACAGUC 199 GACTGTTG GGCTAGCTACAACGA TCCACAGG 1901 877 GUGAAGCA A CAGUCAAU 200 ATTGACTG GGCTAGCTACAACGA TCCTCAC 1902 880 AAGCAACA G UCAAUGGG 201 CCCATTGA GGCTAGCTACAACGA TGCTTCAC 1903 884 AACAGUCA A UGGGCAUU 202 AATGCCC GGCTAGCTACAACGA CCATTGAC 1904 888 GUCAAUGG G CAUUUGUA 203 TACAAATG GGCTAGCTACAACGA CCATTGAC 1905					
812 CUGGGACA G UAGAAAGG 185 CCTTTCTA GGCTAGCTACAACGA TGTCCCAG 1887 821 UAGAAAGG G CUUCAUCA 186 TGATGAAG GGCTAGCTACAACGA CCTTTCTA 1888 826 AGGGCUUC A UCAUAUCA 187 TGATATGA GGCTAGCTACAACGA GAAGCCCT 1889 829 GCUUCAUC A UAUCAAAU 188 ATTTGATA GGCTAGCTACAACGA GAAGCCCT 1889 831 UUCAUCAU A UCAAAUGC 189 GCATTTGA GGCTAGCTACAACGA ATGATGAA 1891 836 CAUAUCAA A UGCAACGU 190 ACGTTGCA GGCTAGCTACAACGA ATGATGAA 1892 838 UAUCAAAU G CAACGUAC 191 GTACGTTG GGCTAGCTACAACGA ATTTGATAT 1893 841 CAAAUGCA A CGUACAAA 192 TTTGTACG GGCTAGCTACAACGA ATTTGATAT 1893 843 AAUGCAAC G UACAAAGA 193 TCTTTGTA GGCTAGCTACAACGA TGCATTTG 1894 843 AAUGCAAC G UACAAAGA 194 TTTCTTTG GGCTAGCTACAACGA ACGTTGCAT 1895 845 UGCAACGU A CAAAGAAA 194 TTTCTTTG GGCTAGCTACAACGA ACGTTGCA 1896 853 ACAAAGAA A UAGGGCUU 195 AAGCCCTA GGCTAGCTACAACGA TCTTTGT 1897 858 GAAAUAGG G CUUCUGAC 196 GTCAGAAG GGCTAGCTACAACGA CCTATTTC 1898 865 GGCUUCUG A CCUGUGAA 197 TTCACAGG GGCTAGCTACAACGA CAGAAGCC 1899 869 UCUGACCU G UGAAGCAA 198 TTGCTTCA GGCTAGCTACAACGA AGGTCAGA 1900 874 CCUGUGAA G CAACAGUC 199 GACTGTTG GGCTAGCTACAACGA TCCACGG 1901 877 GUGAAGCA A CAGUCAAU 200 ATTGACTG GGCTAGCTACAACGA TGCTTCAC 1902 880 AAGCAACA G UCAAUGGG 201 CCCATTGA GGCTAGCTACAACGA TGCTTCAC 1903 884 AACAGUCA A UGGGCAUU 202 AATGCCCA GGCTAGCTACAACGA TGACTGTT 1904 888 GUCAAUGG G CAUUUGUA 203 TACAAATG GGCTAGCTACAACGA CCATTGAC 1905					
821 UAGAAAGG G CUUCAUCA 186 TGATGAAG GGCTAGCTACAACGA CCTTTCTA 1888 826 AGGGCUUC A UCAUAUCA 187 TGATATGA GGCTAGCTACAACGA GAAGCCCT 1889 829 GCUUCAUC A UAUCAAAU 188 ATTTGATA GGCTAGCTACAACGA GATGAAGC 1890 831 UUCAUCAU A UCAAAUGC 189 GCATTTGA GGCTAGCTACAACGA ATGATGAA 1891 836 CAUAUCAA A UGCAACGU 190 ACGTTGCA GGCTAGCTACAACGA ATGATATG 1892 838 UAUCAAAU G CAACGUAC 191 GTACGTTG GGCTAGCTACAACGA ATTTGATA 1893 841 CAAAUGCA A CGUACAAA 192 TTTGTACG GGCTAGCTACAACGA ATTTGATA 1894 843 AAUGCAAC G UACAAAGA 193 TCTTTGTA GGCTAGCTACAACGA GTTGCATT 1895 845 UGCAACGU A CAAAGAAA 194 TTTCTTTG GGCTAGCTACAACGA ACGTTGCA 1896 853 ACAAAGAA A UAGGGCUU 195 AAGCCCTA GGCTAGCTACAACGA ACGTTGCA 1897 858 GAAAUAGG G CUUCUGAC 196 GTCAGAAG GGCTAGCTACAACGA CCTATTTC 1898 865 GGCUUCUG A CCUGUGAA 197 TTCACAGG GGCTAGCTACAACGA CAGAAGCC 1899 869 UCUGACCU G UGAAGCAA 198 TTGCTTCA GGCTAGCTACAACGA AGGTCAGA 1900 874 CCUGUGAA G CAACAGUC 199 GACTGTTG GGCTAGCTACAACGA TGCTTCAC 1902 877 GUGAAGCA A CAGUCAAU 200 ATTGACTG GGCTAGCTACAACGA TGCTTCAC 1902 880 AAGCAACA G UCAAUGGG 201 CCCATTGA GGCTAGCTACAACGA TGCTTCAC 1903 884 AACAGUCA A UGGGCAUU 202 AATGCCCA GGCTAGCTACAACGA TGCTTCAT 1903 884 AACAGUCA A UGGGCAUU 202 AATGCCCA GGCTAGCTACAACGA TGCTTCAT 1903 888 GUCAAUGG G CAUUUGUA 203 TACAAATG GGCTAGCTACAACGA TGACTGCT 1904					
826 AGGGCUUC A UCAUAUCA 187 TGATATGA GGCTAGCTACAACGA GAAGCCCT 1889 829 GCUUCAUC A UAUCAAAU 188 ATTTGATA GGCTAGCTACAACGA GATGAAGC 1890 831 UUCAUCAU A UCAAAUGC 189 GCATTTGA GGCTAGCTACAACGA ATGATGAA 1891 836 CAUAUCAA A UGCAACGU 190 ACGTTGCA GGCTAGCTACAACGA ATGATGAA 1892 838 UAUCAAAU G CAACGUAC 191 GTACGTTG GGCTAGCTACAACGA ATTTGATA 1893 841 CAAAUGCA A CGUACAAA 192 TTTGTACG GGCTAGCTACAACGA TGCATTTG 1894 843 AAUGCAAC G UACAAAGA 193 TCTTTGTA GGCTAGCTACAACGA GTTGCATT 1895 845 UGCAACGU A CAAAGAAA 194 TTTCTTTG GGCTAGCTACAACGA ACGTTGCA 1896 853 ACAAAGAA A UAGGGCUU 195 AAGCCCTA GGCTAGCTACAACGA TCTTTTGT 1897 858 GAAAUAGG G CUUCUGAC 196 GTCAGAAG GGCTAGCTACAACGA CCTATTTC 1898 865 GGCUUCUG A CCUGUGAA 197 TTCACAGG GGCTAGCTACAACGA CAGAAGCC 1899 869 UCUGACCU G UGAAGCAA 198 TTGCTTCA GGCTAGCTACAACGA AGGTCAGA 1900 874 CCUGUGAA G CAACAGUC 199 GACTGTTG GGCTAGCTACAACGA TGCTTCAC 1902 877 GUGAAGCA A CAGUCAAU 200 ATTGACTG GGCTAGCTACAACGA TGCTTCAC 1902 880 AAGCAACA G UCAAUGGG 201 CCCATTGA GGCTAGCTACAACGA TGTTCCT 1903 884 AACAGUCA A UGGGCAUU 202 AATGCCCA GGCTAGCTACAACGA TGACTGTT 1904 888 GUCAAUGG G CAUUUGUA 203 TACAAATG GGCTAGCTACAACGA CCATTGAC 1905	821				
B31 UUCAUCAU A UCAAAUGC 189 GCATTTGA GGCTAGCTACAACGA ATGATGAA 1891 B36 CAUAUCAA A UGCAACGU 190 ACGTTGCA GGCTAGCTACAACGA ATGATATG 1892 B38 UAUCAAAU G CAACGUAC 191 GTACGTTG GGCTAGCTACAACGA ATTTGATA 1893 B41 CAAAUGCA A CGUACAAA 192 TTTGTACG GGCTAGCTACAACGA TGCATTTG 1894 B43 AAUGCAAC G UACAAAGA 193 TCTTTGTA GGCTAGCTACAACGA GTTGCATT 1895 B45 UGCAACGU A CAAAGAAA 194 TTTCTTTG GGCTAGCTACAACGA ACGTTGCA 1896 B53 ACAAAGAA A UAGGGCUU 195 AAGCCCTA GGCTAGCTACAACGA ACGTTGCA 1897 B58 GAAAUAGG G CUUCUGAC 196 GTCAGAAG GGCTAGCTACAACGA CCTATTTC 1898 B65 GGCUUCUG A CCUGUGAA 197 TTCACAGG GGCTAGCTACAACGA CGTAGAGCC 1899 B69 UCUGACCU G UGAAGCAA 198 TTGCTTCA GGCTAGCTACAACGA AGGTCAGA 1900 B74 CCUGUGAA G CAACAGUC 199 GACTGTTG GGCTAGCTACAACGA TTCACAGG 1901 B77 GUGAAGCA A CAGUCAAU 200 ATTGACTG GGCTAGCTACAACGA TGCTTCAC 1902 B80 AAGCAACA G UCAAUGGG 201 CCCATTGA GGCTAGCTACAACGA TGTTGCTT 1903 B84 AACAGUCA A UGGGCAUU 202 AATGCCCA GGCTAGCTACAACGA TGACTGTT 1904 B88 GUCAAUGG G CAUUUGUA 203 TACAAATG GGCTAGCTACAACGA CCATTGAC 1905	826				
831 UUCAUCAU A UCAAAUGC 189 GCATTTGA GGCTAGCTACAACGA ATGATGAA 1891 836 CAUAUCAA A UGCAACGU 190 ACGTTGCA GGCTAGCTACAACGA ATGATATG 1892 838 UAUCAAAU G CAACGUAC 191 GTACGTTG GGCTAGCTACAACGA ATTTGATA 1893 841 CAAAUGCA A CGUACAAA 192 TTTGTACG GGCTAGCTACAACGA TGCATTTG 1894 843 AAUGCAAC G UACAAAGA 193 TCTTTGTA GGCTAGCTACAACGA GTTGCATT 1895 845 UGCAACGU A CAAAGAAA 194 TTTCTTTG GGCTAGCTACAACGA ACGTTGCA 1896 853 ACAAAGAA A UAGGGCUU 195 AAGCCCTA GGCTAGCTACAACGA ACGTTGCA 1897 858 GAAAUAGG G CUUCUGAC 196 GTCAGAAG GGCTAGCTACAACGA CCTATTTC 1898 865 GGCUUCUG A CCUGUGAA 197 TTCACAGG GGCTAGCTACAACGA CAGAAGCC 1899 869 UCUGACCU G UGAAGCAA 198 TTGCTTCA GGCTAGCTACAACGA AGGTCAGA 1900 874 CCUGUGAA G CAACAGUC 199 GACTGTTG GGCTAGCTACAACGA TTCACAGG 1901 877 GUGAAGCA A CAGUCAAU 200 ATTGACTG GGCTAGCTACAACGA TGCTTCAC 1902 880 AAGCAACA G UCAAUGGG 201 CCCATTGA GGCTAGCTACAACGA TGTTGCTT 1903 884 AACAGUCA A UGGGCAUU 202 AATGCCCA GGCTAGCTACAACGA TGACTGTT 1904 888 GUCAAUGG G CAUUUGUA 203 TACAAATG GGCTAGCTACAACGA CCATTGAC 1905	829	GCUUCAUC A UAUCAAAU	188	ATTTGATA GGCTAGCTACAACGA GATGAAGC	1890
836 CAUAUCAA A UGCAACGU 190 ACGTTGCA GGCTAGCTACAACGA TTGATATG 1892 838 UAUCAAAU G CAACGUAC 191 GTACGTTG GGCTAGCTACAACGA ATTTGATA 1893 841 CAAAUGCA A CGUACAAA 192 TTTGTACG GGCTAGCTACAACGA TGCATTTG 1894 843 AAUGCAAC G UACAAAGA 193 TCTTTGTA GGCTAGCTACAACGA GTTGCATT 1895 845 UGCAACGU A CAAAGAAA 194 TTTCTTTG GGCTAGCTACAACGA ACGTTGCA 1896 853 ACAAAGAA A UAGGGCUU 195 AAGCCCTA GGCTAGCTACAACGA ACGTTGCA 1897 858 GAAAUAGG G CUUCUGAC 196 GTCAGAAG GGCTAGCTACAACGA CCTATTTC 1898 865 GGCUUCUG A CCUGUGAA 197 TTCACAGG GGCTAGCTACAACGA CAGAAGCC 1899 869 UCUGACCU G UGAAGCAA 198 TTGCTTCA GGCTAGCTACAACGA AGGTCAGA 1900 874 CCUGUGAA G CAACAGUC 199 GACTGTTG GGCTAGCTACAACGA TTCACAGG 1901 877 GUGAAGCA A CAGUCAAU 200 ATTGACTG GGCTAGCTACAACGA TGCTTCAC 1902 880 AAGCAACA G UCAAUGGG 201 CCCATTGA GGCTAGCTACAACGA TGTTGCTT 1903 884 AACAGUCA A UGGGCAUU 202 AATGCCCA GGCTAGCTACAACGA TGACTGTT 1904 888 GUCAAUGG G CAUUUGUA 203 TACAAATG GGCTAGCTACAACGA CCATTGAC 1905	831				
838 UAUCAAAU G CAACGUAC 191 GTACGTTG GGCTAGCTACAACGA ATTTGATA 1893 841 CAAAUGCA A CGUACAAA 192 TTTGTACG GGCTAGCTACAACGA TGCATTTG 1894 843 AAUGCAAC G UACAAAGA 193 TCTTTGTA GGCTAGCTACAACGA GTTGCATT 1895 845 UGCAACGU A CAAAGAAA 194 TTTCTTTG GGCTAGCTACAACGA ACGTTGCA 1896 853 ACAAAGAA A UAGGGCUU 195 AAGCCCTA GGCTAGCTACAACGA TTCTTTGT 1897 858 GAAAUAGG G CUUCUGAC 196 GTCAGAAG GGCTAGCTACAACGA CCTATTTC 1898 865 GGCUUCUG A CCUGUGAA 197 TTCACAGG GGCTAGCTACAACGA CAGAAGCC 1899 869 UCUGACCU G UGAAGCAA 198 TTGCTTCA GGCTAGCTACAACGA AGGTCAGA 1900 874 CCUGUGAA G CAACAGUC 199 GACTGTTG GGCTAGCTACAACGA TTCACAGG 1901 877 GUGAAGCA A CAGUCAAU 200 ATTGACTG GGCTAGCTACAACGA TGCTTCAC 1902 880 AAGCAACA G UCAAUGGG 201 CCCATTGA GGCTAGCTACAACGA TGTTGCTT 1903 884 AACAGUCA A UGGGCAUU 202 AATGCCCA GGCTAGCTACAACGA TGACTGTT 1904 888 GUCAAUGG G CAUUUGUA 203 TACAAATG GGCTAGCTACAACGA CCATTGAC 1905	836	CAUAUCAA A UGCAACGU	190	ACGTTGCA GGCTAGCTACAACGA TTGATATG	1892
AAUGCAAC G UACAAAGA 193 TCTTTGTA GGCTAGCTACAACGA GTTGCATT 1895  845 UGCAACGU A CAAAGAAA 194 TTTCTTTG GGCTAGCTACAACGA ACGTTGCA 1896  853 ACAAAGAA A UAGGGCUU 195 AAGCCCTA GGCTAGCTACAACGA TTCTTTGT 1897  858 GAAAUAGG G CUUCUGAC 196 GTCAGAAG GGCTAGCTACAACGA CCTATTTC 1898  865 GGCUUCUG A CCUGUGAA 197 TTCACAGG GGCTAGCTACAACGA CAGAAGCC 1899  869 UCUGACCU G UGAAGCAA 198 TTGCTTCA GGCTAGCTACAACGA AGGTCAGA 1900  874 CCUGUGAA G CAACAGUC 199 GACTGTTG GGCTAGCTACAACGA TTCACAGG 1901  877 GUGAAGCA A CAGUCAAU 200 ATTGACTG GGCTAGCTACAACGA TGCTTCAC 1902  880 AAGCAACA G UCAAUGGG 201 CCCATTGA GGCTAGCTACAACGA TGTTGCTT 1903  884 AACAGUCA A UGGGCAUU 202 AATGCCCA GGCTAGCTACAACGA TGACTGTT 1904  888 GUCAAUGG G CAUUUGUA 203 TACAAATG GGCTAGCTACAACGA CCATTGAC 1905	838	UAUCAAAU G CAACGUAC	191	GTACGTTG GGCTAGCTACAACGA ATTTGATA	
AUGCAACG UACAAGA 193 TCTTTGTA GGCTAGCTACAACGA GTTGCATT 1895  845 UGCAACGU A CAAAGAAA 194 TTTCTTTG GGCTAGCTACAACGA ACGTTGCA 1896  853 ACAAAGAA A UAGGGCUU 195 AAGCCCTA GGCTAGCTACAACGA ACGTTGCA 1897  858 GAAAUAGG G CUUCUGAC 196 GTCAGAAG GGCTAGCTACAACGA CCTATTTC 1898  865 GGCUUCUG A CCUGUGAA 197 TTCACAGG GGCTAGCTACAACGA CAGAAGCC 1899  869 UCUGACCU G UGAAGCAA 198 TTGCTTCA GGCTAGCTACAACGA AGGTCAGA 1900  874 CCUGUGAA G CAACAGUC 199 GACTGTTG GGCTAGCTACAACGA TTCACAGG 1901  877 GUGAAGCA A CAGUCAAU 200 ATTGACTG GGCTAGCTACAACGA TGCTTCAC 1902  880 AAGCAACA G UCAAUGGG 201 CCCATTGA GGCTAGCTACAACGA TGTTGCTT 1903  884 AACAGUCA A UGGGCAUU 202 AATGCCCA GGCTAGCTACAACGA TGACTGTT 1904  888 GUCAAUGG G CAUUUGUA 203 TACAAATG GGCTAGCTACAACGA CCATTGAC 1905	841	CAAAUGCA A CGUACAAA	192	TTTGTACG GGCTAGCTACAACGA TGCATTTG	1894
B45 UGCAACGU A CAAAGAAA 194 TTTCTTTG GGCTAGCTACAACGA ACGTTGCA 1896 B53 ACAAAGAA A UAGGGCUU 195 AAGCCCTA GGCTAGCTACAACGA TTCTTTGT 1897 B58 GAAAUAGG G CUUCUGAC 196 GTCAGAAG GGCTAGCTACAACGA CCTATTTC 1898 B65 GGCUUCUG A CCUGUGAA 197 TTCACAGG GGCTAGCTACAACGA CAGAAGCC 1899 B69 UCUGACCU G UGAAGCAA 198 TTGCTTCA GGCTAGCTACAACGA AGGTCAGA 1900 B74 CCUGUGAA G CAACAGUC 199 GACTGTTG GGCTAGCTACAACGA TTCACAGG 1901 B77 GUGAAGCA A CAGUCAAU 200 ATTGACTG GGCTAGCTACAACGA TGCTTCAC 1902 B80 AAGCAACA G UCAAUGGG 201 CCCATTGA GGCTAGCTACAACGA TGTTGCTT 1903 B84 AACAGUCA A UGGGCAUU 202 AATGCCCA GGCTAGCTACAACGA TGACTGTT 1904 B88 GUCAAUGG G CAUUUGUA 203 TACAAATG GGCTAGCTACAACGA CCATTGAC 1905	843	AAUGCAAC G UACAAAGA	193		
ACAAAGAA A UAGGGCUU 195 AAGCCCTA GGCTAGCTACAACGA TTCTTTGT 1897  858 GAAAUAGG G CUUCUGAC 196 GTCAGAAG GGCTAGCTACAACGA CCTATTTC 1898  865 GGCUUCUG A CCUGUGAA 197 TTCACAGG GGCTAGCTACAACGA CAGAAGCC 1899  869 UCUGACCU G UGAAGCAA 198 TTGCTTCA GGCTAGCTACAACGA AGGTCAGA 1900  874 CCUGUGAA G CAACAGUC 199 GACTGTTG GGCTAGCTACAACGA TTCACAGG 1901  877 GUGAAGCA A CAGUCAAU 200 ATTGACTG GGCTAGCTACAACGA TGCTTCAC 1902  880 AAGCAACA G UCAAUGGG 201 CCCATTGA GGCTAGCTACAACGA TGTTGCTT 1903  884 AACAGUCA A UGGGCAUU 202 AATGCCCA GGCTAGCTACAACGA TGACTGTT 1904  888 GUCAAUGG G CAUUUGUA 203 TACAAATG GGCTAGCTACAACGA CCATTGAC 1905	845	UGCAACGU A CAAAGAAA	194	TTTCTTTG GGCTAGCTACAACGA ACGTTGCA	1896
858 GAAAUAGG G CUUCUGAC 196 GTCAGAAG GGCTAGCTACAACGA CCTATTTC 1898 865 GGCUUCUG A CCUGUGAA 197 TTCACAGG GGCTAGCTACAACGA CAGAAGCC 1899 869 UCUGACCU G UGAAGCAA 198 TTGCTTCA GGCTAGCTACAACGA AGGTCAGA 1900 874 CCUGUGAA G CAACAGUC 199 GACTGTTG GGCTAGCTACAACGA TTCACAGG 1901 877 GUGAAGCA A CAGUCAAU 200 ATTGACTG GGCTAGCTACAACGA TGCTTCAC 1902 880 AAGCAACA G UCAAUGGG 201 CCCATTGA GGCTAGCTACAACGA TGTTGCTT 1903 884 AACAGUCA A UGGGCAUU 202 AATGCCCA GGCTAGCTACAACGA TGACTGTT 1904 888 GUCAAUGG G CAUUUGUA 203 TACAAATG GGCTAGCTACAACGA CCATTGAC 1905	853	ACAAAGAA A UAGGGCUU	195	AAGCCCTA GGCTAGCTACAACGA TTCTTTGT	
865 GGCUUCUG A CCUGUGAA 197 TTCACAGG GGCTAGCTACAACGA CAGAAGCC 1899 869 UCUGACCU G UGAAGCAA 198 TTGCTTCA GGCTAGCTACAACGA AGGTCAGA 1900 874 CCUGUGAA G CAACAGUC 199 GACTGTTG GGCTAGCTACAACGA TTCACAGG 1901 877 GUGAAGCA A CAGUCAAU 200 ATTGACTG GGCTAGCTACAACGA TGCTTCAC 1902 880 AAGCAACA G UCAAUGGG 201 CCCATTGA GGCTAGCTACAACGA TGTTGCTT 1903 884 AACAGUCA A UGGGCAUU 202 AATGCCCA GGCTAGCTACAACGA TGACTGTT 1904 888 GUCAAUGG G CAUUUGUA 203 TACAAATG GGCTAGCTACAACGA CCATTGAC 1905	858	GAAAUAGG G CUUCUGAC	196	GTCAGAAG GGCTAGCTACAACGA CCTATTTC	1898
874 CCUGUGAA G CAACAGUC 199 GACTGTTG GGCTAGCTACAACGA TTCACAGG 1901 877 GUGAAGCA A CAGUCAAU 200 ATTGACTG GGCTAGCTACAACGA TGCTTCAC 1902 880 AAGCAACA G UCAAUGGG 201 CCCATTGA GGCTAGCTACAACGA TGTTGCTT 1903 884 AACAGUCA A UGGGCAUU 202 AATGCCCA GGCTAGCTACAACGA TGACTGTT 1904 888 GUCAAUGG G CAUUUGUA 203 TACAAATG GGCTAGCTACAACGA CCATTGAC 1905	865	GGCUUCUG A CCUGUGAA	197	TTCACAGG GGCTAGCTACAACGA CAGAAGCC	
874 CCUGUGAA G CAACAGUC 199 GACTGTTG GGCTAGCTACAACGA TTCACAGG 1901 877 GUGAAGCA A CAGUCAAU 200 ATTGACTG GGCTAGCTACAACGA TGCTTCAC 1902 880 AAGCAACA G UCAAUGGG 201 CCCATTGA GGCTAGCTACAACGA TGTTGCTT 1903 884 AACAGUCA A UGGGCAUU 202 AATGCCCA GGCTAGCTACAACGA TGACTGTT 1904 888 GUCAAUGG G CAUUUGUA 203 TACAAATG GGCTAGCTACAACGA CCATTGAC 1905	869	UCUGACCU G UGAAGCAA	198	TTGCTTCA GGCTAGCTACAACGA AGGTCAGA	1900
880 AAGCAACA G UCAAUGGG 201 CCCATTGA GGCTAGCTACAACGA TGTTGCTT 1903 884 AACAGUCA A UGGGCAUU 202 AATGCCCA GGCTAGCTACAACGA TGACTGTT 1904 888 GUCAAUGG G CAUUUGUA 203 TACAAATG GGCTAGCTACAACGA CCATTGAC 1905	874	CCUGUGAA G CAACAGUC	199		
884 AACAGUCA A UGGGCAUU 202 AATGCCCA GGCTAGCTACAACGA TGACTGTT 1904 888 GUCAAUGG G CAUUUGUA 203 TACAAATG GGCTAGCTACAACGA CCATTGAC 1905	877	GUGAAGCA A CAGUCAAU	200	ATTGACTG GGCTAGCTACAACGA TGCTTCAC	1902
888 GUCAAUGG G CAUUUGUA 203 TACAAATG GGCTAGCTACAACGA CCATTGAC 1905	880	AAGCAACA G UCAAUGGG	201	CCCATTGA GGCTAGCTACAACGA TGTTGCTT	1903
	884	AACAGUCA A UGGGCAUU	202	AATGCCCA GGCTAGCTACAACGA TGACTGTT	1904
	888	GUCAAUGG G CAUUUGUA	203	TACAAATG GGCTAGCTACAACGA CCATTGAC	1905
890   CAAUGGGC A UUUGUAUA   204   TATACAAA GGCTAGCTACAACGA GCCCATTG   1906	890	CAAUGGGC A UUUGUAUA	204	TATACAAA GGCTAGCTACAACGA GCCCATTG	1906

894 GGGCAUUU G UAUAAGAC 205 GTCTTATA GGCTAGCTACAACGA AAATGCCC 896 GCAUUUGU A UAAGACAA 206 TTGTCTTA GGCTAGCTACAACGA ACAAATGC 901 UGUAUAAG A CAAACUAU 207 ATAGTTTG GGCTAGCTACAACGA CTTATACA 905 UAAGACAA A CUAUCUCA 208 TGAGATAG GGCTAGCTACAACGA TTGTCTTA	
901 UGUAUAAG A CAAACUAU 207 ATAGTTTG GGCTAGCTACAACGA CTTATACA	1 2200
	1909
303 CAMBACAA A COADCOCA 200 IGAGATAG GGCTAGCTACAACGA 11G1CTA	
908 GACAAACU A UCUCACAC 209 GTGTGAGA GGCTAGCTACAACGA AGTTTGTC	
913 ACUAUCUC A CACAUCGA 210 TCGATGTG GGCTAGCTACAACGA GAGATAGT	
915 UAUCUCAC A CAUCGACA 211 TGTCGATG GGCTAGCTACAACGA GTGAGATA	
	1913
925 AUCGACAA A CCAAUACA 214 TGTATTGG GGCTAGCTACAACGA TTGTCGAT 929 ACAAACCA A UACAAUCA 215 TGATTGTA GGCTAGCTACAACGA TGGTTTGT	1916
931 AAACCAAU A CAAUCAUA 216 TATGATTG GGCTAGCTACAACGA ATTGGTTT	
934 CCAAUACA A UCAUAGAU 217 ATCTATGA GGCTAGCTACAACGA TGTATTGG	1918
937 AUACAAUC A UAGAUGUC 218 GACATCTA GGCTAGCTACAACGA GATTGTAT	1919
941 AAUCAUAG A UGUCCAAA 219 TTTGGACA GGCTAGCTACAACGA CTATGATT	
943 UCAUAGAU G UCCAAAUA 220 TATTTGGA GGCTAGCTACAACGA ATCTATGA	
949 AUGUCCAA A UAAGCACA 221 TGTGCTTA GGCTAGCTACAACGA TTGGACAT	1922
953 CCAAAUAA G CACACCAC 222 GTGGTGTG GGCTAGCTACAACGA TTGTACAT	1923
955 AAAUAAGC A CACCACGC 223 GCGTGGTG GGCTAGCTACAACGA GCTTATTT	1924
957 AUAAGCAC A CCACGCCC 224 GGGCGTGG GGCTAGCTACAACGA GTGCTTAT	
960 AGCACACC A CGCCCAGU 225 ACTGGGCG GGCTAGCTACAACGA GGTGTGCT	1926
962 CACACCAC G CCCAGUCA 226 TGACTGGG GGCTAGCTACAACGA GTGGTGTG	1927
967 CACGCCCA G UCAAAUUA 227 TAATTTGA GGCTAGCTACAACGA TGGGCGTG	1929
972 CCAGUCAA A UUACUUAG 228 CTAAGTAA GGCTAGCTACAACGA TTGACTGG	1930
975 GUCAAAUU A CUUAGAGG 229 CCTCTAAG GGCTAGCTACAACGA AATTTGAC	1931
983 ACUUAGAG G CCAUACUC 230 GAGTATGG GGCTAGCTACAACGA CTCTAAGT	1932
986 UAGAGGCC A UACUCUUG 231 CAAGAGTA GGCTAGCTACAACGA GGCCTCTA	1933
988 GAGGCCAU A CUCUUGUC 232 GACAAGAG GGCTAGCTACAACGA ATGGCCTC	1934
994 AUACUCUU G UCCUCAAU 233 ATTGAGGA GGCTAGCTACAACGA AAGAGTAT	1935
1001 UGUCCUCA A UUGUACUG 234 CAGTACAA GGCTAGCTACAACGA TGAGGACA	1936
1004 CCUCAAUU G UACUGCUA 235 TAGCAGTA GGCTAGCTACAACGA AATTGAGG	1937
1006 UCAAUUGU A CUGCUACC 236 GGTAGCAG GGCTAGCTACAACGA ACAATTGA	1938
1009 AUUGUACU G CUACCACU 237 AGTGGTAG GGCTAGCTACAACGA AGTACAAT	1939
1012 GUACUGCU A CCACUCCC 238 GGGAGTGG GGCTAGCTACAACGA AGCAGTAC	1940
1015 CUGCUACC A CUCCCUUG 239 CAAGGGAG GGCTAGCTACAACGA GGTAGCAG	1941
1025 UCCCUUGA A CACGAGAG 240 CTCTCGTG GGCTAGCTACAACGA TCAAGGGA	1942
1027 CCUUGAAC A CGAGAGUU 241 AACTCTCG GGCTAGCTACAACGA GTTCAAGG	1943
1033 ACACGAGA G UUCAAAUG 242 CATTTGAA GGCTAGCTACAACGA TCTCGTGT	1944
1039 GAGUUCAA A UGACCUGG 243 CCAGGTCA GGCTAGCTACAACGA TTGAACTC	1945
1042 UUCAAAUG A CCUGGAGU 244 ACTCCAGG GGCTAGCTACAACGA CATTTGAA	1946
1049 GACCUGGA G UUACCCUG 245 CAGGGTAA GGCTAGCTACAACGA TCCAGGTC	
1052 CUGGAGUU A CCCUGAUG 246 CATCAGGG GGCTAGCTACAACGA AACTCCAG	
1058 UUACCCUG A UGAAAAA 247 TTTTTCA GGCTAGCTACAACGA CAGGGTAA	
1067 UGAAAAAA A UAAGAGAG 248 CTCTCTTA GGCTAGCTACAACGA TTTTTTCA	1950
1075 AUAAGAGA G CUUCCGUA 249 TACGGAAG GGCTAGCTACAACGA TCTCTTAT	1951
1081 GAGCUUCC G UAAGGCGA 250 TCGCCTTA GGCTAGCTACAACGA GGAAGCTC	1952
1086 UCCGUAAG G CGACGAAU 251 ATTCGTCG GGCTAGCTACAACGA CTTACGGA	1953
1089 GUAAGGCG A CGAAUUGA 252 TCAATTCG GGCTAGCTACAACGA CGCCTTAC	1954
1093 GGCGACGA A UUGACCAA 253 TTGGTCAA GGCTAGCTACAACGA TCGTCGCC	1955
1097 ACGAAUUG A CCAAAGCA 254 TGCTTTGG GGCTAGCTACAACGA CAATTCGT	1956
1103 UGACCAAA G CAAUUCCC 255 GGGAATTG GGCTAGCTACAACGA TTTGGTCA	1957
1106 CCAAAGCA A UUCCCAUG 256 CATGGGAA GGCTAGCTACAACGA TGCTTTGG	1958

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1118	1112	CAAUUCCC A UGCCAACA	257	TGTTGGCA GGCTACCTACAACGA GGGAATTG	1959
1120		<del></del>			
1122   GCCAACAU A UUCUACAG   261   CTGTAGAA GGCTAGCTACAACGA ATGTTGGC   1953   1127   CAUAUUCU A CAGUGUUC   262   GARACATG GGCTAGCTACAACGA AGAATATG   1964   1130   AUUCUACA G GUULUUACU   263   TAAGAACA GGCTAGCTACAACGA TATGAGAT   1965   1132   UCUACAGU G UUCUUACU   264   AGTAGAA GGCTAGCTACAACGA AGTAGAAT   1965   1133   GUGUUCUU A CUAUUGAC   265   GTCAATAG GGCTAGCTACAACGA AGGAACAC   1967   1141   UUCUACUA U UUGACAAA   266   TTGTCTA GGCTAGCTACAACGA AGGAACAC   1968   1145   UACUAUUGA C 267   GCATTTTG GGCTAGCTACAACGA AGGAACA   1968   1145   UACUAUUGA C 267   GCATTTTG GGCTAGCTACAACGA AGGAACA   1968   1150   UUGACAAA C 268   GTTCTGCA GGCTAGCTACAACGA ACTTTGTCA   1970   1151   UUGACAAA C 268   GTTCTGCA GGCTAGCTACAACGA ACTTTGTCA   1971   1151   AAUGCAGA A CAAGACACA   269   TTGTCTTG GGCTAGCTACAACGA ATTTTGTC   1971   1151   AAUGCAGA A CAAGACACA   270   TGTCTTTG GGCTAGCTACAACGA ATTTTGTC   1971   1151   AAUGCAGA A CAAGACACA   270   TGTCTTTG GGCTAGCTACAACGA ATTTTGTC   1971   1170   GACAAAGG A CUAUAUAC   273   GACAAGTA GGCTAGCTACAACGA ATTTTGTC   1971   1171   AGGACUUAU A CUUGUUGU   274   GACAAAGG A CUUUAUAC   275   GTTCATAAA GGCTAGCTACAACGA ATTTAGAGT   1975   1177   GACUUAUU A CUUGUUGU   274   GACGACAG GGCTAGCTACAACGA ATAGAGTC   1975   1177   GACUUAUU A CUUGUUGU   274   GACGACAG GGCTAGCTACAACGA AAAGTCCT   1976   1181   UUADACUU G UGUAGGA   276   TCCTTACA   GGCTAGCTACAACGA AAAGTCT   1976   1181   UUADACUU G UGUAGGA   276   TCCTTACA   GGCTAGCTACAACGA AAAGTCTA   1976   1181   UUADACUU G UAUAAGGA   276   TCCTTACA   GGCTAGCTACAACGA ACAGATA   1978   1184   UUADACACC   GUAUAGGA   277   ACTCCTTA   GGCTAGCTACAACGA ACAGATA   1978   1184   UUADACACC   GACAACAA   278   ATTGACGA   GCCTAGCTACAACGA ACAGATA   1978   1184   UUADACAC   UCAUUCAA   280   TTGATAGA   GGCTAGCTACAACGA ACAGATA   1978   1197   AGGAGUGA   UUCAAAUC   278   AATGATCG   GGCTAGCTACAACGA ACAGATA   1980   1197   AGGAGUA A UUCAAAUC   281   ATTGATAG   GGCTAGCTACAACGA   ACAGATAG   1981   1197   AGGAGUA A UUCAAAUC   281   ATTGATAG   GGCTAGCTACAACGA   AGGATTCA   1981   1200   UAUU			259		1961
1127					1962
1130					
1132			262		1964
1138		AUUCUACA G UGUUCUUA	263	TAAGAACA GGCTAGCTACAACGA TGTAGAAT	1965
1141   UUCUUACU A UUGACAAA   266   TTIGTCAA GGCTAGCTACAACGA AGTAACAA   1958     1145   UUCUUACU A UUGACAAA   267   GCATTITTG GGCTAGCTACAACGA CAATAGTA   1959     1150   UUGACAAA A UGCAGAAC   268   GTTCTGCA GGCTAGCTACAACGA TTTGTCAA   1970     1151   GACAAAAU C CAGAACAA   269   TTIGTTCTG GGCTAGCTACAACGA TTTGTCAA   1971     1157   AAUGCAGA A CAAAGACA   270   TGTCTTTG GGCTAGCTACAACGA TTTTGTCA   1971     1158   GACAAAGA A CAAAGACA   270   TGTCTTTG GGCTAGCTACAACGA TTTTGTC   1971     1159   GACAAAGA A CAAAGACA   271   GTCCTTTG GGCTAGCTACAACGA CTTTGTTC   1972     1170   GACAAAGA A CUUUAUAC   272   GTATAAAG GGCTAGCTACAACGA CTTTGTTC   1974     1177   GACUUAU A UUCUUCUC   273   GACAAGTA GGCTAGCTACAACGA CTTTGTTC   1975     1181   UUAUACUU G UCCUUGUA   275   TTACACGA GGCTAGCTACAACGA AAAGTTCT   1976     1184   UUAUACUU G UCCUUGUA   275   TTACACGA GGCTAGCTACAACGA AAAAGTTCT   1976     1186   CUUGUCGU G UUAAGGAG   276   TCCTTACA GGCTAGCTACAACGA ACGAACTA   1977     1181   UUAUAGGA G UGGACCAU   278   TAGTCCA GGCTAGCTACAACGA ACGAACGA   1979     1193   UUAAAGGA G UGGACCAU   278   TAGTCCA GGCTAGCTACAACGA ACGACAA   1980     1197   AGGAGUGG A CCALICAUU   279   AATGATGG GGCTAGCTACAACGA CCACTCCT   1981     1200   AGUGAGCA UCCAAUUCAA   280   TTGAATGA GGCTAGCTACAACGA CACTCCCT   1981     1201   AGUGAGCA UUCAAAUCA   281   GATTGTAGA GGCTAGCTACAACGA CACTCCCT   1982     1202   UCAUUCAA A UCUCAAUC   281   GATTGTAGA GGCTAGCTACAACGA GATGGTCC   1982     1217   AUCUGUUA C 282   TTACAGA GGCTAGCTACAACGA GATGGTCC   1981     1218   UUACAAUC G UUACAAUC   281   GATTGTAG GACTAGCTAACAGA GATGGTCC   1981     1219   CUUUAAC A CCUCAGUG   285   CACTGAGG GGCTAGCTACAACGA GATGGTCC   1981     1210   CUGUUAAC A CCUCAGUG   286   CTATGTAGA GGCTAGCTAACAACGA TTGAATGA   1986     1211   AUCUGUUA C ACCUCAGU   286   CATATATA GGCTAGCTAACAACGA TTGAATGA   1986     1221   AUCUGUUA A UUACAAUC   286   CATATATA GGCTAGCTAACAACGA TTGAATGA   1986     1222   CUCUGUGA A UUACAAUC   286   CATATATA GGCTAGCTACAACGA GATGACTA   1986     1223   CUCUGUGA A UUACAAUC   286   CATATATA GGCTAGCTAC			264	AGTAAGAA GGCTAGCTACAACGA ACTGTAGA	1966
1145			265	GTCAATAG GGCTAGCTACAACGA AAGAACAC	1967
1150			266	TTTGTCAA GGCTAGCTACAACGA AGTAAGAA	1968
1152		UACUAUUG A CAAAAUGC	267	GCATTITG GGCTAGCTACAACGA CAATAGTA	1969
1157			268		1970
1163	<b>——</b>	GACAAAAU G CAGAACAA	269	TTGTTCTG GGCTAGCTACAACGA ATTTTGTC	1971
1170		AAUGCAGA A CAAAGACA	270	TGTCTTTG GGCTAGCTACAACGA TCTGCATT	1972
1175	1163	GAACAAAG A CAAAGGAC	271	GTCCTTTG GGCTAGCTACAACGA CTTTGTTC	1973
1177	1170	GACAAAGG A CUUUAUAC	272	GTATAAAG GGCTAGCTACAACGA CCTTTGTC	1974
1181   UNADACUU G UGUGUDA   275   TTACACGA GGCTAGCTACAACGA AAGTATAA   1978     1184   UACUUGUC G UGUAAGGA   276   TCCTTACA GGCTAGCTACAACGA GACAAGTA   1978     1186   CUUGUCGU G UBAAGGAGU   277   ACTCCTTA GGCTAGCTACAACGA ACGACAAG   1979     1193   UGUAAGGA G UGGACCAU   278   ATGGTCA GGCTAGCTACAACGA TCCTTACA   1980     1197   AGGAGUGG A CCAUCAUU   279   AATGATGG GGCTAGCTACAACGA TCCTTACA   1980     1200   AGUGGACC A UCAUACAA   280   TTGAATGA GGCTAGCTACAACGA GGCTCACT   1981     1201   AGUGGACC A UCUCAAAUC   281   GATTTGAA GGCTAGCTACAACGA GGTCCACT   1982     1203   GGACCAUC A UUCAAAUC   281   GATTTGAA GGCTAGCTACAACGA GATGGTC   1983     1209   UCAUACAA   UCUGUUAA   282   TTAACAGA GGCTAGCTACAACGA GATGGTC   1983     1213   UCAAAUCU G UUAACACC   284   CTGAGGTG GGCTAGCTACAACGA TGAACGAT   1986     1217   AUCUGUUAA   ACACCUCAG   284   CTGAGGTG GGCTAGCTACAACGA TGAACGAT   1986     1219   UUGUUAAC   CCUCAGUG   285   CACTGAGG GGCTAGCTACAACGA TGAACGAT   1986     1225   ACACCUCA G UGCAUAUA   286   TATATGCA GGCTAGCTACAACGA TGAACGAT   1986     1226   ACACCUCA G UGCAUAUA   287   TATATGTA GGCTAGCTACAACGA ACTGAGGT   1988     1227   ACCUCAGU G CAUAUAUA   287   TATATATA GGCTAGCTACAACGA ACTGAGGT   1991     1231   CAGUGCAU   UAUAUGAU   289   ATCATATA GGCTAGCTACAACGA ACTGAGGT   1991     1231   CAGUGCAU   UAUAUGAU   289   ATCATATA GGCTAGCTACAACGA ATGACGT   1991     1233   GUGCAUAU   UAUAUGAU   289   ATCATATA GGCTAGCTACAACGA ATATGCAC   1992     1234   CAGUGAUAU   UAUAUAGU   289   ATCATATA GGCTAGCTACAACGA ATATGCAC   1992     1235   GCAUAUU   UAUAUAGU   290   TATACCATA GGCTAGCTACAACGA ATATGCAC   1992     1243   AUGAUAAA   GCAUCAUC   294   GTGATGAA GGCTAGCTACAACGA ATATTACA   1994     1244   AAGCAUU   UAUACAC   294   GTGATGAA GGA GATGAAGA ATATATAC   1995     1245   GAUAAAAG   AUCAUCAC   294   GTGATGAA GGCTAGCTACAACGA ATATATAC   1996     1246   GAUAAAAG   AUCAUCAC   294   GTGATGAA GGCTAGCTACAACGA ATATATAC   1996     1247   AAGCAUC   GUGAAACAU   297   ATGTTTA GGCTAGCTACAACGA ATATATAC   1996     1248   UAUAAAG   AUCAUCAC   294   GTGATGAA GGCTAGC		AGGACUUU A UACUUGUC	273	GACAAGTA GGCTAGCTACAACGA AAAGTCCT	1975 .
1184	1177	GACUUUAU A CUUGUCGU	274	ACGACAAG GGCTAGCTACAACGA ATAAAGTC	1976
1186	1181	UUAUACUU G UCGUGUAA	275	TTACACGA GGCTAGCTACAACGA AAGTATAA	1977
1193	1184	UACUUGUC G UGUAAGGA	276	TCCTTACA GGCTAGCTACAACGA GACAAGTA	1978
1197   AGGAGUGG A CCAUCAUU   279   AATGATGG GGCTAGCTACAACGA CCACTCCT   1981   1200   AGUGGACC A UCAUUCAA   280   TTGAATGA GGCTAGCTACAACGA GGTCCACT   1982   1203   GGACCAUC A UUCAAAUC   281   GATTTGAA GGCTAGCTACAACGA GATGGTCC   1983   1209   UCAUUCAA A UCUGUUAA   282   TTAACAGA GGCTAGCTACAACGA GATGGTCC   1983   1213   UCAAAUCU G UUAACAACC   283   GGTGTTAA GGCTAGCTACAACGA TGGAATTGA   1984   1213   UCAAUUCA G UUAACAACC   284   CTGAGGTG GGCTAGCTACAACGA TGAATGA   1985   1217   AUCUGUUAA C CACCUCAG   284   CTGAGGTG GGCTAGCTACAACGA TAACAGAT   1986   1219   CUUGUUAAC A CCUCAGUG   285   CACTGAGG GGCTAGCTACAACGA TGAGGTT   1986   1225   ACACCUCA G UGCAUAUA   286   TATATGCA GGCTAGCTACAACGA TGAGGTG   1987   1227   ACCUCAGU G CAUAUAUA   287   TATATATG GGCTAGCTACAACGA ACTGAGGT   1989   1229   CUCAGUGCA A UAUAUAUG   288   CATATATA GGCTAGCTACAACGA ACTGAGGT   1990   1231   CAGUGCAU A UAUAUAGAU   289   ATCATATA GGCTAGCTACAACGA ATCGACTT   1991   1233   GUGCAUAUA A UAUGAUAA   290   TTATCATA GGCTAGCTACAACGA ATATGCAC   1992   1235   GCAUAUAU A UAUGAUAA   291   CTTTATCA GGCTAGCTACAACGA ATATGCAC   1992   1238   UAUAUAUG A UAAAGCAU   292   ATGCTTTA GGCTAGCTACAACGA ATATATGCAC   1993   1243   AUGAUAAA G CAUUCAUC   293   GATGATG GGCTAGCTACAACGA CATATTAT   1994   1243   AUGAUAAA G CAUUCAUC   293   GATGATG GGCTAGCTACAACGA CATATTATA   1995   1245   GAUAAAGC A UUCAUCAC   294   GTGATGAA GGCTAGCTACAACGA CATATTATA   1996   1249   AAGCAUUC A UCACUGUG   295   CACAGTGA GGCTAGCTACAACGA GATTATTAT   1997   1252   CAUUCAUC A UUGAUAAA   296   TTTCACAG GGCTAGCTACAACGA GATTATTAT   1998   1249   AAGCAUUC A UUGAGAAA   296   TTTCACAG GGCTAGCTACAACGA GATTATTAT   1998   1255   UCAUCAUC A UUGAAAA   297   ATGTTTCA GGCTAGCTACAACGA GATTATTT   1998   1260   ACUGUAAA A CAUCGAAA   298   TTTCACAG GGCTAGCTACAACGA GATTATTC   1998   1260   ACUGAAAAC   299   GTTTCACAG GGCTAGCTACAACGA GATTATTC   2001   1260   CAUCGAAA A CAUCGAAA   296   TTTCACAG GGCTAGCTACAACGA TTTCACAG   2001   1260   CAUCGAAA A CAUCGAAA   297   ATGTTTCA GGCTAGCTACAACGA TTTCACAG   2001   1260   CAUCGAAA	1186	CUUGUCGU G UAAGGAGU	277	ACTCCTTA GGCTAGCTACAACGA ACGACAAG	1979
1200   AGUGGACC A UCAUUCAA   280   TTGAATGA GGCTAGCTACAACGA GGTCCACT   1982   1203   GGACCAUC A UUCAAAUC   281   GATTTGAA GGCTAGCTACAACGA GATGGTCC   1983   1209   UCAUUCAA A UCUGUUAA   282   TTAACAGA GGCTAGCTACAACGA TTGAATGA   1984   1213   UCAAAUCU G UUAACACC   283   GGTGTTAA GGCTAGCTACAACGA AGATTTGA   1985   1217   AUCUGUUAA   CACCUCAG   284   CTGAGGTG GGCTAGCTACAACGA AGATTTGA   1986   1219   CUGUUAAC   CCUCAGUG   285   CACTGAGG GGCTAGCTACAACGA AGATTTGA   1987   1225   ACACCUCA G UGCAUAUA   286   TATATGCA GGCTAGCTACAACGA GTTAACAGT   1987   1227   ACCUCAGU G CAUAUAUA   287   TATATATG GGCTAGCTACAACGA ACTGAGGT   1989   1229   CUCAGUGC   AUAUAUAUG   288   CATATATA GGCTAGCTACAACGA ACTGAGGT   1989   1231   CAGUGCAU   A UAUAUGAU   289   ATCATATA GGCTAGCTACAACGA ATGCACTG   1991   1233   GUGCAUAU   A UAUAUAUG   289   ATCATATA GGCTAGCTACAACGA ATGCACTG   1992   1235   GCAUAUAU   A UGAUAAAG   290   TTATCATA GGCTAGCTACAACGA ATATGCAC   1992   1235   GCAUAUAU   A UGAUAAAG   291   CTTTATCA GGCTAGCTACAACGA ATATATGC   1993   1238   UAUAUAUG   A UAAAGCAU   292   ATGCTTTA GGCTAGCTACAACGA ATATATGC   1993   1243   AUGAUAAA   GCAUCAUC   293   GATGAATG GGCTAGCTACAACGA CATATATA   1994   1243   AUGAUAAA   GCAUCAUC   294   GTGATGAA   GGCTAGCTACAACGA CATATATA   1995   1245   GAUAAAGC   UUCAUCAC   294   GTGATGAA   GGCTAGCTACAACGA GCTTTATC   1996   1249   AAGCAUUC   A UCAUUGUG   295   CACAGTGA   GGCTAGCTACAACGA GATGCAT   1997   1252   CAUUCAUC   UGAAACAU   297   ATGTTTCA GGCTAGCTACAACGA GATGCAT   1997   1252   CAUUCAUC   UGAAACAU   297   ATGTTTCA GGCTAGCTACAACGA AGTGCAT   1998   1255   UCAUCAUC   UGAAACAU   297   ATGTTTCA GGCTAGCTACAACGA AGTGCAT   1998   1255   UCAUCAUC   UGAAACAU   297   ATGTTTCA GGCTAGCTACAACGA AGTGCAT   1998   1256   ACUGGAAA   CAUCGAAA   296   TTTCACAG GGCTAGCTACAACGA AGTGATGCA   1998   1256   ACUGGAAA   CAUCGAAA   296   TTTCACAG GGCTAGCTACAACGA AGTGATCA   2000   1262   UGUAAAC   UCGAAACAU   297   ATGTTTCAG GGCTAGCTACAACGA ATTCACAG   2000   1262   UGUAAACC   UGCAGAA   296   TTTCAGA GGCTAGCTACAACGA ATTCACAG   2000	1193	UGUAAGGA G UGGACCAU	278	ATGGTCCA GGCTAGCTACAACGA TCCTTACA	1980
1203   GGACCAUC A UUCAAAUC   281   GATTTGAA GGCTAGCTACAACGA GATGGTCC   1983   1209   UCAUUCAA A UCUGUUAA   282   TTAACAGA GGCTAGCTACAACGA TTGAATGA   1984   1213   UCAAAUCU G UUAACACC   283   GGTGTTAA GGCTAGCTACAACGA AGATTTGA   1985   1217   AUCUGUUAA   CACCUCAG   284   CTGAGGTG GGCTAGCTACAACGA AGATTTGA   1986   1219   CUGUUAAC   CCUCAGUG   285   CACTGAGG GGCTAGCTACAACGA TAACAGAT   1986   1225   ACACCUCA G   UGCAUAUA   286   TATATGCA   GGCTAGCTACAACGA   TGAGGTGT   1988   1227   ACCUCAGU G   CAUAUAUA   287   TATATATG GGCTAGCTACAACGA   ACTGAGGT   1989   1229   CUCAGUGC   A UAUAUAUA   287   TATATATA   GGCTAGCTACAACGA   ACTGAGGT   1989   1231   CAGUCAGU   A UAUAUGAU   288   CATATATA   GGCTAGCTACAACGA   ACTGAGGT   1991   1233   GUGCAUAU   A UAUAUAA   290   TTATCATA   GGCTAGCTACAACGA   ATATGCAC   1992   1235   GCAUAUAU   A UAUAUAA   290   TTATCATA   GGCTAGCTACAACGA   ATATGCAC   1992   1238   UAUAUAUG   A UAUAUAGA   291   CTTTATCA   GGCTAGCTACAACGA   ATATTGCAC   1993   1238   UAUAUAUG   A UAUAUAGA   291   CTTTATCA   GGCTAGCTACAACGA   ATATTATCAC   1993   1249   AUGAUAAA   G CAUUCAUC   292   ATGCTTTA   GGCTAGCTACAACGA   ATATTATAC   1994   1243   AUGAUAAA   G CAUUCAUC   293   GATGAATG   GGCTAGCTACAACGA   CATATATA   1995   1245   GAUAAAGC   A UUCAUCAC   294   GTGATGAA   GGCTAGCTACAACGA   GATGCTT   1996   1249   AAGCAUUC   A UCAUCAC   294   GTGATGAA   GGCTAGCTACAACGA   GATGCTT   1997   1252   CAUUCAUC   A UCAUCAC   295   CACAGTGA   GGCTAGCTACAACGA   GATGCTT   1997   1252   CAUUCAUC   A UCAUCAC   295   CACAGTGA   GGCTAGCTACAACGA   GATGATT   1998   1255   UCAUCAC   UGAAACAU   297   ATGTTCA   GGCTAGCTACAACGA   GATGATT   1998   1255   UCAUCAC   UGAAACAU   297   ATGTTCA   GGCTAGCTACAACGA   GATGATT   1999   1260   ACUGUGAA   CAUGUAAA   296   TTTCACAG   GGCTAGCTACAACGA   GATGATT   1998   1255   UCAUCACA   A CUGUAAA   296   TTTCACAG   GGCTAGCTACAACGA   GTTTACA   2001   1262   UGUGAAA   CAGCAGGU   300   ACCTGCTG   GGCTAGCTACAACGA   GTTTCACA   2001   1262   UGUGAAA   CAGCAGGU   301   AGCACCTG   GGCTAGCTACAACGA   ACCTGCTG   2003   1	1197	AGGAGUGG A CCAUCAUU	279	AATGATGG GGCTAGCTACAACGA CCACTCCT	1981
1209	1200	AGUGGACC A UCAUUCAA	280	TTGAATGA GGCTAGCTACAACGA GGTCCACT	1982
1213         UCAAAUCU G UUAACACC         283         GGTGTTAA GGCTAGCTACAACGA AGATTTGA         1985           1217         AUCUGUUA A CACCUCAG         284         CTGAGGTG GGCTAGCTACAACGA TAACAGAT         1986           1219         CUGUUAAC A CCUCAGUG         285         CACTGAGG GGCTAGCTACAACGA GTTAACAG         1987           1225         ACACCUCA G UGCAUAUA         286         TATATATG GGCTAGCTACAACGA TGAGGTGT         1988           1227         ACCUCAGUG C AUAUAUA         287         TATATATG GGCTAGCTACAACGA ACTGAGGT         1989           1229         CUCAGUGC A UAUAUAUG         288         CATATATA GGCTAGCTACAACGA ACTGACTG         1990           1231         CAGUGCAU A UAUAUGAU         289         ATCATATA GGCTAGCTACAACGA ATGACTG         1991           1233         GUGCAUAU A UAUAUAAG         290         TATACATA GGCTAGCTACAACGA ATATAGCAC         1992           1235         GCAUAUAU A UGAUAAG         291         CTTTATCA GGCTAGCTACAACGA ATATATGCAC         1992           1235         GCAUAUAUA A UGAUAAG         291         CTTTATCA GGCTAGCTACAACGA ATATATA         1993           1236         GAUAAAGA         292         ATGATTA GGCTACAACGA ATATATA         1993           1243         AUGAUAAG         294         GTGATGATA         GGCTAGCTACAACGA GATGATT         1995	1203	GGACCAUC A UUCAAAUC	281	GATTTGAA GGCTAGCTACAACGA GATGGTCC	1983
1217 AUCUGUUA A CACCUCAG 284 CTGAGGTG GGCTAGCTACAACGA TAACAGAT 1986 1219 CUGUUAAC A CCUCAGUG 285 CACTGAGG GGCTAGCTACAACGA GTTAACAG 1987 1225 ACACCUCA G UGCAUAUA 286 TATATGCA GGCTAGCTACAACGA TGAGGTGT 1988 1227 ACCUCAGU G CAUAUAUA 287 TATATATG GGCTAGCTACAACGA ACTGAGGT 1989 1229 CUCAGUGC A UAUAUAUG 288 CATATATA GGCTAGCTACAACGA GCACTGAG 1990 1231 CAGUGCAU A UAUAUAUAU 289 ATCATATA GGCTAGCTACAACGA ATGCACTG 1991 1233 GUGCAUAU A UAUAUAUA 290 TTATCATA GGCTAGCTACAACGA ATATGCAC 1992 1235 GCAUAUAU A UAUAUAUA 290 TTATCATA GGCTAGCTACAACGA ATATGCAC 1992 1238 UAUAUAUG A UAAAGCAU 292 ATGCTTTA GGCTAGCTACAACGA ATATATGC 1993 1243 AUGAUAAA G CAUUCAUC 293 GATGAATG GGCTAGCTACAACGA CATATATA 1994 1243 AUGAUAAG C AUUCAUC 294 GTGATGAA GGCTAGCTACAACGA CATATATA 1995 1244 GAUAAAGC A UCACUGUG 295 CACAGTGA GGCTAGCTACAACGA GATTATCAT 1995 1245 GAUAAAGC A UCACUGUG 295 CACAGTGA GGCTAGCTACAACGA GATGATTA 1996 1249 AAGCAUUC A CUGUGAAA 296 TTTCACAG GGCTAGCTACAACGA GATGAATG 1997 1252 CAUUCAUC A CUGUGAAA 296 TTTCACAG GGCTAGCTACAACGA GATGAATG 1998 1255 UCAUCAUC A CUGUGAAA 296 TTTCACAG GGCTAGCTACAACGA GATGAATG 1999 1256 ACUGUGAA A CAUCGAAA 298 TTTCGACG GGCTAGCTACAACGA GTTTCACAG 2000 1262 UGUGAAACA UCGAAAAC 299 GTTTTCGA GGCTAGCTACAACGA GTTTCACA 2001 1269 CAUCGAAA CAUCGAAA 298 TTTCGATG GGCTAGCTACAACGA TTTCACAGT 2000 1262 UGUGAAACA UCGAAAAC 299 GTTTTCGA GGCTAGCTACAACGA TTTCACAGT 2000 1262 UGUGAAACA CAUCGAAA 298 TTTCGATG GGCTAGCTACAACGA TTTCACAG 2001 1269 CAUCGAAA CAGCGU 300 ACCTGCTG GGCTAGCTACAACGA TTTCACAG 2001 1269 CAUCGAAA CAGCAGGU 301 AGCACCTG GGCTAGCTACAACGA TTTCGACG 2000 1272 CGAAAACA G CAGGUGCU 301 AGCACCTG GGCTAGCTACAACGA TTTCGACG 2001 1269 CAUCGAAA A CAGCAGGU 300 ACCTGCTG GGCTAGCTACAACGA TTTCGACG 2001 1276 AACAGCAG G UGCUGAA 302 TTCAAGCA GGCTAGCTACAACGA TTTCAACG 2001 1277 CGAAAACA G CAGGUGCU 301 AGCACCTG GGCTAGCTACAACGA TTTCAACG 2001 1278 CAGCAGGU G CUUGAAAC 303 GTTTCAAG GGCTAGCTACAACGA TTTCAAGCA 2001 1278 CAGCAGGU G CUUGAAAC 303 GTTTCAAG GGCTAGCTACAACGA TTCAAGCA 2006 1288 UUGAAACC G UAGCUGC 305 GCCAGCTA GGCTAGCTACAACGA TTCAAGCA 2007 1291 AAACCGUA	1209	UCAUUCAA A UCUGUUAA	282	TTAACAGA GGCTAGCTACAACGA TTGAATGA	1984
1219         CUGUUAAC A CCUCAGUG         285         CACTGAGG GGCTAGCTACAACGA GTTAACAG         1987           1225         ACACCUCA G UGCAUAUA         286         TATATGCA GGCTAGCTACAACGA TGAGGTGT         1988           1227         ACCUCAGU G CAUAUAUA         287         TATATATG GGCTAGCTACAACGA ACTGAGGT         1989           1229         CUCAGUGC A UAUAUAUG         288         CATATATA GGCTAGCTACAACGA ACTGAGG         1990           1231         CAGUGCAU A UAUAUAUA         289         ATCATATA GGCTAGCTACAACGA ATATGCAC         1991           1233         GUGCAUAU A UAUAUAUA         290         TTATCATA GGCTAGCAACGA ATATGCAC         1992           1235         GCAUAUAU A UAUAUAAAG         291         CTTTATCA GGCTAGCAACGA ATATATGC         1993           1238         UAUAUAUG A UAAAGCAU         292         ATGCTTTA GGCTACAACGA CATATATA         1994           1243         AUGAUAAA G CAUUCAUC         293         GATGATAA         GGCTAGCTACAACGA CATATATA         1995           1245         GAUAAAGC A UUCAUCAC         294         GTGATGAA         GGCTAGCTACAACGA GCTTTATC         1997           1252         CAUCAUCA A CUGUAAA         295         CACAGTGA GGCTAGCTACAACGA GATGAATG         1998           1255         UCAUCAUC A CUGAAACA         297         ATGTTTCA GGCTAGCTACAACGA ATT	1213	UCAAAUCU G UUAACACC	283	GGTGTTAA GGCTAGCTACAACGA AGATTTGA	1985
1225         ACACCUCA G UGCAUAUA         286         TATATGCA GGCTAGCTACAACGA TGAGGTGT         1988           1227         ACCUCAGU G CAUAUAUA         287         TATATATG GGCTAGCTACAACGA ACTGAGGT         1989           1229         CUCAGUGC A UAUAUAUG         288         CATATATA GGCTAGCTACAACGA GCACTGAG         1990           1231         CAGUGCAU A UAUAUGAU         289         ATCATATA GGCTAGCTACAACGA ATATGCAC         1991           1233         GUGCAUAU A UAUGAUAA         290         TTATCATA GGCTAGCTACAACGA ATATGCAC         1992           1235         GCAUAUAU A UAUAGAG         291         CTTTATCA GGCTAGCTACAACGA ATATATGC         1993           1238         UAUAUAUG A UAAAGCAU         292         ATGCTTTA GGCTAGCTACAACGA CATATATA         1994           1243         AUGAUAAA G CAUUCAUC         293         GATGAATG GGCTAGCTACAACGA CTTATATC         1995           1245         GAUAAAGC A UUCAUCAC         294         GTGATGAA         GGCTAGCTACAACGA GCTTATATC         1996           1249         AAGCAUUC A UCACUGUG         295         CACAGTGA GGCTAGCTACAACGA GATGATT         1997           1252         CAUUCAUC A CUGUGAAA         296         TTTCACAG GGCTAGCTACAACGA AGTGATGA         1999           1255         UCAUCACU G UGAAACAU         297         ATGTTTCA GGCTAGCTACAACGA TTCACAGT </td <td>1217</td> <td>AUCUGUUA A CACCUCAG</td> <td>284</td> <td>CTGAGGTG GGCTAGCTACAACGA TAACAGAT</td> <td>1986</td>	1217	AUCUGUUA A CACCUCAG	284	CTGAGGTG GGCTAGCTACAACGA TAACAGAT	1986
1227 ACCUCAGU G CAUAUAUA 287 TATATATG GGCTAGCTACAACGA ACTGAGGT 1989 1229 CUCAGUGC A UAUAUAUG 288 CATATATA GGCTAGCTACAACGA GCACTGAG 1990 1231 CAGUGCAU A UAUAUGAU 289 ATCATATA GGCTAGCTACAACGA ATGCACTG 1991 1233 GUGCAUAU A UAUGAUAA 290 TTATCATA GGCTAGCTACAACGA ATATGCAC 1992 1235 GCAUAUAU A UAUAUAAG 291 CTTTATCA GGCTAGCTACAACGA ATATATGC 1993 1238 UAUAUAUAG A UAAAGCAU 292 ATGCTTTA GGCTAGCTACAACGA ATATATA 1994 1243 AUGAUAAA G CAUUCAUC 293 GATGAATG GGCTAGCTACAACGA CATATATA 1995 1245 GAUAAAGC A UUCAUCAC 294 GTGATGAA GGCTAGCTACAACGA GCTTTATC 1996 1249 AAGCAUUC A UCACUGUG 295 CACAGTGA GGCTAGCTACAACGA GATGCTT 1997 1252 CAUUCAUC A CUGUGAAA 296 TTTCACAG GGCTAGCTACAACGA GATGATG 1998 1255 UCAUCACU G UGAAACAU 297 ATGTTTCA GGCTAGCTACAACGA ATGTATA 1999 1260 ACUGUGAA CAUCGAAA 298 TTTCGATG GGCTAGCTACAACGA ATGTATA 1999 1260 ACUGUGAA CAUCGAAA 299 GTTTTCGA GGCTAGCTACAACGA TTCACAGT 2000 1262 UGUGAAACA UCGAAAAC 299 GTTTTCGA GGCTAGCTACAACGA TTCACAGT 2001 1269 CAUCGAAA CAGCAGGU 300 ACCTGCTG GGCTAGCTACAACGA TTTCGATG 2002 1272 CGAAAACA G CAGGUGCU 301 AGCACCTG GGCTAGCTACAACGA TTTTCGATG 2002 1276 AACAGCAG G UGCUUGAA 302 TTCAAGCA GGCTAGCTACAACGA TTTTCGATG 2002 1277 CGAAAACA G CAGGUGCU 301 AGCACCTG GGCTAGCTACAACGA CTGCTGT 2004 1278 CAGCAGGU G CUUGAAAC 303 GTTTCAAG GGCTAGCTACAACGA CTGCTGT 2004 1278 CAGCAGGU G CUUGAAAC 303 GTTTCAAG GGCTAGCTACAACGA ACCTGCTG 2005 1285 UGCUUGAA A CGUAGCCU 304 AGCTACGG GGCTAGCTACAACGA TTCAAGCA 2006 1288 UUGAAACC G UAGCUGCC 305 GCCAGCTA GGCTAGCAACGA ACCTGCTG 2005 1289 CGUAGCUG G CAAGCGGU 307 ACCGCTTG GGCTAGCTACAACGA TTCAAGCA 2007 1291 AAACCGUA G CUGGCAAG 306 CTTGCCAG GGCTAGCTACAACGA TTCAAGCA 2007 1291 AAACCGUA G CUGGCAAG 306 CTTGCCAG GGCTAGCTACAACGA TCCAGCTTCAA	1219	CUGUUAAC A CCUCAGUG	285	CACTGAGG GGCTAGCTACAACGA GTTAACAG	1987
1229 CUCAGUGC A UAUAUAUG 288 CATATATA GGCTAGCTACAACGA GCACTGAG 1990 1231 CAGUGCAU A UAUAUGAU 289 ATCATATA GGCTAGCTACAACGA ATGCACTG 1991 1233 GUGCAUAU A UAUGAUAA 290 TTATCATA GGCTAGCTACAACGA ATATGCAC 1992 1235 GCAUAUAU A UGAUAAAG 291 CTTTATCA GGCTAGCTACAACGA ATATATGC 1993 1238 UAUAUAUGA UAAAGCAU 292 ATGCTTTA GGCTAGCTACAACGA ATATATGC 1993 1243 AUGAUAAA G CAUUCAUC 293 GATGAATG GGCTAGCTACAACGA CATATATA 1994 1243 AUGAUAAA G CAUUCAUC 294 GTGATGAA GGCTAGCTACAACGA TTTATCAT 1995 1245 GAUAAAGC A UUCAUCAC 294 GTGATGAA GGCTAGCTACAACGA GCTTTATC 1996 1249 AAGCAUUC A UCACUGUG 295 CACAGTGA GGCTAGCTACAACGA GATGCTT 1997 1252 CAUUCAUC A CUGUGAAA 296 TTTCACAG GGCTAGCTACAACGA GATGATG 1998 1255 UCAUCACU G UGAAACAU 297 ATGTTTCA GGCTAGCTACAACGA AGTGATGA 1999 1260 ACUGUGAA A CAUCGAAA 298 TTTCGATG GGCTAGCTACAACGA AGTGATGA 1999 1261 ACUGGAAAC A UCGAAAAC 299 GTTTTCGA GGCTAGCTACAACGA GTTTCACA 2001 1262 UGUGAAAC A UCGAAAAC 299 GTTTTCGA GGCTAGCTACAACGA GTTTCACA 2001 1269 CAUCGAAA A CAGCAGGU 300 ACCTGCTG GGCTAGCTACAACGA TTTCGATG 2002 1272 CGAAAACA G CAGGUGCU 301 AGCACCTG GGCTAGCTACAACGA TTTCGATG 2003 1276 AACAGCAG G UGCUUGAA 302 TTCAAGCA GGCTAGCTACAACGA TTTTCGC 2003 1276 AACAGCAG G UGCUUGAA 302 TTCAAGCA GGCTAGCTACAACGA ACCTGCTGT 2004 1278 CAGCAGGU G CUUGAAAC 303 GTTTCAAG GGCTAGCTACAACGA ACCTGCTG 2005 1285 UGCUUGAA A CCGUAGCU 304 AGCTACG GGCTAGCTACAACGA ACCTGCTG 2005 1286 UUGAAACC G UAGCUGGC 305 GCCAGCTA GGCTAGCTACAACGA TTCAAGCA 2006 1288 UUGAAACC G UAGCUGGC 306 CTTGCCAG GGCTAGCTACAACGA TTCAAGCA 2007 1291 AAACCGUA G CUGGCAAG 307 ACCGCTTG GGCTAGCTACAACGA TTCAAGCA 2007 1291 AAACCGUA G CUGGCAAG 307 ACCGCTTG GGCTAGCTACAACGA TTCAAGCA 2007 1291 AAACCGUA G CUGGCAAG 307 ACCGCTTG GGCTAGCTACAACGA TACGGTTT 2008 1295 CGUAGCUG G CAAGCCGU 307 ACCGCTTG GGCTAGCTACAACGA TACGGTTT 2008	1225	ACACCUCA G UGCAUAUA	286	TATATGCA GGCTAGCTACAACGA TGAGGTGT	1988
1231 CAGUGCAU A UAUAUGAU 289 ATCATATA GGCTAGCTACAACGA ATGCACTG 1991 1233 GUGCAUAU A UAUGAUAA 290 TTATCATA GGCTAGCTACAACGA ATATGCAC 1992 1235 GCAUAUAU A UGAUAAAG 291 CTTTATCA GGCTAGCTACAACGA ATATATGC 1993 1238 UAUAUAUG A UAAAGCAU 292 ATGCTTTA GGCTAGCTACAACGA ATATATATG 1994 1243 AUGAUAAA G CAUUCAUC 293 GATGAATG GGCTAGCTACAACGA CATATATA 1994 1244 AUGAUAAA G CAUUCAUC 294 GTGATGAA GGCTAGCTACAACGA CTTATCAT 1995 1245 GAUAAAGC A UUCAUCAC 294 GTGATGAA GGCTAGCTACAACGA GCTTTATC 1996 1249 AAGCAUUC A UCACUGUG 295 CACAGTGA GGCTAGCTACAACGA GATGCTT 1997 1252 CAUUCAUC A CUGUGAAA 296 TTTCACAG GGCTAGCTACAACGA GATGATG 1998 1255 UCAUCACU G UGAAACAU 297 ATGTTTCA GGCTAGCTACAACGA AGTGATGA 1999 1260 ACUGUGAA A CAUCGAAA 298 TTTCGATG GGCTAGCTACAACGA ATTCACAGT 2000 1262 UGUGAAAC A UCGAAAAC 299 GTTTTCGA GGCTAGCTACAACGA GTTTCACA 2001 1269 CAUCGAAA A CAGCAGGU 300 ACCTGCTG GGCTAGCTACAACGA TTTCGATG 2002 1272 CGAAAACA G CAGGUGCU 301 AGCACCTG GGCTAGCTACAACGA TTTCGATG 2003 1276 AACAGCAG G UGCUUGAA 302 TTCAAGCA GGCTAGCTACAACGA CTGCTGTT 2004 1278 CAGCAGGU G CUUGAAAC 303 GTTTCAAG GGCTAGCTACAACGA ACCTGCTG 2005 1285 UGCUUGAA A CCGUAGCU 304 AGCTACGG GGCTAGCTACAACGA ACCTGCTG 2005 1286 UUGAAACC G UAGCUGGC 305 GCCAGCTA GGCTAGCTACAACGA TTCAAGCA 2006 1288 UUGAAACC G UAGCUGGC 305 GCCAGCTA GGCTAGCTACAACGA TTCAAGCA 2007 1291 AAACCGUA G CUGGCAAG 307 ACCGCTTG GGCTAGCTACAACGA TTCAAGCA 2007 1291 AAACCGUA G CUGGCAAG 307 ACCGCTTG GGCTAGCTACAACGA TACAGGTTT 2008	1227	ACCUCAGU G CAUAUAUA	287	TATATATG GGCTAGCTACAACGA ACTGAGGT	1989
1233 GUGCAUAU A UAUGAUAA 290 TTATCATA GGCTAGCTACAACGA ATATGCAC 1992 1235 GCAUAUAU A UGAUAAAG 291 CTTTATCA GGCTAGCTACAACGA ATATATGC 1993 1238 UAUAUAUG A UAAAGCAU 292 ATGCTTTA GGCTAGCTACAACGA CATATATA 1994 1243 AUGAUAAA G CAUUCAUC 293 GATGAATG GGCTAGCTACAACGA CTTTATCAT 1995 1245 GAUAAAGC A UUCAUCAC 294 GTGATGAA GGCTAGCTACAACGA GCTTTATC 1996 1249 AAGCAUUC A UCACUGUG 295 CACAGTGA GGCTAGCTACAACGA GATGCTT 1997 1252 CAUUCAUC A CUGUGAAA 296 TTTCACAG GGCTAGCTACAACGA GATGAATG 1998 1255 UCAUCACU G UGAAACAU 297 ATGTTTCA GGCTAGCTACAACGA AGTGATGA 1999 1260 ACUGUGAA A CAUCGAAA 298 TTTCGATG GGCTAGCTACAACGA AGTGATGA 1999 1262 UGUGAAAC A UCGAAAAC 299 GTTTTCGA GGCTAGCTACAACGA GTTTCACA 2001 1262 UGUGAAAC A UCGAAAAC 299 GTTTTCGA GGCTAGCTACAACGA GTTTCACA 2001 1269 CAUCGAAA A CAGCAGGU 300 ACCTGCTG GGCTAGCTACAACGA TTTCGATG 2002 1272 CGAAAACA G CAGGUGCU 301 AGCACCTG GGCTAGCTACAACGA TTTCGATG 2002 1274 CGAAAACA G CAGGUGCU 301 AGCACCTG GGCTAGCTACAACGA TTTCGATG 2003 1276 AACAGCAG G UGCUUGAA 302 TTCAAGCA GGCTAGCTACAACGA TTTTCGT 2004 1278 CAGCAGGU G CUUGAAAC 303 GTTTCAAG GGCTAGCTACAACGA CTGCTGTT 2004 1278 CAGCAGGU G CUUGAAAC 303 GTTTCAAG GGCTAGCTACAACGA ACCTGCTG 2005 1285 UGCUUGAA A CCGUAGCU 304 AGCTACGG GGCTAGCTACAACGA TTCAAGCA 2006 1288 UUGAAACC G UAGCUGGC 305 GCCAGCTA GGCTAGCTACAACGA TTCAAGCA 2007 1291 AAACCGUA G CUGGCAAG 306 CTTGCCAG GGCTAGCTACAACGA TACCGTTT 2008 1295 CGUAGCUG G CAAGCGGU 307 ACCGCTTG GGCTAGCTACAACGA TACCGTTT 2008	1229	CUCAGUGC A UAUAUAUG	288	CATATATA GGCTAGCTACAACGA GCACTGAG	1990
1235 GCAUAUAU A UGAUAAAG 291 CTTTATCA GGCTAGCTACAACGA ATATATGC 1993 1238 UAUAUAUG A UAAAGCAU 292 ATGCTTTA GGCTAGCTACAACGA CATATATA 1994 1243 AUGAUAAA G CAUUCAUC 293 GATGAATG GGCTAGCTACAACGA TTTATCAT 1995 1245 GAUAAAGC A UUCAUCAC 294 GTGATGAA GGCTAGCTACAACGA GCTTTATC 1996 1249 AAGCAUUC A UCACUGUG 295 CACAGTGA GGCTAGCTACAACGA GATGCTT 1997 1252 CAUUCAUC A CUGUGAAA 296 TTTCACAG GGCTAGCTACAACGA GATGATG 1998 1255 UCAUCACU G UGAAACAU 297 ATGTTCA GGCTAGCTACAACGA AGTGATGA 1999 1260 ACUGUGAA A CAUCGAAA 298 TTTCGATG GGCTAGCTACAACGA AGTGATGA 1999 1262 UGUGAAAC A UCGAAAAC 299 GTTTTCGA GGCTAGCTACAACGA GTTTCACA 2000 1262 UGUGAAAC A UCGAAAAC 299 GTTTTCGA GGCTAGCTACAACGA TTCCACGT 2000 1269 CAUCGAAA A CAGCAGGU 300 ACCTGCTG GGCTAGCTACAACGA TTTCGATG 2002 1272 CGAAAACA G CAGGUGCU 301 AGCACCTG GGCTAGCTACAACGA TGTTTTCG 2003 1276 AACAGCAG G UGCUUGAA 302 TTCAAGCA GGCTAGCTACAACGA TGTTTTCG 2003 1278 CAGCAGGU G CUUGAAAC 303 GTTTCAAG GGCTAGCTACAACGA ACCTGCTG 2004 1278 CAGCAGGU G CUUGAAAC 303 GTTTCAAG GGCTAGCTACAACGA ACCTGCTG 2005 1285 UGCUUGAA A CCGUAGCU 304 AGCTACGG GGCTAGCTACAACGA ACCTGCTG 2005 1286 UUGAAACC G UAGCUGCC 305 GCCAGCTA GGCTAGCTACAACGA TTCAAGCA 2007 1291 AAACCGUA G CUGGCAAG 306 CTTGCCAG GGCTAGCTACAACGA TACGGTTT 2008 1295 CGUAGCUG G CAAGCCGU 307 ACCGCTTG GGCTAGCTACAACGA CAGCTACG		CAGUGCAU A UAUAUGAU	289	ATCATATA GGCTAGCTACAACGA ATGCACTG	1991
1238 UAUAUAUG A UAAAGCAU 292 ATGCTTTA GGCTAGCTACAACGA CATATATA 1994 1243 AUGAUAAA G CAUUCAUC 293 GATGAATG GGCTAGCTACAACGA TTTATCAT 1995 1245 GAUAAAGC A UUCAUCAC 294 GTGATGAA GGCTAGCTACAACGA GCTTTATC 1996 1249 AAGCAUUC A UCACUGUG 295 CACAGTGA GGCTAGCTACAACGA GAATGCTT 1997 1252 CAUUCAUC A CUGUGAAA 296 TTTCACAG GGCTAGCTACAACGA GATGATG 1998 1255 UCAUCACU G UGAAACAU 297 ATGTTTCA GGCTAGCTACAACGA AGTGATGA 1999 1260 ACUGUGAA A CAUCGAAA 298 TTTCGATG GGCTAGCTACAACGA AGTGATGA 1999 1262 UGUGAAAC A UCGAAAAC 299 GTTTTCGA GGCTAGCTACAACGA TTCACAGT 2000 1262 UGUGAAAC A UCGAAAAC 299 GTTTTCGA GGCTAGCTACAACGA TTTCGATG 2002 1272 CGAAAACA G CAGGUGCU 300 ACCTGCTG GGCTAGCTACAACGA TTTCGATG 2002 1272 CGAAAACA G CAGGUGCU 301 AGCACCTG GGCTAGCTACAACGA TTTTCGAT 2003 1276 AACAGCAG G UGCUUGAA 302 TTCAAGCA GGCTAGCTACAACGA CTGCTGTT 2004 1278 CAGCAGGU G CUUGAAAC 303 GTTTCAAG GGCTAGCTACAACGA CTGCTGTT 2004 1278 CAGCAGGU G CUUGAAAC 303 GTTTCAAG GGCTAGCTACAACGA TTCAAGCA 2006 1288 UUGAAACC G UAGCUGGC 304 AGCTACGA GGCTAGCTACAACGA TTCAAGCA 2007 1281 AAACCGUA G CUGGCAAG 305 GCCAGCTA GGCTAGCTACAACGA TTCAAGCA 2007 1291 AAACCGUA G CUGGCAAG 306 CTTGCCAG GGCTAGCTACAACGA TACGGTTT 2008 1295 CGUAGCUG G CAAGCGGU 307 ACCGCTTG GGCTAGCTACAACGA CAGCTACG	1233	GUGCAUAU A UAUGAUAA	290	TTATCATA GGCTAGCTACAACGA ATATGCAC	1992
1243 AUGAUAAA G CAUUCAUC 293 GATGAATG GGCTAGCTACAACGA TTTATCAT 1995 1245 GAUAAAGC A UUCAUCAC 294 GTGATGAA GGCTAGCTACAACGA GCTTTATC 1996 1249 AAGCAUUC A UCACUGUG 295 CACAGTGA GGCTAGCTACAACGA GATGCTT 1997 1252 CAUUCAUC A CUGUGAAA 296 TTTCACAG GGCTAGCTACAACGA GATGATG 1998 1255 UCAUCACU G UGAAACAU 297 ATGTTCA GGCTAGCTACAACGA AGTGATGA 1999 1260 ACUGUGAA A CAUCGAAA 298 TTTCGATG GGCTAGCTACAACGA TTCACAGT 2000 1262 UGUGAAAC A UCGAAAAC 299 GTTTTCGA GGCTAGCTACAACGA GTTTCACA 2001 1269 CAUCGAAA A CAGCAGGU 300 ACCTGCTG GGCTAGCTACAACGA TTTCGATG 2002 1272 CGAAAACA G CAGGUGCU 301 AGCACCTG GGCTAGCTACAACGA TTTCGATG 2003 1276 AACAGCAG G UGCUUGAA 302 TTCAAGCA GGCTAGCTACAACGA CTGCTGTT 2004 1278 CAGCAGGU G CUUGAAAC 303 GTTTCAAG GGCTAGCTACAACGA CTGCTGTT 2004 1278 CAGCAGGU G CUUGAAAC 303 GTTTCAAG GGCTAGCTACAACGA ACCTGCTG 2005 1285 UGCUUGAA A CCGUAGCU 304 AGCTACGG GGCTAGCTACAACGA TTCAAGCA 2006 1288 UUGAAACC G UAGCUGGC 305 GCCAGCTA GGCTAGCTACAACGA TTCAAGCA 2007 1291 AAACCGUA G CUGGCAAG 306 CTTGCCAG GGCTAGCTACAACGA TACGGTTT 2008 1295 CGUAGCUG G CAAGCGGU 307 ACCGCTTG GGCTAGCTACAACGA CAGCTACG	1235	GCAUAUAU A UGAUAAAG	291	CTTTATCA GGCTAGCTACAACGA ATATATGC	1993
1245 GAUAAAGC A UUCAUCAC 294 GTGATGAA GGCTAGCTACAACGA GCTTTATC 1996 1249 AAGCAUUC A UCACUGUG 295 CACAGTGA GGCTAGCTACAACGA GATGCTT 1997 1252 CAUUCAUC A CUGUGAAA 296 TTTCACAG GGCTAGCTACAACGA GATGATG 1998 1255 UCAUCACU G UGAAACAU 297 ATGTTCA GGCTAGCTACAACGA AGTGATGA 1999 1260 ACUGUGAA A CAUCGAAA 298 TTTCGATG GGCTAGCTACAACGA TTCACAGT 2000 1262 UGUGAAAC A UCGAAAAC 299 GTTTCGA GGCTAGCTACAACGA GTTTCACA 2001 1269 CAUCGAAA A CAGCAGGU 300 ACCTGCTG GGCTAGCTACAACGA TTTCGATG 2002 1272 CGAAAACA G CAGGUGCU 301 AGCACCTG GGCTAGCTACAACGA TGTTTTCG 2003 1276 AACAGCAG G UGCUUGAA 302 TTCAAGCA GGCTAGCTACAACGA CTGCTGTT 2004 1278 CAGCAGGU G CUUGAAAC 303 GTTTCAAG GGCTAGCTACAACGA ACCTGCTG 2005 1285 UGCUUGAA A CCGUAGCU 304 AGCTACGG GGCTAGCTACAACGA TCAAGGA 2006 1288 UUGAAACC G UAGCUGGC 305 GCCAGCTA GGCTAGCTACAACGA TTCAAGCA 2007 1291 AAACCGUA G CUGGCAAG 306 CTTGCCAG GGCTAGCTACAACGA TACGGTTT 2008 1295 CGUAGCUG G CAAGCGGU 307 ACCGCTTG GGCTAGCTACAACGA CAGCTACG	1238		292	ATGCTTTA GGCTAGCTACAACGA CATATATA	1994
1249 AAGCAUUC A UCACUGUG 295 CACAGTGA GGCTAGCTACAACGA GAATGCTT 1997 1252 CAUUCAUC A CUGUGAAA 296 TTTCACAG GGCTAGCTACAACGA GATGATG 1998 1255 UCAUCACU G UGAAACAU 297 ATGTTCA GGCTAGCTACAACGA AGTGATGA 1999 1260 ACUGUGAA A CAUCGAAA 298 TTTCGATG GGCTAGCTACAACGA TTCACAGT 2000 1262 UGUGAAAC A UCGAAAAC 299 GTTTTCGA GGCTAGCTACAACGA GTTTCACA 2001 1269 CAUCGAAA A CAGCAGGU 300 ACCTGCTG GGCTAGCTACAACGA TTTCGATG 2002 1272 CGAAAACA G CAGGUGCU 301 AGCACCTG GGCTAGCTACAACGA TGTTTTCG 2003 1276 AACAGCAG G UGCUUGAA 302 TTCAAGCA GGCTAGCTACAACGA CTGCTGTT 2004 1278 CAGCAGGU G CUUGAAAC 303 GTTTCAAG GGCTAGCTACAACGA ACCTGCTG 2005 1285 UGCUUGAA A CCGUAGCU 304 AGCTACGG GGCTAGCTACAACGA TTCAAGCA 2006 1288 UUGAAACC G UAGCUGGC 305 GCCAGCTA GGCTAGCTACAACGA TTCAAGCA 2007 1291 AAACCGUA G CUGGCAAG 306 CTTGCCAG GGCTAGCTACAACGA TACGGTTT 2008 1295 CGUAGCUG G CAAGCGGU 307 ACCGCTTG GGCTAGCTACAACGA CAGCTACG	1243	AUGAUAAA G CAUUCAUC	293	GATGAATG GGCTAGCTACAACGA TTTATCAT	1995
1252 CAUUCAUC A CUGUGAAA 296 TTTCACAG GGCTAGCTACAACGA GATGAATG 1998 1255 UCAUCACU G UGAAACAU 297 ATGTTTCA GGCTAGCTACAACGA AGTGATGA 1999 1260 ACUGUGAA A CAUCGAAA 298 TTTCGATG GGCTAGCTACAACGA TTCACAGT 2000 1262 UGUGAAAC A UCGAAAAC 299 GTTTTCGA GGCTAGCTACAACGA GTTTCACA 2001 1269 CAUCGAAA A CAGCAGGU 300 ACCTGCTG GGCTAGCTACAACGA TTTCGATG 2002 1272 CGAAAACA G CAGGUGCU 301 AGCACCTG GGCTAGCTACAACGA TGTTTTCG 2003 1276 AACAGCAG G UGCUUGAA 302 TTCAAGCA GGCTAGCTACAACGA CTGCTGTT 2004 1278 CAGCAGGU G CUUGAAAC 303 GTTTCAAG GGCTAGCTACAACGA ACCTGCTG 2005 1285 UGCUUGAA A CCGUAGCU 304 AGCTACGG GGCTAGCTACAACGA TTCAAGCA 2006 1288 UUGAAACC G UAGCUGGC 305 GCCAGCTA GGCTAGCTACAACGA GGTTTCAA 2007 1291 AAACCGUA G CUGGCAAG 306 CTTGCCAG GGCTAGCTACAACGA TACGGTTT 2008 1295 CGUAGCUG G CAAGCGGU 307 ACCGCTTG GGCTAGCTACAACGA CAGCTACG		·	294		1996
1255 UCAUCACU G UGAAACAU 297 ATGTTTCA GGCTAGCTACAACGA AGTGATGA 1999 1260 ACUGUGAA A CAUCGAAA 298 TTTCGATG GGCTAGCTACAACGA TTCACAGT 2000 1262 UGUGAAAC A UCGAAAAC 299 GTTTTCGA GGCTAGCTACAACGA GTTTCACA 2001 1269 CAUCGAAA A CAGCAGGU 300 ACCTGCTG GGCTAGCTACAACGA TTTCGATG 2002 1272 CGAAAACA G CAGGUGCU 301 AGCACCTG GGCTAGCTACAACGA TGTTTTCG 2003 1276 AACAGCAG G UGCUUGAA 302 TTCAAGCA GGCTAGCTACAACGA CTGCTGTT 2004 1278 CAGCAGGU G CUUGAAAC 303 GTTTCAAG GGCTAGCTACAACGA CTGCTGT 2005 1285 UGCUUGAA A CCGUAGCU 304 AGCTACGG GGCTAGCTACAACGA TTCAAGCA 2006 1288 UUGAAACC G UAGCUGGC 305 GCCAGCTA GGCTAGCTACAACGA GTTTCAA 2007 1291 AAACCGUA G CUGGCAAG 306 CTTGCCAG GGCTAGCTACAACGA TACGGTTT 2008 1295 CGUAGCUG G CAAGCGGU 307 ACCGCTTG GGCTAGCTACAACGA CAGCTACG 2009					
1260 ACUGUGAA A CAUCGAAA 298 TTTCGATG GGCTAGCTACAACGA TTCACAGT 2000 1262 UGUGAAAC A UCGAAAAC 299 GTTTTCGA GGCTAGCTACAACGA GTTTCACA 2001 1269 CAUCGAAA A CAGCAGGU 300 ACCTGCTG GGCTAGCTACAACGA TTTCGATG 2002 1272 CGAAAACA G CAGGUGCU 301 AGCACCTG GGCTAGCTACAACGA TGTTTTCG 2003 1276 AACAGCAG G UGCUUGAA 302 TTCAAGCA GGCTAGCTACAACGA CTGCTGTT 2004 1278 CAGCAGGU G CUUGAAAC 303 GTTTCAAG GGCTAGCTACAACGA ACCTGCTG 2005 1285 UGCUUGAA A CCGUAGCU 304 AGCTACGG GGCTAGCTACAACGA TTCAAGCA 2006 1288 UUGAAACC G UAGCUGGC 305 GCCAGCTA GGCTAGCTACAACGA GGTTTCAA 2007 1291 AAACCGUA G CUGGCAAG 306 CTTGCCAG GGCTAGCTACAACGA TACGGTTT 2008 1295 CGUAGCUG G CAAGCGGU 307 ACCGCTTG GGCTAGCTACAACGA CAGCTACG 2009	<del></del>		296	TTTCACAG GGCTAGCTACAACGA GATGAATG	1998
1262 UGUGAAAC A UCGAAAAC 299 GTTTTCGA GGCTAGCTACAACGA GTTTCACA 2001 1269 CAUCGAAA A CAGCAGGU 300 ACCTGCTG GGCTAGCTACAACGA TTTCGATG 2002 1272 CGAAAACA G CAGGUGCU 301 AGCACCTG GGCTAGCTACAACGA TGTTTTCG 2003 1276 AACAGCAG G UGCUUGAA 302 TTCAAGCA GGCTAGCTACAACGA CTGCTGTT 2004 1278 CAGCAGGU G CUUGAAAC 303 GTTTCAAG GGCTAGCTACAACGA ACCTGCTG 2005 1285 UGCUUGAA A CCGUAGCU 304 AGCTACGG GGCTAGCTACAACGA TTCAAGCA 2006 1288 UUGAAACC G UAGCUGGC 305 GCCAGCTA GGCTAGCTACAACGA GGTTTCAA 2007 1291 AAACCGUA G CUGGCAAG 306 CTTGCCAG GGCTAGCTACAACGA TACGGTTT 2008 1295 CGUAGCUG G CAAGCGGU 307 ACCGCTTG GGCTAGCTACAACGA CAGCTACG 2009					1999
1269 CAUCGAAA A CAGCAGGU 300 ACCTGCTG GGCTAGCTACAACGA TTTCGATG 2002 1272 CGAAAACA G CAGGUGCU 301 AGCACCTG GGCTAGCTACAACGA TGTTTTCG 2003 1276 AACAGCAG G UGCUUGAA 302 TTCAAGCA GGCTAGCTACAACGA CTGCTGTT 2004 1278 CAGCAGGU G CUUGAAAC 303 GTTTCAAG GGCTAGCTACAACGA ACCTGCTG 2005 1285 UGCUUGAA A CCGUAGCU 304 AGCTACGG GGCTAGCTACAACGA TTCAAGCA 2006 1288 UUGAAACC G UAGCUGGC 305 GCCAGCTA GGCTAGCTACAACGA GGTTTCAA 2007 1291 AAACCGUA G CUGGCAAG 306 CTTGCCAG GGCTAGCTACAACGA TACGGTTT 2008 1295 CGUAGCUG G CAAGCGGU 307 ACCGCTTG GGCTAGCTACAACGA CAGCTACG 2009			298		2000
1272 CGAAAACA G CAGGUGCU 301 AGCACCTG GGCTAGCTACAACGA TGTTTTCG 2003 1276 AACAGCAG G UGCUUGAA 302 TTCAAGCA GGCTAGCTACAACGA CTGCTGTT 2004 1278 CAGCAGGU G CUUGAAAC 303 GTTTCAAG GGCTAGCTACAACGA ACCTGCTG 2005 1285 UGCUUGAA A CCGUAGCU 304 AGCTACGG GGCTAGCTACAACGA TTCAAGCA 2006 1288 UUGAAACC G UAGCUGGC 305 GCCAGCTA GGCTAGCTACAACGA GGTTTCAA 2007 1291 AAACCGUA G CUGGCAAG 306 CTTGCCAG GGCTAGCTACAACGA TACGGTTT 2008 1295 CGUAGCUG G CAAGCGGU 307 ACCGCTTG GGCTAGCTACAACGA CAGCTACG 2009					2001
1276 AACAGCAG G UGCUUGAA 302 TTCAAGCA GGCTAGCTACAACGA CTGCTGTT 2004 1278 CAGCAGGU G CUUGAAAC 303 GTTTCAAG GGCTAGCTACAACGA ACCTGCTG 2005 1285 UGCUUGAA A CCGUAGCU 304 AGCTACGG GGCTAGCTACAACGA TTCAAGCA 2006 1288 UUGAAACC G UAGCUGGC 305 GCCAGCTA GGCTAGCTACAACGA GGTTTCAA 2007 1291 AAACCGUA G CUGGCAAG 306 CTTGCCAG GGCTAGCTACAACGA TACGGTTT 2008 1295 CGUAGCUG G CAAGCGGU 307 ACCGCTTG GGCTAGCTACAACGA CAGCTACG 2009		~ <del></del>	300	ACCTGCTG GGCTAGCTACAACGA TTTCGATG	2002
1278 CAGCAGGU G CUUGAAAC 303 GTTTCAAG GGCTAGCTACAACGA ACCTGCTG 2005 1285 UGCUUGAA A CCGUAGCU 304 AGCTACGG GGCTAGCTACAACGA TTCAAGCA 2006 1288 UUGAAACC G UAGCUGGC 305 GCCAGCTA GGCTAGCTACAACGA GGTTTCAA 2007 1291 AAACCGUA G CUGGCAAG 306 CTTGCCAG GGCTAGCTACAACGA TACGGTTT 2008 1295 CGUAGCUG G CAAGCGGU 307 ACCGCTTG GGCTAGCTACAACGA CAGCTACG 2009	-	<del></del>			2003
1285 UGCUUGAA A CCGUAGCU 304 AGCTACGG GGCTAGCTACAACGA TTCAAGCA 2006 1288 UUGAAACC G UAGCUGGC 305 GCCAGCTA GGCTAGCTACAACGA GGTTTCAA 2007 1291 AAACCGUA G CUGGCAAG 306 CTTGCCAG GGCTAGCTACAACGA TACGGTTT 2008 1295 CGUAGCUG G CAAGCGGU 307 ACCGCTTG GGCTAGCTACAACGA CAGCTACG 2009					2004
1288 UUGAAACC G UAGCUGGC 305 GCCAGCTA GGCTAGCTACAACGA GGTTTCAA 2007 1291 AAACCGUA G CUGGCAAG 306 CTTGCCAG GGCTAGCTACAACGA TACGGTTT 2008 1295 CGUAGCUG G CAAGCGGU 307 ACCGCTTG GGCTAGCTACAACGA CAGCTACG 2009			303	GTTTCAAG GGCTAGCTACAACGA ACCTGCTG	2005
1291 AAACCGUA G CUGGCAAG 306 CTTGCCAG GGCTAGCTACAACGA TACGGTTT 2008 1295 CGUAGCUG G CAAGCGGU 307 ACCGCTTG GGCTAGCTACAACGA CAGCTACG 2009			304		2006
1295 CGUAGCUG G CAAGCGGU 307 ACCGCTTG GGCTAGCTACAACGA CAGCTACG 2009			305		2007
Total Control of the		AAACCGUA G CUGGCAAG	306	CTTGCCAG GGCTAGCTACAACGA TACGGTTT	2008
1299 GCUGGCAA G CGGUCUUA 308 TAAGACCG GGCTAGCTACAACGA TTGCCAGC 2010			307	ACCGCTTG GGCTAGCTACAACGA CAGCTACG	2009
	1299	GCUGGCAA G CGGUCUUA	308	TAAGACCG GGCTAGCTACAACGA TTGCCAGC	2010

1307   GCGGUCUU A CCGGCUCU   310   AGAGCCGG GGCTAGCTACAACGA AAGACCGC   2012   1311   UCUUACCG G CUCUCUAU   311   ATAGAGAG GGCTAGCTACAACGA CGGTAACA   2013   1318   GGGUCUCU A UGAAAGGG   312   CACTTACA GGCTAGCTACAACGA AGAGAGCC   2014   1324   CUADGAAA G UGAAAGGC   313   TGCCTTCA GGCTAGCTACAACGA ATTCACTAG   2015   1324   CUGAAAGG A UUUCCCC   314   GGGAAATG GGCTACCTACAACGA CTTCACTT   2016   1332   GUGAAAGG A UUUCCCC   315   GAGGAAA GGCTAGCTACAACGA GCCTTACA   2017   1341   UUUCCCUC G CCGGAAGU   316   ACTTCCGG GGCTAGCTACAACGA GCCTTACAC   2017   1341   UUUCCCUC G CCGGAAGU   316   ACTTCCGG GGCTAGCTACAACGA GAGGGGAA   2018   1351   CGGAAGGU   GUUGAUAGG   317   CCATACAA GGCTAGCTACAACGA AACTTCC   2021   1353   GGAAGUU   UGGUUAAA   319   TTTAACCA GGCTAGCTACAACGA ACCTTCC   2021   1354   GUUAAAAGA   UGGGUUAA   319   TTTAACCA GGCTAGCTACAACGA ACCTTCC   2021   1356   GUUGAAAGA   UGGGUUAA   320   TCTTTTAA GGCTAGCTACAACGA CTTTTAAC   2022   1368   AAAGAUGG   UUACAUAG   321   GTAACCA   GGCTAGCTACAACGA CTTTTAAC   2023   1368   AAAGAUGG   UUACAUGC   322   GCAGGTAA GGCTAGCTACAACGA CTTTTAAC   2023   1371   GAUGGGUUA   CUUCCGC   322   GCAGGTAA GGCTAGCTACAACGA CCATCTTT   2024   1371   GAUGGGUUA   CUUCCGC   323   GTCGCAGG GGCTAGCTACAACGA CACCATC   2025   1378   UACCUGCG   CUUCAAAAA   325   TTTCTCAG GGCTAGCTACAACGA CACCATC   2025   1378   UACCUGCG   CUGAGAAA   325   TTTCTCAG GGCTAGCTACAACGA CAGCAACCAACGA   2026   1378   UACCUGCG   CUGAGAAA   325   TTTCTCAG GGCTAGCTACAACGA CAGCAGT   2027   1386   ACUGAGAA   UCUCCUGC   326   CGAGCAGA GGCTAGCTACAACGA CAGCAACCAACCAACGA   CACCATC   2028   1391   UACCUGCG   CUGAGAAA   325   TTTCTCAG GGCTAGCTACAACGA CAGCAACCAACCAACCAACCAACCAACCAACC	1302	GGCAAGCG G UCUUACCG	309	CGGTAAGA GGCTAGCTACAACGA CGCTTGCC	2011
1311				*	
1318					
1324	<b>—</b>				
1330					
1332   GUGAAGGC A UUUCCCUC   315   GAGGGAAA GGCTAGCTACAACGA GCCTTCAC   2017   1341   UUUCCCUC G CCGGAAGU   316   ACTTCCGG GGCTAGCTACAACGA GAGGGAAA   2018   1348   CGCCGGAA G UUGUAUGG   317   CCATACAA GGCTAGCTACAACGA TCCGGCG   2019   1351   CGGAAGUU G UUGUGUUA   318   TAACCATA GGCTAGCTACAACGA ACTTCCG   2020   1353   GAAGUUGU A UGGUUAAA   319   TTTAACCA GGCTAGCTACAACGA ACACTTC   2021   1356   GUUGUAUG G UUAAAAGA   320   TCTTTTAA GGCTAGCTACAACGA ACACTTC   2021   1356   GUUGUAUG G UUAACUG   321   GTAACCAA GGCTAGCTACAACGA CTATCAAC   2022   1368   AAAGAUGG G UUACCUGC   322   GCAGGTAA GGCTAGCTACAACGA CTATCTAC   2021   1371   GAUGGGUUA   2321   GTAACCAA GGCTAGCTACAACGA CTATCTAC   2023   1375   GGUUACCUG   323   GTGGCAGG GGCTAGCTACAACGA CTATCTAC   2024   1371   GAUGGGUU A CCUGCGAC   323   GTGGCAGG GGCTAGCTACAACGA AGCCATC   2025   1375   GGUUACCU G CCACUGAG   324   CTCAGTCG GGCTAGCTACAACGA AGGTAAC   2027   1376   AUCCUGCG   A CUGAGAAA   325   TTTTCTCAG GGCTAGCTACAACGA AGGTAAC   2027   1386   ACUGAGAA   UCUGCUCG   326   CGAGCGAG GGCTAGCTACAACGA AGGTAAC   2027   1390   AGAAAUCU G CUGACUGA   327   ATAGCGAG GGCTAGCTACAACGA AGGTAAC   2027   1394   AUCUGCUC G CUAUUUGA   328   TCAAATAG GGCTAGCTACAACGA AGCAGT   2028   1390   AGAAAUCU G CUAUUUGA   328   TCAAATAG GGCTAGCTACAACGA AGCAGAT   2030   1402   GCUUAUUGA   2028   GAGTCAAA GGCTAGCTACAACGA AGCAGAT   2031   1402   GCUUAUUG A CUGGUUACU   331   AGTAGCCA GGCTAGCTACAACGA AGCAGAT   2031   1404   GAUCUGCU G UUACUGACU   329   GAGTCAAA GGCTAGCTACAACGA AGCAGAT   2031   1405   GAUCUGU G UUACUGACU   332   ACGAGTAG GGCTAGCTACAACGA AGCAGAT   2031   1406   UUUGACUC G UUACUGAU   333   AGTAGCCA GGCTAGCTACAACGA AGCAGAT   2031   1407   GACUCUGU G UUACUGACU   332   ACGAGTAG GGCTAGCTACAACGA AGCAGAT   2031   1407   GACUCUGU G UUACUGACU   332   ACGAGTAG GGCTAGCTACAACGA CACAGAT   2031   1416   GCUACUCG UUACUGACU   331   AGTAGCCA GGCTAGCTACAACGA CACAGAT   2031   1416   GCUACUC G UUACUGAU   333   AGTAGCCA GGCTAGCTACAACGA AGCAGAT   2031   1416   GCUACUC G UUACUGA   331   AGTAGCA GGCTAGCTACAACGA AGCA					
1341   UUUCCCUC G CCGGAAGU   316   ACTTCCGG GGCTAGCTACAACGA GAGGGAA   2018   1348   GCCCGGAA G UUGUAUGG   317   CCATACAA GGCTAGCTACAACGA TCCGGGG   2019   1351   CCGAAGUU G UAUGGUUA   318   TAACCATA GGCTAGCTACAACGA AACTTCCG   2020   1353   GAAGUUGU A UGGUUAAA   319   TTTTAACCA GGCTAGCTACAACGA ACACTTC   2021   1356   GUUGUAUG G UUAAAAGA   320   TCTTTTAA GGCTAGCTACAACGA CATACAAC   2022   1364   GUUAAAAGA   10GGGUUAC   321   GTAACCCA GGCTAGCTACAACGA CATACAAC   2022   1364   GUUAAAAGA   10GGGUUAC   322   GCAGGTAA GGCTAGCTACAACGA CATACTAC   2021   1371   GAUGGGUU A CCUGCGAC   323   GTCGCAGG GGCTAGCTACAACGA CATCTTT   2024   1371   GAUGGGUU A CCUGCGAC   323   GTCGCAGG GGCTAGCTACAACGA CACTCTT   2025   1375   GGUUACCUG C CACCUGAG   324   CTCAGTCG GGCTAGCTACAACGA AACCCATC   2025   1376   UACCUGCG A CUGAGAAA   325   TTTCTCAG GGCTAGCTACAACGA AGGTAACC   2026   1386   ACUGAGAA   UCUGCUCG   326   CGAGGCAG GGCTAGCTACAACGA AGGTAACC   2027   1390   AGAAAUCU G CUAUUUGA   328   TCAAATAG GGCTAGCTACAACGA AGATTCT   2029   1391   AUCUGCUC G CUAUUUGA   328   TCAAATAG GGCTAGCTACAACGA AGATTCT   2029   1394   AUCUGCUC G CUAUUUGA   328   TCAAATAG GGCTAGCTACAACGA AGACCAT   2031   1402   GCUAUUUG A CUCGUGC   330   GCCACGAG GGCTAGCTACAACGA AGACCAAC   2031   1402   GCUAUUUG A CUCGUGC   331   AGTAGCA GGCTAGCTACAACGA AGACCAAC   2031   1402   GCUAUUUG A CUCGUGU   332   ACAGTACA GGCTAGCTACAACGA AGACCACA   2031   1402   GCUAUUUG A CUCGUUA   331   AGTAGCA GGCTAGCTACAACGA AGACCACA   2031   1402   GCUAUUUG A CUCGUUAA   333   TTAACGAG GGCTAGCTACAACGA AGACCACA   2031   1402   GCUAUUUG A CUCGUUAA   333   AGTAGCA GGCTAGCTACAACGA AGACCACA   2031   1404   GCUACUCU G UUAAUCAAG   335   GCCACGAG GGCTAGCTACAACGA AGCCACA   2031   1404   CUCGUGA A CUAACAG   333   AGTAGCA GGCTAGCTACAACGA AGCCACA   2034   1404   CUCGUGA A CUACUCU   332   ACAGTTAG GGCTAGCTACAACGA AGCCACA   2034   1404   ACAGAGTU A CUACUCU   332   ACAGTTAG GGCTAGCTACAACGA AGCTACAC   2034   1404   ACAGAGTU A CUACUCU   334   AGATTAG GGCTAGCTACAACGA ACTCATCA   2041   1404   ACAGAGGU A CUACUCU   334   A	<del></del>				
1348	<b>—</b>				
1351	<b>—</b>				
1353					
1356	<del> </del>				
1364   GUUAANAG A UGGGUUAC   321   GTAACCCA GGCTAGCTACAACGA CTTTTACA   2023   1368   AAAGAUGG G UUACCUGC   322   GCAGGTAA GGCTAGCTACAACGA CCATCTTT   2024   1371   GAUGGGUU A CCUGCGAC   323   GTGGCAGG GGCTAGCTACAACGA AACCCATC   2025   1375   GGUUACCU G CGACUGAG   324   CTCAGTCG GGCTAGCTACAACGA AACCCATC   2025   1375   GGUUACCU G CGACUGAG   324   CTCAGTCG GGCTAGCTACAACGA AGGTAACC   2026   1378   UACCUGCG A CUGAGAAA   325   TTTTCTCAG GGCTAGCTACAACGA AGGTAACC   2027   1386   ACUĞAGAA A UCUĞCUCG   326   CGAGCAG GGCTAGCTACAACGA AGATTTCT   2028   1390   AGAAUCU G CUCĞCUAU   327   ATAGCGAG GGCTAGCTACAACGA AGATTTCT   2029   1394   AUCUĞCUC G CUAUUUGA   328   TCAAATAG GGCTAGCTACAACGA AGATTTCT   2029   1397   UGCUCĞCU A UUUĞACUC   329   GAĞTCAAA GĞCTAĞCTACAACGA AĞCGAĞÇA   2031   1402   GCUAUUUĞ A CUCĞUĞCCU   331   AĞTAĞCCA GĞCTAĞCTACAACĞA AĞCĞAĞÇA   2031   1406   UUUĞACUC G UĞĞCUACUCU   331   AĞTAĞCCA GĞCTAĞCTACAACĞA GAĞCÇAĞC   2032   1406   UUUĞACUC G UĞĞCUACUCU   332   ACGAĞTĞĞ GĞCTAĞCTACAACĞA GAĞCÇAĞC   2034   1412   UCĞÜĞĞCU A CUCĞUUAA   333   TTAACĞAĞ GĞCTAĞCTACAACĞA GAĞCÇAĞC   2035   1416   GĞCUACUC G UUAUUAU   334   ATAATTAA GĞCTAĞCTACAACĞA AĞCCACĞA   2035   1420   ACUCĞUUA A UUAUCAAĞ   335   CTTĞATAA GĞCTAĞCTACAACĞA AĞCTAĞCA   2036   1420   ACUCĞUUA A UUAUCAAĞ   336   GTCCTTĞA GĞCTAĞCTACAACĞA AĞTTAACĞ   2038   1430   UAUCAAĞĞA C GUAACUĞ   337   CAĞTTAÇĞ GĞCTAĞCTACAACĞA AĞTTAACĞ   2038   1430   UAUCAAĞĞA C GUAACUĞ   337   CAĞTTAÇĞ GĞCTAĞCTACAACĞA AĞTTAACĞ   2038   1430   UAUCAAĞĞA C GUAACUĞ   337   TTCATTA GĞCTAĞCTACAACĞA TACGTCT   2041   1445   UĞAĞĞĞA   UĞAACĞA   338   TTCAĞTTA GĞCTAĞCTACAACĞA ATTTAACĞ   2038   1430   UAUCAAĞĞA C GUAACUĞ   337   TTCATTA GĞCTAĞCTACAACĞA ATTTAACĞ   2041   1447   AĞAĞĞĞA   UĞAACĞA   340   TCCCTĞA GĞCTAĞCTACAACĞA ATTTAACĞ   2041   1447   AĞAĞĞAĞA   UĞAÇAĞĞA   340   TCCCTĞA GĞCTAĞCTACAACĞA ATTTAACĞ   2041   1447   AĞAĞĞAĞA   UĞAĞAĞA   341   ATTTCCTĞ GĞCTAĞCTACAACĞA ATTTATT   2041   1447   AĞAĞĞAĞA   UĞAĞAĞA   342   TTTTATĞA GĞCTAĞCTACAACĞA ATTTATT   2046   1447   AĞAĞĞAĞA   UĞAĞAĞA	<del></del>			<del></del>	
1368					
1371	<del> </del>				
1375   GGUIACCU G CGACUGAG   324   CTCAGTCG GGCTAGCTACAACGA AGGTAACC   2026   1378   UACCUGCG A CUGAGAAA   325   TTTCTCAG GGCTAGCTACAACGA CGCAGGTA   2027   1386   ACUGAGAA A UCUGCUCG   326   CGAGCAGA GGCTAGCTACAACGA TTCTTCAT   2028   1390   AGAANUCU G CUCGCUAU   327   ATAGCCAG GGCTAGCTACAACGA TACTTCT   2029   1394   AUCUGCUC G CUAUUUGA   328   TCAAATAG GGCTAGCTACAACGA AGACTATTCT   2029   1394   AUCUGCUC G CUAUUUGA   329   GAGTCAAA GGCTAGCTACAACGA AGCCAGCA   2031   1402   GCUAUUUG A CUCGUGCU   330   GCCACGAG GGCTAGCTACAACGA AGCCAGCA   2031   1402   GCUAUUUG A CUCGUGCU   331   AGTAGCCA GGCTAGCTACAACGA AGCCAGCA   2031   1409   GACUCGUG G CUACUCGU   331   AGTAGCCA GGCTAGCTACAACGA CAAATAGC   2032   1406   UUUGACUC G UGGCUACU   331   AGTAGCCA GGCTAGCTACAACGA CAACGAA CACCAAATAGC   2034   1412   UCGUGGCU A CUCGUUAA   333   TTAACCAA GGCTAGCTACAACGA CACGAATC   2034   1412   UCGUGGCU A CUCGUUAA   334   ATAATTAA GGCTAGCTACAACGA AGCCACCA   2035   1416   GGCUACUC G UUAAUUAU   334   ATAATTAA GGCTAGCTACAACGA AGCCACCA   2035   1420   ACUCGUUA A UUAUCAAG   335   CTTGATAA GGCTAGCTACAACGA AGCCACCA   2037   1423   CGUUAAUU A UCAAAGGA   336   GTCCTTGA GGCTAGCTACAACGA ATTAACG   2038   1432   UCAAGGAC   CUAACUUG   337   CAGTTAGC GGCTAGCTACAACGA ATTAACG   2039   1432   UCAAGGAC   CUAACUUG   337   TCTCTGA GGCTAGCTACAACGA ATTAACG   2039   1432   UCAAGGAC   UAUACAA   338   TTCAGTTA GGCTAGCTACAACGA CCTTGATA   2040   1445   UGAAGGAG   AUGAGAGA   340   TCCCTGCA GGCTAGCTACAACGA CCTCTTCA   2040   1445   UGAAGGAG   AUGAGAGA   340   TCCCTGCA GGCTAGCTACAACGA CCTCTTCA   2041   1445   UGAAGGAG   AUGAGAGA   340   TCCCTGCA GGCTAGCTACAACGA ATCCCTCT   2041   1447   AAGAGAGU   A CUGAGAGA   340   TCCCTGCA GGCTAGCTACAACGA ATCCCTCT   2041   1447   AAGAGAG   AUGACAA   342   TTGATATA GGCTAGCTACAACGA ATCCCTTCA   2042   1447   AAGAGAU   A UACAAAUCU   344   AGATTGTA GGCTAGCTACAACGA ATCCCTCT   2045   1459   GGAAUUAU   A CAAUCUU   344   CAAGATG GGCTAGCTACAACGA ATCCCTTCT   2045   1462   AUUAUACA   AUCUUGCUG   345   AGATTGA GGCTAGCTACAACGA ATCCCTCTC   2046   1462	<del></del>				
1378	<del></del>				
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1390					
1394   AUCUGCUC G CUAUUUGA   328   TCAAATAG GGCTAGCTACAACGA GGCAGAT   2030   1397   UGCUCGCU A UUUGACUC   329   GAGTCAAA GGCTAGCTACAACGA AGCGAGCA   2031   1402   GCUAUUUG A CUCGUGGC   330   GCCACGAG GGCTAGCTACAACGA CAAATAGC   2032   1406   UUUGACUC G UGGCUACU   331   AGTAGCCA GGCTAGCTACAACGA CAAATAGC   2034   1419   GACUCGUG G CUACUCGU   332   ACGAGTAG GGCTAGCTACAACGA CACGAGTC   2034   1412   UCGUGGCU A CUCGUUAA   333   TTAACGAG GGCTAGCTACAACGA AGCCACGA   2035   1416   GGCUACUC G UUAAUUAU   334   ATAATTAA GGCTAGCTACAACGA AGCCACGA   2036   1420   ACUCGUUA A UUAUCAAG   335   CTTGATAA GGCTAGCTACAACGA TAACGAGT   2037   1423   CGUUAAUU A UCAAGGAC   336   GTCCTTGA GGCTAGCTACAACGA TAACGAGT   2037   1430   UAUCAAGG A CGUAACUG   337   CAGTTACG GGCTAGCTACAACGA TAACGAGT   2039   1432   UCAAGGAC G UAACUGGA   338   TTCAGTTA GGCTAGCTACAACGA TATTAACG   2039   1432   UCAAGGAC G UAACUGGA   338   TTCAGTTA GGCTAGCTACAACGA TACGTCCT   2041   1445   UGAAGAGG A UCUAGAGA   339   CTCTTCAG GGCTAGCTACAACGA TACGTCCT   2041   1445   UGAAGAGG A UCCAGGGA   340   TCCCTGCA GGCTAGCTACAACGA TCCCTCTC   2042   1447   AAGAGGAU G CAGGGAAU   341   ATTCCCTG GGCTAGCTACAACGA TCCCTCTC   2044   1457   AAGAGGAU G CAGGGAAU   341   ATTCCCTG GGCTAGCTACAACGA ATCCTCTT   2043   1454   UGCAGGGA A UUAUACAA   342   TTGTATAA GGCTAGCTACAACGA ATCCTCCT   2045   1459   GGAAUUAU A CAAUCUU   343   AGATTGTA GGCTAGCTACAACGA ATCCTCCT   2046   1462   AUUAUACAA   AUCUACUU   344   CAAGATTG GGCTAGCTACAACGA ATAATTCCC   2046   1462   AUUAUACAA   UCUUGCUG   345   CAGCAAGA GGCTAGCTACAACGA ATAATTCCC   2046   1462   AUUAUACAA   AUCUACAG   346   ATGCTCAG GGCTAGCTACAACGA ATAATTCCC   2046   1462   AUUAUACAA   AUCUACAA   346   ATGCTCAG GGCTAGCTACAACGA ATAATTCCC   2046   1462   AUUAUACAA   AUCUACAA   346   ATGCTCAG GGCTAGCTACAACGA ATAATTCC   2046   1462   AUUAUACAA   AUCUACAA   347   GTTTTATG GGCTAGCTACAACGA ATGATTCC   2046   1462   AUUAUACAA   AUCUACAA   347   GTTTTATG GGCTAGCTACAACGA ATGATTCC   2046   1462   AUUAUACAA   AUCUACAA   347   GTTTTATG GGCTAGCTACAACGA ATGATCC   2050   1466	-				
1397   UGCUCGCU A UUUGACUC   329   GAGTCAAA GGCTAGCTACAACGA AGCGAGCA 2031     1402   GCUAUUUG A CUCGUGGC   330   GCCACGAG GGCTAGCTACAACGA CAAATAGC 2032     1406   UUUGACUC G UGGCUACU   331   AGTAGCCA GGCTAGCTACAACGA CAAATAGC 2033     1409   GACUCGUG G CUACUCGU   332   ACGASTAG GGCTAGCTACAACGA CACGAGTC 2034     1412   UCGUGGCU A CUCGUUAA   333   TTAACGAG GGCTAGCTACAACGA AGCCACGA 2035     1416   GGCUACUC G UUAAUUAU   334   ATAATTAA GGCTAGCTACAACGA AGCCACGA 2036     1420   ACUCGUUA A UUAUCAAG   335   CTTGATAA GGCTAGCTACAACGA ATACAGAGC 2036     1421   CGUUAAUU A UCAAGGAC   336   GTCCTTGA GGCTAGCTACAACGA AATTAACG 2037     1423   CGUUAAUU A UCAAGGAC   336   GTCCTTGA GGCTAGCTACAACGA AATTAACG 2038     1430   UAUCAAGG A CGUAACUG   337   CAGTTACG GGCTAGCTACAACGA AATTAACG 2039     1432   UCAAGGAC G UAACUGAA   338   TTCAGTTA GGCTAGCTACAACGA CCTTGATA 2039     1433   AGAACGUA A CUGAAGAG   339   CTCTTCAG GGCTAGCTACAACGA TACGTCCT 2041     1445   UGAAGAGG A UGCAAGGA   340   TCCCTGCA GGCTAGCTACAACGA TCCCTCTC 2042     1447   AAGAGAGU G CAGGGAAU   341   ATTCCCTG GGCTAGCTACAACGA ATCCTCT 2043     1454   UGCAGGGA A UUAUACAA   342   TTGTATAA GGCTAGCTACAACGA TCCCTCT 2044     1457   AGGGAAUU A UACAAUCUU   343   AGATTGTA GGCTAGCTACAACGA ATCCTCT 2045     1459   GGAAUUAU A CAAUCUU   344   CAACATTG GGCTAGCTACAACGA ATCCTCT 2045     1462   AUUAUACA A UCUUGCUG   345   CAGCAAGA GGCTAGCTACAACGA ATAATTCC 2046     1462   AUUAUACA A UCUUGCUG   346   ATGCTCAG GGCTAGCTACAACGA ATAATTCC 2046     1463   ACAAUCUU G CUGAGCAU   346   ATGCTCAG GGCTAGCTACAACGA ATAATTCC 2046     1464   UGCAGGA A UAAAACA   347   GTTTTATG GGCTAGCTACAACGA ATAATTCC 2046     1465   ACAAUCUU G CUGAGCAU   346   ATGCTCAG GGCTAGCTACAACGA ATAATTCC 2046     1467   ACAAUCUU G CUGAGCAU   346   ATGCTCAG GGCTAGCTACAACGA ATAATTCC 2046     1478   CUUGCUGA G CAUAAAAC   347   GTTTTATG GGCTAGCTACAACGA ATAATTCC 2051     1479   ACAAUCAA A UGUUUAAA   349   TTGACT GGCTAGCTACAACGA ATTTAGCT 2051     1479   ACACUAAA A CAGUCAAA   349   TTTGACT GGCTAGCTACAACGA TTTATGCT 2051     1489   AUUAAAACA G UCAAA				** ****	
1402         GCUAUUUG A CUCGUGGC         330         GCCACGAG GGCTAGCTACAACGA CAATAGC         2032           1406         UUUGACUC G UGGCUACU         331         AGTAGCCA GGCTAGCTACAACGA GAGTCAAA         2033           1409         GACUCGUG G CUACUCGU         332         ACGAGTAG GGCTAGCTACAACGA CACGAGTC         2034           1412         UCGUGGCU A CUCGUUAA         333         TTAACGAG GGCTAGCTACAACGA AGCCACGA         2035           1416         GGCUACUC G UUAAUUAU         334         ATAATTAA GGCTAGCTACAACGA AGCACGA         2036           1420         ACUCGUUA A UUAUCAAG         335         CTTGATAA GGCTAGCTACAACGA AATTAACC         2037           1433         CAGUAACUG         336         GTCCTTGA GGCTAGCTACAACGA AATTAACC         2038           1430         UAUCAAGG A CGUAACUG         337         CAGTTACA         GGCTAGCTACAACGA ACTTGATA         2039           1432         UCAAGGAC G UAACUGA         338         TTCAGTTA GGCTACAACGA GTCCTTGA         2040           1435         AGGACGU A CUGAACAG         339         CTCTTCAG GGCTACAACGA TACGACGA CTCTTCA         2041           1445         UGAAGAGG A UGCAGGA         340         TCCCTGCA GGCTAGCTACAACGA ACCCTCTTCA         2042           1447         AAGAGGAU G CAGGGAAU         341         ATTCCCTG GGCTAGCTACAACGA ACCCCTCTTCA	<del></del>				
1406         UUUGACUC G UGGCUACU         331         AGTAGCCA GGCTAGCACGA GAGTCAAA         2033           1409         GACUCGUG G CUACUCGU         332         ACGAGTAG GGCTAGCTACAACGA CACGAGTC         2034           1412         UCGUGGCU A CUCGUUAA         333         TTAACGAG GGCTAGCTACAACGA AGCCACGA         2035           1416         GGCUACUC G UUAAUUAU         334         ATAATTAA GGCTAGCTACAACGA GAGTAGCC         2036           1420         ACUCGUUA A UUAUCAAG         335         CTTGATAA GGCTAGCTACAACGA TAACGAGT         2037           1423         CGUUAAUU A UCAAGGAC         336         GTCCTTGA GGCTACCAACGA AATTAACG         2038           1430         UAUCAAGGA C GUAACUGA         337         CAGTTACA         GGCTAGCTACAACGA CCTTGATA         2039           1432         UCAAGGAC G UAACUGAA         338         TTCAGTTA GGCTACAACGA TACCACGA TACGTCCT         2040           1435         AGGACGUA A CUGAAGAG         339         CTCTTCAG GGCTAGCTACAACGA CCTCTTCA         2042           1445         UGAAGAGG A UGCAGGGA         340         TCCCTGCA GGCTAGCTACAACGA CCTCTTCA         2042           1447         AAGAGGAGA A UUAUACAA         341         ATTCCCTG GGCTAGCTACAACGA ATCCCTTCT         2043           1454         UGCAGGGA A UUAUACAA         342         TTGATAA GGCTAGCAACGA ATTTCCCT <td></td> <td>· · · · · · · · · · · · · · · · · · ·</td> <td></td> <td></td> <td></td>		· · · · · · · · · · · · · · · · · · ·			
1409         GACUCGUG G CUACUCGU         332         ACGAGTAG GGCTAGCTACAACGA CACGAGTC         2034           1412         UCGUGGCU A CUCGUUAA         333         TTAACGAG GGCTAGCTACAACGA AGCCACGA         2035           1416         GGCUACUC G UUAAUUAU         334         ATAATTAA GGCTAGCTACAACGA GAGTAGCC         2036           1420         ACUCGUUA A UUAUCAAG         335         CTTGATAA GGCTAGCTACAACGA TAACGAGT         2037           1423         CGUUAAUU A UCAAGGAC         336         GTCCTTGA GGCTAGCTACAACGA AATTAACG         2038           1430         UAUCAAGGA C GUAACUG         337         CAGTTACG GGCTAGCTACAACGA CCTTGATA         2039           1432         UCAAGGAC G UAACUGAA         338         TTCAGTTA GGCTAGCTACAACGA GTCCTTGA         2040           1435         AGGACGUA A CUGAAGG         339         CTCTTCAG GGCTAGCTACAACGA TACGTCCT         2041           1445         UGAAGAGG A UGCAGGGA         340         TCCCTGCA GGCTAGCTACAACGA ATCCTCTT         2042           1447         AAGAGGAU G CAGGGAAU         341         ATTCCCTG GGCTAGCTACAACGA ATCCTCTT         2044           1454         UGCAGGGA A UUAUACAA         342         TTGTATAA GGCTAGCTACAACGA ATCCTCT         2044           1457         AGGAAUAU A CAAUCUU         343         AGATTGTA GGCTAGCTACAACGA ATTATTCC         204					•
1412 UCGUGGCU A CUCGUUAA 333 TTAACGAG GGCTAGCTACAACGA AGCCACGA 2035 1416 GGCUACUC G UJAAUJAU 334 ATAATTAA GGCTAGCTACAACGA GAGTAGCC 2036 1420 ACUCGUUA A UJAUCAAG 335 CTTGATAA GGCTAGCTACAACGA TAACGAGT 2037 1423 CGUUAAUU A UCAAGGAC 336 GTCCTTGA GGCTAGCTACAACGA AATTAACG 2038 1430 UAUCAAGG A CGUAACUG 337 CAGTTACG GGCTAGCTACAACGA CCTTGATA 2039 1432 UCAAGGAC G UAACUGAA 338 TTCAGTTA GGCTAGCAACGA GTCCTTGA 2040 1435 AGGACGUA A CUGAAGAG 339 CTCTTCAG GGCTAGCTACAACGA TACGTCCT 2041 1445 UGAAGAGG A UGCAGGGA 340 TCCCTGCA GGCTAGCTACAACGA TCCTCTCA 2042 1447 AAGAGGAU G CAGGGAAU 341 ATTCCCTG GGCTAGCTACAACGA TCCTCTT 2043 1454 UGCAGGGA A UJAUACAA 342 TTGTATAA GGCTAGCTACAACGA ATTCCCTT 2045 1457 AGGGAAUU A UACAAUCU 343 AGATTGTA GGCTAGCTACAACGA ATTCCCT 2045 1459 GGAAUJAU A CAAUCUUG 344 CAAGATTG GGCTAGCTACAACGA ATATTCC 2046 1462 AUJAUACAA UCUUGCUG 345 CAGCAAGA GGCTAGCTACAACGA ATATTCC 2046 1462 AUJAUACA A UCUUGCUG 346 ATGCTCAG GGCTAGCTACAACGA AGATTGT 2048 1472 CUUGCUGA G CAUAAAAC 347 GTTTTATG GGCTAGCTACAACGA AGATTGT 2048 1474 UGCUGAGC A UAAAACAG 348 CTGTTTTA GGCTAGCTACAACGA TCAGCAAG 2049 1474 UGCUGAGC A UAAAACAG 348 CTGTTTTA GGCTAGCTACAACGA TCAGCAAG 2050 1479 AGCAUAAA A CAGUCAAA 349 TTTGACTG GGCTAGCTACAACGA TTTATGCT 2051 1482 AUAAAACA G UCAAAUGU 350 ACATTTGA GGCTAGCTACAACGA TTTATGCT 2051 1483 AGACAAAA G GUCAAAUGU 350 ACATTTGA GGCTAGCTACAACGA TTTATGCT 2051 1484 ACAGUCAA A UGUGUUAA 351 TAAACACA GGCTAGCTACAACGA TTTATGCT 2051 1487 ACAGUCAA A UGUGUUAA 351 TAAACACA GGCTAGCTACAACGA TTTATGCT 2053 1489 AGUCAAAU G UGUAAAAA 352 TTTAAACA GGCTAGCTACAACGA ATTTGACT 2054 1491 UCAAAUGU G UUUAAAAA 352 TTTAAACA GGCTAGCTACAACGA ACTTTGACT 2054					
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1445 UGAAGAGG A UGCAGGGA 340 TCCCTGCA GGCTAGCTACAACGA CCTCTTCA 2042 1447 AAGAGGAU G CAGGGAAU 341 ATTCCCTG GGCTAGCTACAACGA ATCCTCTT 2043 1454 UGCAGGGA A UUAUACAA 342 TTGTATAA GGCTAGCTACAACGA ATCCCTGCA 2044 1457 AGGGAAUU A UACAAUCU 343 AGATTGTA GGCTAGCTACAACGA ATTCCCT 2045 1459 GGAAUUAU A CAAUCUUG 344 CAAGATTG GGCTAGCTACAACGA ATAATTCC 2046 1462 AUUAUACA A UCUUGCUG 345 CAGCAAGA GGCTAGCTACAACGA AGATTGT 2047 1467 ACAAUCUU G CUGAGCAU 346 ATGCTCAG GGCTAGCTACAACGA AAGATTGT 2048 1472 CUUGCUGA G CAUAAAAC 347 GTTTTATG GGCTAGCTACAACGA TCAGCAAG 2049 1474 UGCUGAGC A UAAAACAG 348 CTGTTTTA GGCTAGCTACAACGA GCTCAGCA 2050 1479 AGCAUAAA A CAGUCAAA 349 TTTGACTG GGCTAGCTACAACGA TTTATGCT 2051 1482 AUAAAACA G UCAAAUGU 350 ACATTTGA GGCTAGCTACAACGA TGTTTTAT 2052 1487 ACAGUCAA A UGUGUUUA 351 TAAACACA GGCTAGCTACAACGA TTGACTGT 2053 1489 AGUCAAAU G UGUUUAAAA 352 TTTAAACA GGCTAGCTACAACGA ATTTGACT 2054 1491 UCAAAUGU G UUUAAAAA 353 TTTTTAAAC GGCTAGCTACAACGA ACATTTGA 2055 1499 GUUUAAAAA A CCUCACUG 354 CAGTGAGG GGCTAGCTACAACGA ACATTTGA 2056	1435	AGGACGUA A CUGAAGAG	339		
1447 AAGAGGAU G CAGGGAAU 341 ATTCCCTG GGCTAGCTACAACGA ATCCTCTT 2043 1454 UGCAGGGA A UUAUACAA 342 TTGTATAA GGCTAGCTACAACGA TCCCTGCA 2044 1457 AGGGAAUU A UACAAUCU 343 AGATTGTA GGCTAGCTACAACGA AATTCCCT 2045 1459 GGAAUUAU A CAAUCUUG 344 CAAGATTG GGCTAGCTACAACGA ATAATTCC 2046 1462 AUUAUACA A UCUUGCUG 345 CAGCAAGA GGCTAGCTACAACGA TGTATAAT 2047 1467 ACAAUCUU G CUGAGCAU 346 ATGCTCAG GGCTAGCTACAACGA AAGATTGT 2048 1472 CUUGCUGA G CAUAAAAC 347 GTTTTATG GGCTAGCTACAACGA TCAGCAAG 2049 1474 UGCUGAGC A UAAAACAG 348 CTGTTTTA GGCTAGCTACAACGA GCTCAGCA 2050 1479 AGCAUAAA A CAGUCAAA 349 TTTGACTG GGCTAGCTACAACGA TGTTTTAT 2051 1482 AUAAAACA G UCAAAUGU 350 ACATTTGA GGCTAGCTACAACGA TGTTTTAT 2052 1487 ACAGUCAA A UGUGUUUA 351 TAAACACA GGCTAGCTACAACGA TTGACTGT 2053 1489 AGUCAAAU G UGUUUAAA 352 TTTAAACA GGCTAGCTACAACGA ATTTGACT 2054 1491 UCAAAUGU G UUUAAAAA 353 TTTTTAAAC GGCTAGCTACAACGA TTTTAAAC 2056	1445	UGAAGAGG A UGCAGGGA	340		
1457 AGGGAAUU A UACAAUCU 343 AGATTGTA GGCTAGCTACAACGA AATTCCCT 2045 1459 GGAAUUAU A CAAUCUUG 344 CAAGATTG GGCTAGCTACAACGA ATAATTCC 2046 1462 AUUAUACA A UCUUGCUG 345 CAGCAAGA GGCTAGCTACAACGA TGTATAAT 2047 1467 ACAAUCUU G CUGAGCAU 346 ATGCTCAG GGCTAGCTACAACGA AAGATTGT 2048 1472 CUUGCUGA G CAUAAAAC 347 GTTTTATG GGCTAGCTACAACGA TCAGCAAG 2049 1474 UGCUGAGC A UAAAACAG 348 CTGTTTTA GGCTAGCTACAACGA GCTCAGCA 2050 1479 AGCAUAAA A CAGUCAAA 349 TTTGACTG GGCTAGCTACAACGA TTTATGCT 2051 1482 AUAAAACA G UCAAAUGU 350 ACATTTGA GGCTAGCTACAACGA TGTTTTAT 2052 1487 ACAGUCAA A UGUGUUUA 351 TAAACACA GGCTAGCTACAACGA TTGACTGT 2053 1489 AGUCAAAU G UGUUUAAA 352 TTTAAACA GGCTAGCTACAACGA ATTTGACT 2054 1491 UCAAAUGU G UUUAAAAA 353 TTTTTAAAC GGCTAGCTACAACGA ACATTGA 2055	1447	AAGAGGAU G CAGGGAAU	341		2043
1459 GGAAUUAU A CAAUCUUG 344 CAAGATTG GGCTAGCTACAACGA ATAATTCC 2046 1462 AUUAUACA A UCUUGCUG 345 CAGCAAGA GGCTAGCTACAACGA TGTATAAT 2047 1467 ACAAUCUU G CUGAGCAU 346 ATGCTCAG GGCTAGCTACAACGA AAGATTGT 2048 1472 CUUGCUGA G CAUAAAAC 347 GTTTTATG GGCTAGCTACAACGA TCAGCAAG 2049 1474 UGCUGAGC A UAAAACAG 348 CTGTTTTA GGCTAGCTACAACGA GCTCAGCA 2050 1479 AGCAUAAA A CAGUCAAA 349 TTTGACTG GGCTAGCTACAACGA TTTATGCT 2051 1482 AUAAAACA G UCAAAUGU 350 ACATTTGA GGCTAGCTACAACGA TGTTTTAT 2052 1487 ACAGUCAA A UGUGUUUA 351 TAAACACA GGCTAGCTACAACGA TTGACTGT 2053 1489 AGUCAAAU G UGUUUAAAA 352 TTTAAACA GGCTAGCTACAACGA ATTTGACT 2054 1491 UCAAAUGU G UUUAAAAA 353 TTTTTAAA GGCTAGCTACAACGA ACATTGA 2055	1454	UGCAGGGA A UUAUACAA	342	TTGTATAA GGCTAGCTACAACGA TCCCTGCA	2044
1462 AUUAUACA A UCUUGCUG 345 CAGCAAGA GGCTAGCTACAACGA TGTATAAT 2047 1467 ACAAUCUU G CUGAGCAU 346 ATGCTCAG GGCTAGCTACAACGA AAGATTGT 2048 1472 CUUGCUGA G CAUAAAAC 347 GTTTTATG GGCTAGCTACAACGA TCAGCAAG 2049 1474 UGCUGAGC A UAAAACAG 348 CTGTTTTA GGCTAGCTACAACGA GCTCAGCA 2050 1479 AGCAUAAA A CAGUCAAA 349 TTTGACTG GGCTAGCTACAACGA TTTATGCT 2051 1482 AUAAAACA G UCAAAUGU 350 ACATTTGA GGCTAGCTACAACGA TGTTTTAT 2052 1487 ACAGUCAA A UGUGUUUA 351 TAAACACA GGCTAGCTACAACGA TTGACTGT 2053 1489 AGUCAAAU G UGUUUAAA 352 TTTAAACA GGCTAGCTACAACGA ATTTGACT 2054 1491 UCAAAUGU G UUUAAAAA 353 TTTTTAAA GGCTAGCTACAACGA ACATTTGA 2055 1499 GUUUAAAA A CCUCACUG 354 CAGTGAGG GGCTAGCTACAACGA TTTTAAAC 2056	1457	AGGGAAUU A UACAAUCU	343	AGATTGTA GGCTAGCTACAACGA AATTCCCT	2045
1467 ACAAUCUU G CUGAGCAU 346 ATGCTCAG GGCTAGCTACAACGA AAGATTGT 2048 1472 CUUGCUGA G CAUAAAAC 347 GTTTTATG GGCTAGCTACAACGA TCAGCAAG 2049 1474 UGCUGAGC A UAAAACAG 348 CTGTTTTA GGCTAGCTACAACGA GCTCAGCA 2050 1479 AGCAUAAA A CAGUCAAA 349 TTTGACTG GGCTAGCTACAACGA TTTATGCT 2051 1482 AUAAAACA G UCAAAUGU 350 ACATTTGA GGCTAGCTACAACGA TGTTTTAT 2052 1487 ACAGUCAA A UGUGUUUA 351 TAAACACA GGCTAGCTACAACGA TTGACTGT 2053 1489 AGUCAAAU G UGUUUAAA 352 TTTAAACA GGCTAGCTACAACGA ATTTGACT 2054 1491 UCAAAUGU G UUUAAAAA 353 TTTTTAAA GGCTAGCTACAACGA ACATTTGA 2055 1499 GUUUAAAA A CCUCACUG 354 CAGTGAGG GGCTAGCTACAACGA TTTTAAAC 2056	1459	GGAAUUAU A CAAUCUUG	344	CAAGATTG GGCTAGCTACAACGA ATAATTCC	2046
1472 CUUGCUGA G CAUAAAAC 347 GTTTTATG GGCTAGCTACAACGA TCAGCAAG 2049 1474 UGCUGAGC A UAAAACAG 348 CTGTTTTA GGCTAGCTACAACGA GCTCAGCA 2050 1479 AGCAUAAA A CAGUCAAA 349 TTTGACTG GGCTAGCTACAACGA TTTATGCT 2051 1482 AUAAAACA G UCAAAUGU 350 ACATTTGA GGCTAGCTACAACGA TGTTTTAT 2052 1487 ACAGUCAA A UGUGUUUA 351 TAAACACA GGCTAGCTACAACGA TTGACTGT 2053 1489 AGUCAAAU G UGUUUAAA 352 TTTAAACA GGCTAGCTACAACGA ATTTGACT 2054 1491 UCAAAUGU G UUUAAAAA 353 TTTTTAAA GGCTAGCTACAACGA ACATTTGA 2055 1499 GUUUAAAA A CCUCACUG 354 CAGTGAGG GGCTAGCTACAACGA TTTTAAAC 2056	1462	AUUAUACA A UCUUGCUG	345	CAGCAAGA GGCTAGCTACAACGA TGTATAAT	2047
1474 UGCUGAGC A UAAAACAG 348 CTGTTTTA GGCTAGCTACAACGA GCTCAGCA 2050 1479 AGCAUAAA A CAGUCAAA 349 TTTGACTG GGCTAGCTACAACGA TTTATGCT 2051 1482 AUAAAACA G UCAAAUGU 350 ACATTTGA GGCTAGCTACAACGA TGTTTTAT 2052 1487 ACAGUCAA A UGUGUUUA 351 TAAACACA GGCTAGCTACAACGA TTGACTGT 2053 1489 AGUCAAAU G UGUUUAAA 352 TTTAAACA GGCTAGCTACAACGA ATTTGACT 2054 1491 UCAAAUGU G UUUAAAAA 353 TTTTTAAA GGCTAGCTACAACGA ACATTTGA 2055 1499 GUUUAAAA A CCUCACUG 354 CAGTGAGG GGCTAGCTACAACGA TTTTAAAC 2056	1467	ACAAUCUU G CUGAGCAU	346	ATGCTCAG GGCTAGCTACAACGA AAGATTGT	2048
1479 AGCAUAAA A CAGUCAAA 349 TTTGACTG GGCTAGCTACAACGA TTTATGCT 2051 1482 AUAAAACA G UCAAAUGU 350 ACATTTGA GGCTAGCTACAACGA TGTTTTAT 2052 1487 ACAGUCAA A UGUGUUUA 351 TAAACACA GGCTAGCTACAACGA TTGACTGT 2053 1489 AGUCAAAU G UGUUUAAA 352 TTTAAACA GGCTAGCTACAACGA ATTTGACT 2054 1491 UCAAAUGU G UUUAAAAA 353 TTTTTAAA GGCTAGCTACAACGA ACATTTGA 2055 1499 GUUUAAAA A CCUCACUG 354 CAGTGAGG GGCTAGCTACAACGA TTTTAAAC 2056	1472	CUUGCUGA G CAUAAAAC	347	GTTTTATG GGCTAGCTACAACGA TCAGCAAG	2049
1482 AUAAAACA G UCAAAUGU 350 ACATTTGA GGCTAGCTACAACGA TGTTTTAT 2052 1487 ACAGUCAA A UGUGUUUA 351 TAAACACA GGCTAGCTACAACGA TTGACTGT 2053 1489 AGUCAAAU G UGUUUAAA 352 TTTAAACA GGCTAGCTACAACGA ATTTGACT 2054 1491 UCAAAUGU G UUUAAAAA 353 TTTTTAAA GGCTAGCTACAACGA ACATTTGA 2055 1499 GUUUAAAA A CCUCACUG 354 CAGTGAGG GGCTAGCTACAACGA TTTTAAAC 2056	1474	UGCUGAGC A UAAAACAG	348	CTGTTTTA GGCTAGCTACAACGA GCTCAGCA	2050
1487 ACAGUCAA A UGUGUUUA 351 TAAACACA GGCTAGCTACAACGA TTGACTGT 2053 1489 AGUCAAAU G UGUUUAAA 352 TTTAAACA GGCTAGCTACAACGA ATTTGACT 2054 1491 UCAAAUGU G UUUAAAAA 353 TTTTTAAA GGCTAGCTACAACGA ACATTTGA 2055 1499 GUUUAAAA A CCUCACUG 354 CAGTGAGG GGCTAGCTACAACGA TTTTAAAC 2056	1479	AGCAUAAA A CAGUCAAA	349	TTTGACTG GGCTAGCTACAACGA TTTATGCT	2051
1487 ACAGUCAA A UGUGUUUA 351 TAAACACA GGCTAGCTACAACGA TTGACTGT 2053 1489 AGUCAAAU G UGUUUAAA 352 TTTAAACA GGCTAGCTACAACGA ATTTGACT 2054 1491 UCAAAUGU G UUUAAAAA 353 TTTTTAAA GGCTAGCTACAACGA ACATTTGA 2055 1499 GUUUAAAA A CCUCACUG 354 CAGTGAGG GGCTAGCTACAACGA TTTTAAAC 2056	1482	AUAAAACA G UCAAAUGU	350	ACATTTGA GGCTAGCTACAACGA TGTTTTAT	2052
1491 UCAAAUGU G UUUAAAAA 353 TTTTTAAA GGCTAGCTACAACGA ACATTTGA 2055 1499 GUUUAAAA A CCUCACUG 354 CAGTGAGG GGCTAGCTACAACGA TTTTAAAC 2056	1487	ACAGUCAA A UGUGUUUA	351		2053
1499 GUUUAAAA A CCUCACUG 354 CAGTGAGG GGCTAGCTACAACGA TTTTAAAC 2056	1489	AGUCAAAU G UGUUUAAA	352	TTTAAACA GGCTAGCTACAACGA ATTTGACT	2054
	1491	UCAAAUGU G UUUAAAAA	353	TTTTTAAA GGCTAGCTACAACGA ACATTTGA	2055
1504 AAAACCUC A CUGCCACU 355 AGTGGCAG GGCTAGCTACAACGA GAGGTTTT 2057		GUUUAAAA A CCUCACUG	354	CAGTGAGG GGCTAGCTACAACGA TTTTAAAC	2056
			355	AGTGGCAG GGCTAGCTACAACGA GAGGTTTT	2057
1507 ACCUCACU G CCACUCUA 356 TAGAGTGG GGCTAGCTACAACGA AGTGAGGT 2058	1507		356	TAGAGTGG GGCTAGCTACAACGA AGTGAGGT	2058
1510 UCACUGCC A CUCUAAUU 357 AATTAGAG GGCTAGCTACAACGA GGCAGTGA 2059	-		357	AATTAGAG GGCTAGCTACAACGA GGCAGTGA	2059
1516 CCACUCUA A UUGUCAAU 358 ATTGACAA GGCTAGCTACAACGA TAGAGTGG 2060			358	ATTGACAA GGCTAGCTACAACGA TAGAGTGG	2060
1519 CUCUAAUU G UCAAUGUG 359 CACATTGA GGCTAGCTACAACGA AATTAGAG 2061			359		2061
1523 AAUUGUCA A UGUGAAAC 360 GTTTCACA GGCTAGCTACAACGA TGACAATT 2062	1523	AAUUGUCA A UGUGAAAC	360	GTTTCACA GGCTAGCTACAACGA TGACAATT	2062

7505		2.55	COCCUTACY COMPACTOR OF THE COLUMN	
1525	UUGUCAAU G UGAAACCC	361	GGGTTTCA GGCTAGCTACAACGA ATTGACAA	2063
1530	AAUGUGAA A CCCCAGAU	362	ATCTGGGG GGCTAGCTACAACGA TTCACATT	2064
1537	AACCCCAG A UUUACGAA	363	TTCGTAAA GGCTAGCTACAACGA CTGGGGTT	2065
1541	CCAGAUUU A CGAAAAGG	364	CCTTTTCG GGCTAGCTACAACGA AAATCTGG	2066
1549	ACGAAAAG G CCGUGUCA	365	TGACACGG GGCTAGCTACAACGA CTTTTCGT	2067
1552	AAAAGGCC G UGUCAUCG	366	CGATGACA GGCTAGCTACAACGA GGCCTTTT	2068
1554	AAGGCCGU G UCAUCGUU	367	AACGATGA GGCTAGCTACAACGA ACGGCCTT	2069
1557	GCCGUGUC A UCGUUUCC	368	GGAAACGA GGCTAGCTACAACGA GACACGGC	2070
1560	GUGUCAUC G UUUCCAGA	369	TCTGGAAA GGCTAGCTACAACGA GATGACAC	2071
1568	GUUUCCAG A CCCGGCUC	370	GAGCCGGG GGCTAGCTACAACGA CTGGAAAC	2072
1573	CAGACCCG G CUCUCUAC	371	GTAGAGAG GGCTAGCTACAACGA CGGGTCTG	2073
1580	GGCUCUCU A CCCACUGG	372	CCAGTGGG GGCTAGCTACAACGA AGAGAGCC	2074
1584	CUCUACCC A CUGGGCAG	373	CTGCCCAG GGCTAGCTACAACGA GGGTAGAG	2075
1589	CCCACUGG G CAGCAGAC	374	GTCTGCTG GGCTAGCTACAACGA CCAGTGGG	2076
1592	ACUGGGCA G CAGACAAA	375	TTTGTCTG GGCTAGCTACAACGA TGCCCAGT	2077
1596	GGCAGCAG A CAAAUCCU	376	AGGATTTG GGCTAGCTACAACGA CTGCTGCC	2078
1600	GCAGACAA A UCCUGACU	377	AGTCAGGA GGCTAGCTACAACGA TTGTCTGC	2079
1606	AAAUCCUG A CUUGUACC	378	GGTACAAG GGCTAGCTACAACGA CAGGATTT	2080
1610	CCUGACUU G UACCGCAU	379	ATGCGGTA GGCTAGCTACAACGA AAGTCAGG	2081
1612	UGACUUGU A CCGCAUAU	380	ATATGCGG GGCTAGCTACAACGA ACAAGTCA	2082
1615	CUUGUACC G CAUAUGGU	381	ACCATATG GGCTAGCTACAACGA GGTACAAG	2083
1617	UGUACCGC A UAUGGUAU	382	ATACCATA GGCTAGCTACAACGA GCGGTACA	20B4
1619	UACCGCAU A UGGUAUCC	383	GGATACCA GGCTAGCTACAACGA ATGCGGTA	2085
1622	CGCAUAUG G UAUCCCUC	384	GAGGGATA GGCTAGCTACAACGA CATATGCG	2086
1624	CAUAUGGU A UCCCUCAA	385	TTGAGGGA GGCTAGCTACAACGA ACCATATG	2087
1632	AUCCCUCA A CCUACAAU	386	ATTGTAGG GGCTAGCTACAACGA TGAGGGAT	2088
1636	CUCAACCU A CAAUCAAG	387	CTTGATTG GGCTAGCTACAACGA AGGTTGAG	2089
1639	AACCUACA A UCAAGUGG	388	CCACTTGA GGCTAGCTACAACGA TGTAGGTT	2090
1644	ACAAUCAA G UGGUUCUG	389	CAGAACCA GGCTAGCTACAACGA TTGATTGT	2091
1647	AUCAAGUG G UUCUGGCA	390	TGCCAGAA GGCTAGCTACAACGA CACTTGAT	2092
1653	UGGUUCUG G CACCCCUG	391	CAGGGGTG GGCTAGCTACAACGA CAGAACCA	2093
1655	GUUCUGGC A CCCCUGUA	392	TACAGGGG GGCTAGCTACAACGA GCCAGAAC	2094
1661	GCACCCCU G UAACCAUA	393	TATGGTTA GGCTAGCTACAACGA AGGGGTGC	2095
1664	CCCCUGUA A CCAUAAUC	394	GATTATGG GGCTAGCTACAACGA TACAGGGG	2096
1667	CUGUAACC A UAAUCAUU	395	AATGATTA GGCTAGCTACAACGA GGTTACAG	2097
1670	UAACCAUA A UCAUUCCG	396	CGGAATGA GGCTAGCTACAACGA TATGGTTA	2098
1673	CCAUAAUC A UUCCGAAG	397	CTTCGGAA GGCTAGCTACAACGA GATTATGG	2099
1681	AUUCCGAA G CAAGGUGU	398	ACACCTTG GGCTAGCTACAACGA TTCGGAAT	2100
1686	GAAGCAAG G UGUGACUU	399	AAGTCACA GGCTAGCTACAACGA CTTGCTTC	2101
1688	AGCAAGGU G UGACUUUU	400	AAAAGTCA GGCTAGCTACAACGA ACCTTGCT	2102
1691	AAGGUGUG A CUUUUGUU	401	AACAAAAG GGCTAGCTACAACGA CACACCTT	2103
1697	UGACUUUU G UUCCAAUA	402	TATTGGAA GGCTAGCTACAACGA AAAAGTCA	2104
1703	UUGUUCCA A UAAUGAAG	403	CTTCATTA GGCTAGCTACAACGA TGGAACAA	2105
1706	UUCCAAUA A UGAAGAGU	404	ACTOTTCA GGCTAGCTACAACGA TATTGGAA	2106
1713	AAUGAAGA G UCCUUUAU	405	ATAAAGGA GGCTAGCTACAACGA TCTTCATT	2107
1720	AGUCCUUU A UCCUGGAU	406	ATCCAGGA GGCTAGCTACAACGA AAAGGACT	2108
1727	UAUCCUGG A UGCUGACA	407	TGTCAGCA GGCTAGCTACAACGA CCAGGATA	2109
1729	UCCUGGAU G CUGACAGC	408	GCTGTCAG GGCTAGCTACAACGA ATCCAGGA	2110
1733	GGAUGCUG A CAGCAACA	409	TGTTGCTG GGCTAGCTACAACGA CAGCATCC	2111
1736	UGCUGACA G CAACAUGG	410	CCATGTTG GGCTAGCTACAACGA TGTCAGCA	2112
1739	UGACAGCA A CAUGGGAA	411	TTCCCATG GGCTAGCTACAACGA TGCTGTCA	2113
1741	ACAGCAAC A UGGGAAAC	412	GTTTCCCA GGCTAGCTACAACGA GTTGCTGT	2114
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1748	CALICOGNA A CACANITIC	1 412	CA AMMONG COOMA COMA CA A COA MINICOCAMO	2225
	CAUGGGAA A CAGAAUUG	413	CAATTCTG GGCTAGCTACAACGA TTCCCATG	
1753	GAAACAGA A UUGAGAGC	414	GCTCTCAA GGCTAGCTACAACGA TCTGTTTC	2116
1760	AAUUGAGA G CAUCACUC	415	GAGTGATG GGCTAGCTACAACGA TCTCAATT	2117
1762	UUGAGAGC A UCACUCAG	416	CTGAGTGA GCCTACCTACAACGA GCCCTCAA	2118
1765	AGAGCAUC A CUCAGCGC	417	GCGCTGAG GGCTAGCTACAACGA GATGCTCT	2119
1770	AUCACUCA G CGCAUGGC	418	GCCATGCG GGCTAGCTACAACGA TGAGTGAT	
1772	CACUCAGC G CAUGGCAA	419	TTGCCATG GGCTAGCTACAACGA GCTGAGTG	
1774	CUCAGCGC A UGGCAAUA	420	TATTGCCA GGCTAGCTACAACGA GCGCTGAG	
1777	AGCGCAUG G CAAUAAUA	421	TATTATTG GGCTAGCTACAACGA CATGCGCT	2123
1780	GCAUGGCA A UAAUAGAA	422	TTCTATTA GGCTAGCTACAACGA TGCCATGC	2124
1783	UGGCAAUA A UAGAAGGA	423	TCCTTCTA GGCTAGCTACAACGA TATTGCCA	2125
1796	AGGAAAGA A UAAGAUGG	424	CCATCTTA GGCTAGCTACAACGA TCTTTCCT	2126
1801	AGAAUAAG A UGGCUAGC	425	GCTAGCCA GGCTAGCTACAACGA CTTATTCT	2127
1804	AUAAGAUG G CUAGCACC	426	GGTGCTAG GGCTAGCTACAACGA CATCTTAT	2128
1808	GAUGGCUA G CACCUUGG	427	CCAAGGTG GGCTAGCTACAACGA TAGCCATC	2129
1810	UGGCUAGC A CCUUGGUU	428	AACCAAGG GGCTAGCTACAACGA GCTAGCCA	2130
1816	GCACCUUG G UUGUGGCU	429	AGCCACAA GGCTAGCTACAACGA CAAGGTGC	2131
1819	CCUUGGUU G UGGCUGAC	430	GTCAGCCA GGCTAGCTACAACGA AACCAAGG	2132
1822	UGGUUGUG G CUGACUCU	431	AGAGTCAG GGCTAGCTACAACGA CACAACCA	2133
1826	UGUGGCUG A CUCUAGAA	432	TTCTAGAG GGCTAGCTACAACGA CAGCCACA	2134
1834	ACUCUAGA A UUUCUGGA	433	TCCAGAAA GGCTAGCTACAACGA TCTAGAGT	2135
1843	UUUCUGGA A UCUACAUU	434	AATGTAGA GGCTAGCTACAACGA TCCAGAAA	2136
1847	UGGAAUCU A CAUUUGCA	435	TGCAAATG GGCTAGCTACAACGA AGATTCCA	2137
1849	GAAUCUAC A UUUGCAUA	436	TATGCAAA GGCTAGCTACAACGA GTAGATTC	2138
1853	CUACAUUU G CAUAGCUU	437	AAGCTATG GGCTAGCTACAACGA AAATGTAG	2139
1855	ACAUUUGC A UAGCUUCC	438	GGAAGCTA GGCTAGCTACAACGA GCAAATGT	2140
1858	UUUGCAUA G CUUCCAAU	439	ATTGGAAG GGCTAGCTACAACGA TATGCAAA	2141
1865	AGCUUCCA A UAAAGUUG	440	CAACTTTA GGCTAGCTACAACGA TGGAAGCT	2142
1870	CCAAUAAA G UUGGGACU	441	AGTCCCAA GGCTAGCTACAACGA TTTATTGG	2143
1876	AAGUUGGG A CUGUGGGA	442	TCCCACAG GGCTAGCTACAACGA CCCAACTT	2144
1879	UUGGGACU G UGGGAAGA	443	TCTTCCCA GGCTAGCTACAACGA AGTCCCAA	2145
1889	GGGAAGAA A CAUAAGCU	444	AGCTTATG GGCTAGCTACAACGA TTCTTCCC	2146
1891	GAAGAAAC A UAAGCUUU	445	AAAGCTTA GGCTAGCTACAACGA GTTTCTTC	2147
1895	AAACAUAA G CUUUUAUA	446	TATAAAAG GGCTAGCTACAACGA TTATGTTT	2148
1901	AAGCUUUU A UAUCACAG	447	CTGTGATA GGCTAGCTACAACGA AAAAGCTT	2149
1903	GCUUUUAU A UCACAGAU	448	ATCTGTGA GGCTAGCTACAACGA ATAAAAGC	2150
1906	UUUAUAUC A CAGAUGUG	449	CACATCTG GGCTAGCTACAACGA GATATAAA	2151
1910	UAUCACAG A UGUGCCAA	450	TTGGCACA GGCTAGCTACAACGA CTGTGATA	2152
1912	UCACAGAU G UGCCAAAU	451	ATTTGGCA GGCTAGCTACAACGA ATCTGTGA	2153
1914	ACAGAUGU G CCAAAUGG	452	CCATTTGG GGCTAGCTACAACGA ACATCTGT	2154
1919	UGUGCCAA A UGGGUUUC	453	GAAACCCA GGCTAGCTACAACGA TTGGCACA	2155
1923	CCAAAUGG G UUUCAUGU	454	ACATGAAA GGCTAGCTACAACGA CCATTTGG	2156
1928	UGGGUUUC A UGUUAACU	455	AGTTAACA GGCTAGCTACAACGA GAAACCCA	2157
1930	GGUUUCAU G UUAACUUG	456	CAAGTTAA GGCTAGCTACAACGA ATGAAACC	2158
1934	UCAUGUUA A CUUGGAAA	457	TTTCCAAG GGCTAGCTACAACGA TAACATGA	2159
1945	UGGAAAAA A UGCCGACG	458	CGTCGGCA GGCTAGCTACAACGA TTTTTCCA	2160
1947	GAAAAAAU G CCGACGGA	459	TCCGTCGG GGCTAGCTACAACGA ATTTTTTC	2161
1951	AAAUGCCG A CGGAAGGA	460	TCCTTCCG GGCTAGCTACAACGA CGGCATTT	2162
1964	AGGAGAGG A CCUGAAAC	461	GTTTCAGG GGCTAGCTACAACGA CCTCTCCT	2163
1971	GACCUGAA A CUGUCUUG	462	CAAGACAG GGCTAGCTACAACGA TTCAGGTC	2164
1974	CUGAAACU G UCUUGCAC	463	GTGCAAGA GGCTAGCTACAACGA AGTTTCAG	
1979	ACUGUCUU G CACAGUUA	464	TAACTGTG GGCTAGCTACAACGA AAGACAGT	2166

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1981	HOLIGITICS & CACITIANS	465	CHETA A CINC OCCURA COMA CITA COMA COMA COMA COMA COMA COMA COMA COM	0165
1984	CHICCAGA C HILAACAAC	466	GTTAACTG GGCTAGCTACAACGA GCAAGACA	2167
1988	CUUGCACA G UUAACAAG CACAGUUA A CAAGUUCU	467	CTTGTTAA GGCTAGCTACAACGA TGTGCAAG	2168
1992	GUUAACAA G UUCUUAUA	468	AGAACTTG GGCTAGCTACAACGA TAACTGTG	2169
1998			TATAAGAA GGCTAGCTACAACGA TTGTTAAC	2170
2000	AAGUUCUU A UACAGAGA	469	TCTCTGTA GGCTAGCTACAACGA AAGAACTT	2171
2006	GUUCUUAU A CAGAGACG	470	CGTCTCTG GGCTAGCTACAACGA ATAAGAAC	
2008	AUACAGAG A CGUUACUU	471	AAGTAACG GGCTAGCTACAACGA CTCTGTAT	2173
2011	ACAGAGAC G UUACUUGG	472	CCAAGTAA GGCTAGCTACAACGA GTCTCTGT	
2017	GAGACGUU A CUUGGAUU	473	AATCCAAG GGCTAGCTACAACGA AACGTCTC	
2022	UUACUUGG A UUUUACUG UGGAUUUU A CUGCGGAC	474	CAGTAAAA GGCTAGCTACAACGA CCAAGTAA	2176
2025	AUUUUACU G CGGACAGU	475	GTCCGCAG GGCTAGCTACAACGA AAAATCCA	2177
2029	UACUGCGG A CAGUUAAU	476	ACTGTCCG GGCTAGCTACAACGA AGTAAAAT	2178
2032	UGCGGACA G UUAAUAAC	477	ATTAACTG GGCTAGCTACAACGA CCGCAGTA	2179
2036	GACAGUUA A UAACAGAA	478	GTTATTAA GGCTAGCTACAACGA TGTCCGCA	2180
2039	AGUUAAUA A CAGAACAA	480	TTCTGTTA GGCTAGCTACAACGA TAACTGTC	2181
2044	AUAACAGA A CAAUGCAC		TTGTTCTG GGCTAGCTACAACGA TATTAACT	2182
2047		481	GTGCATTG GGCTAGCTACAACGA TCTGTTAT	2183
2049	ACAGAACA A UGCACUAC AGAACAAU G CACUACAG	482	GTAGTGCA GGCTAGCTACAACGA TGTTCTGT	2184
2051		483	CTGTAGTG GGCTAGCTACAACGA ATTGTTCT	2185
2054	AACAAUGC A CUACAGUA AAUGCACU A CAGUAUUA	484	TACTGTAG GGCTAGCTACAACGA GCATTGTT	2186
2057		485	TAATACTG GGCTAGCTACAACGA AGTGCATT	2187
2059	GCACUACA G UAUUAGCA ACUACAGU A UUAGCAAG	486	TGCTAATA GGCTAGCTACAACGA TGTAGTGC	2188
2063	CAGUADUA G CAAGCAAA	487	CTTGCTAA GGCTAGCTACAACGA ACTGTAGT	2189 ·
2067	AUUAGCAA G CAAAAAAU	488	TTTGCTTG GGCTAGCTACAACGA TAATACTG	2190
2074	AGCAAAAA A UGGCCAUC	489	ATTTTTTG GGCTAGCTACAACGA TTGCTAAT	2191
2077	AAAAAAUG G CCAUCACU	491	GATGGCCA GGCTAGCTACAACGA TTTTTGCT	2192
2080	AAAUGGCC A UCACUAAG		AGTGATGG GGCTAGCTACAACGA CATTTTT	2193
2083	UGGCCAUC A CUAAGGAG	492	CTTAGTGA GGCTAGCTACAACGA GGCCATTT	2194
2091	ACUAAGGA G CACUCCAU	494	CTCCTTAG GGCTAGCTACAACGA GATGGCCA	2195
2093	UAAGGAGC A CUCCAUCA	495	ATGGAGG GCCTACCTACA ACCA CCTTAGT	2196
2098	AGCACUCC A UCACUCUU	496	TGATGGAG GGCTAGCTACAACGA GCTCCTTA	2197
2101	ACUCCAUC A CUCUUAAU	497	AAGAGTGA GGCTAGCTACAACGA GGAGTGCT	2198
2108	CACUCUUA A UCUUACCA	498	ATTAAGAG GGCTAGCTACAACGA GATGGAGT TGGTAAGA GGCTAGCTACAACGA TAAGAGTG	2199
2113	UUAAUCUU A CCAUCAUG	499	CATGATGG GGCTAGCTACAACGA AAGATTAA	2200
2116	AUCUUACC A UCAUGAAU	500	ATTCATGA GGCTAGCTACAACGA GGTAAGAT	2201
2119	UUACCAUC A UGAAUGUU	501	AACATTCA GGCTAGCTACAACGA GATGGTAA	2202
2123	CAUCAUGA A UGUUUCCC	502	GGGAAACA GGCTAGCTACAACGA TCATGATG	
2125	UCAUGAAU G UUUCCCUG	503	CAGGGAAA GGCTAGCTACAACGA ATTCATGA	2204
2133	GUUUCCCU G CAAGAUUC	504		2205
2138	CCUGCAAG A UUCAGGCA	505	GAATCTTG GGCTAGCTACAACGA AGGGAAAC TGCCTGAA GGCTAGCTACAACGA CTTGCAGG	
2144	AGAUUCAG G CACCUAUG	506	CATAGGTG GGCTAGCTACAACGA CTGAATCT	
2146	AUUCAGGC A CCUAUGCC	507	GGCATAGG GGCTAGCTACAACGA GCCTGAAT	2208
2150	AGGCACCU A UGCCUGCA	508	TGCAGGCA GGCTAGCTACAACGA AGGTGCCT	2209
2152	GCACCUAU G CCUGCAGA	509	TCTGCAGG GGCTAGCTACAACGA ATAGGTGC	2210
2156	CUAUGCCU G CAGAGCCA	510	TGGCTCTG GGCTAGCTACAACGA AGGCATAG	2212
2161	CCUGCAGA G CCAGGAAU	511	ATTCCTGG GGCTAGCTACAACGA TCTGCAGG	
2168	AGCCAGGA A UGUAUACA	512	TGTATACA GGCTAGCTACAACGA TCCTGGCT	2213
2170	CCAGGAAU G UAUACACA	513	TGTGTATA GGCTAGCTACAACGA ATTCCTGG	2214
2172	AGGAAUGU A UACACAGG	514	CCTGTGTA GGCTAGCTACAACGA ACATTCCT	2215
2174	GAAUGUAU A CACAGGGG	515	CCCCTGTG GGCTAGCTACAACGA ACATTCCT	
2176	AUGUAUAC A CAGGGGAA	516		2217
	TOTAL A CAGGGAA	240	TTCCCCTG GGCTAGCTACAACGA GTATACAT	2218

2206   AGAANGAA A UUACAAUC   518   GATTGTAA GGCTAGCTACAACGA TTCTTTCT   2220	2100	CCCARCAR A MCCMCCAC	517	CERCUACIO COCERCOTA CA ACCA TENCETECCO	2210
2209   AAGARAUU A CANUCAGA   519   TCTGATTG GGCTAGCTACAACGA ANTTCTT   2221	2188	GGGAAGAA A UCCUCCAG			
2212         ANDURACA A UCAGAGAU         520         ATCTCTGA GGCTAGCTACAAGGA TOTAATT         2222           2217         ANUCAGGAA G         521         CTTCCTGA GGCTAGCTACAAGGA TCTGATT         223           2227         ANUCAGGAA G         522         GTATGGTG GGCTAGCTACAAGGA TCTCGTGAT         2225           2229         CAGGAAGC A CACUACCU         524         AGGAGTG GGCTAGCTACAAGGA GCTTCCTO         2225           2221         AGACCCAU A COUCCUGC         524         AGGAGGA GGCTAGCTACAAGGA GCTTCCTO         2226           2224         AGACCCAU G COUCCUGC         525         CAGGGAGG GGCTAGCTACAAGGA ATGGTGCT         2227           2246         COUGCGAA A CCUCAGUG         526         CAGGGAGG GGCTAGCTACAAGGA ATGGGTT         2228           2246         COUGCGAA A CCUCAGUG         527         CACTGAGG GGCTAGCTACAAGGA TCGGAGG         2229           2255         CACUAGUG A UCACACG         529         CTGTGTGA GGCTAGCAAGGA ATCACTGAGG         2231           2266         CAGUAGA C ACAGGUGG         530         CCACTGTG GGCTAGCTACAAGGA ATCACTGAGG         2231           2266         ACACAGUG G CAGUAGG         531         GCCACTG GGCTAGCTACAAGGA ATCACTGAGG         2232           2267         ACGGGCA D UCACACA         536         ACTGCTGA GGCTACACAGGA ATCACTGAGGA         2236      <	<b>———</b>				
2219					
2227         AUCAGGAR G CACCAUACC         522         GTATGGTG GGCTAGCTACACGA TTCCTGAT         2224           2229         CAGGARGC A CCAUACCU         523         AGGARGG G GGCTAGCTACACGA GGTGTCTC         2225           2234         AGCACCAU A CCUCCUGC         524         AGGAGGTA GGCTAGCTACAACGA GGTGTCT         2225           2234         AGCACCAU A CCUCCUGC         525         GCAGGAG GCTAGCTACAACGA AGGAGGTCT         2227           2241         UUCCUCCUG G CAAACCU         526         AGGTTTCG GGCTAGCTACAACGA AGGAGTATCGCAG         2229           2242         CUCCUCAGUG G UGAUCACA         528         TGTGATCA GGCTAGCTACAACGA TAGGAGTACACGA         2229           2255         CACCACAG G UGAUCACA         529         CTGTGTGA GGCTAGCTACAACGA TAGGAGTACACGA         2231           2258         CAGGAGU C ACACCAGG         530         CACCATGGA GGCTAGCTACAACGA CACTGAGG         2231           2260         GUGAUCAC A CAGGUGC         531         GGCCACTG GGCTAGCACACAGA TATGTCACACCA         2232           2263         ACACACAUG G GCAGUCCA         532         GATGGTAGCACACACACACACACACACACACACACACACA	<u> </u>				
2229         CAGGARAGC A CCAUACCU         523         AGGTATGG GGCTAGCTACAGAG GCTTCCTO         2225           22314         AGAGCCAU A CCUCCUGC         525         AGGAGGAG GGCTAGCTACAGAG GGTCCTC         2226           22341         AGACCAU A CCUCCUGC         525         AGGAGGAG GGCTAGCTACAAGGA ARGAGGT         2227           22441         UACCUCCU G CGAAACCU         526         AGGTTTCG GGCTAGCTACAACGA ARGAGTACCACGA         2228           2246         CCUCGGGA A CCUCAGUG         527         CACTGAGG GGCTAGCTACAACGA ARGAGTTCCACGC         2229           2252         AAACCUCA G UGAUCAC         528         TGTGATCA GGCTAGCTACAACGA CACTGAGG         2231           2255         CCUCAGUG A UCACACAG         529         CTOTGTGA GGCTAGCTACAACGA CACTGAGG         2221           2266         GUBAUCAC A CACUGGG         531         GCCACTG GGCTAGCTACAACGA GTTCATCA         2232           2267         AUCACACA G UGGCCAUC         532         GATGACTACAACGA TGTGTACAACGA TGTGTACA         2233           2263         AUCACACA G UGCCACC         533         GCTGATGCTACAACGA TGTGTACA         2236           22669         CAGUGGCC A UCAGCAGU         534         ACTGTCTGA         GGCTAGCTACAACGA TGTGTGTT         2236           2277         GCAUCAG G UUCCACCA         536         TGGATGAGCTACAACGA TGTGTGTACAACGA					
22321         GARGCACC A UACCUCCU         524         AGGAGGATA GCTAGATACAGA GGTGCTTC         2226           22341         AGCACCAU A CCUCCUGC         525         GCAGGAGG GGCTAGCTACAGAGA ATGGTGCT         2227           22411         LACCUCCU G GARAACCU         526         AGGTTTCG GGCTAGCTACAGAGA ATGGGTTA         2228           2246         CCUGGGAA A CCUCAGUG         527         CACTGAGG GGCTAGCTACAACGA TTGGCGTA         2229           2252         AAACCUCA G UGALCACA         528         TGTGTTGA GGCTAGCTACAACGA TTGGGTTA         2230           2255         CCUCAGUG A UCACACAG         529         CTGTGTTGA GGCTAGCTACAACGA GATCACTO         2231           2256         CAGUGAUC A CACAGUGG         531         GGCCACTG GGCTAGCTACAACGA GATCATCA         2232           2266         AUCACACA G UGGCCAUC         532         GATGGTCACAACGA CACAGA TGTGTTA         2232           2266         ACACAGUG G CAGUCAG         533         GCTGATGCTACAACGA CACAGA TGTGTAT         2232           2273         GGCCAUCA G CAGUUCCA         535         TGGTGATCTACACGA CACACAT TGTTACA         2237           2274         CAUCAGCA G UGUCCACA         535         TGGTGAGA GGCTAGCTACAACGA TGCTGCACACA         2236           2286         GAGUGUCC A CACAUUAGA         537         TAAAGTG         GGCTAGCTACAACGA TGATCACACA <td></td> <td></td> <td></td> <td></td> <td></td>					
2234 AGCACCAU A CCUCCUGC 525 GCAGGNGG GGCTAGCTACAACGA ATGGTGCT 2227 2241 UACCUCCU G CGAAACCU 526 AGGTTTCG GGCTAGCTACAACGA AGGAGTA 2228 2446 CCUGGGAA A CCUCAGUG 527 CATCHAGG GGCTAGCTACAACGA ATGGTGCT 2229 2252 AAACCUCA G UGADUCACA 528 TGTGATCA GGCTAGCTACAACGA TTCGCGGG 2239 2255 CCUCAGUG A UCACACAG 529 CTGTGTGA GGCTAGCTACAACGA CACTGAGG 2231 2258 CAGUGAUC A CACAUGGG 530 CCACTGTG GGCTAGCTACAACGA CACTGAGG 2231 2258 CAGUGAUC A CACAUGGG 530 CCACTGTG GGCTAGCTACAACGA CACTGAGG 2232 2266 GUGAUCAC A CACUUGGC 531 GGCCACTG GGCTAGCTACAACGA GTCACTO 2232 2266 GUGAUCAC A CAGUGGC 531 GGCCACTG GGCTAGCTACAACGA GTGATCAC 2232 2266 AUCACACA G UGGCCAUC 532 GATGACCA GGCTAGCTACAACGA TGTGTACA 2232 2266 ACACAGUG G CCAUCAGC 533 GCTGATG GGCTAGCTACAACGA TGTGTGT 2234 2266 ACACAGUG G CCAUCAGC 533 GCTGATG GGCTAGCTACAACGA TGTGTGT 2234 2267 CAGUGGCC A UCAGCAGU 534 ACTGCTGA GGCTAGCTACAACGA TGATGGC 2236 2273 GGCCAUCA G CAGUUCCA 535 TGGAACTA GGCTACAACGA TGATGGCC 2237 2276 CAUCAGGA G UUCCACCA 536 TGGTGGAA GGCTAGCTACAACGA TGATGGCC 2237 2281 GCAGUUCCA CCAC 536 TGGTGGAA GGCTAGCTACAACGA TGATGGCC 2237 2284 GUUCCACC A CUUUAGAC 538 GTCTAAAG GGCTAGCTACAACGA TGATGGCC 2239 2284 GUUCCACC A CUUUAGAC 538 GTCTAAAG GGCTAGCTACAACGA GGAACTAC 2229 2291 CACUUUAGA A UGUUCAUG 539 CATGACGA GGCTAGCTACAACGA GGTAGACA 2292 ACUUUCAU A UGCUAUGG 540 CACACGA GGCTAGCTACAACGA CGAACGA CCACGA CCACGA CCACGA GACACGA CCACGA ACCGA CCACGA ACCGA CCACGA					
2241         URCCUCCU G CGANACCU         526         AGGITTCG GCTAGCTACACGA AGGA AGGAGGTA         2228           2246         CCUGGGAA A CCUCAGUG         527         CACTGAGG GGCTAGCTACAACGA TCCCACA         2229           2252         ANACCUCA G UGAUCACA         528         TGTGATCA GGCTAGCTACAACGA TGAGGTT         2230           2255         CCUCAGUG A UCACACAG         529         CTGTGTGA GGCTAGCTACAACGA CACTGAGG         2231           2260         GUGAUCAC A CACAGUGG         530         CCACTGG GGCTAGCTACAACGA GATCACTO         2232           2263         AUCACACAG G GGCCAUC         532         GATGGCCA GGCTACCAACGA GATCACACGA         2246           2266         ACACAGUG G CAGUCAC         532         GATGGCCA GGCTAGCTACAACGA         CACTGTGT         2235           2266         ACACAGUG G CAGUUCCA         534         ACTGCTGA GGCTAGCTACAACGA         CACTGTT         2235           2273         GGCCAUCA G CUGUUCCA         535         TGGAGCTG CAACAGA GGCTAGCTACAACGA         GACTGCTCAACAGA         2236           2274         CAUCAGCA G UUCACCA         536         TGGTGAGA GGCTAGCTACAACGA         GACACTC         2237           2284         GUCCACCA         537         TAAAGTG         GGCTAGCTACAACGA         GACACTC         2239           2284         GUUCAACCA </td <td></td> <td></td> <td></td> <td></td> <td></td>					
2246         CCUEGGAA A CCUCAGUG         527         CACTGAGG GGCTAGCTACAACA TTCGCAGG         2229           2252         AAACCUCA G UGAUCACA         528         TOTGATAC GGCTAGCTACAACGA TGAGGTT         2230           2255         CCUCAGUG A UCACACAG         529         CTOTGTGA GGCTAGCTACAACGA CACTGAGG         2231           2256         CAGUGAUC A CACAGUG         530         CCACTGTG GGCTACAACGA GACTACTC         2232           2260         GUGAUCAC A CAGUGGC         531         GGCCACTG GGCTACAACGA GTTACAACGA GTTACTCAC         2233           2263         AUCACACA G UGGCCAUC         532         GATGGCCA GGCTACAACGA GTTACAACGA TGTGTGAT         2236           2266         ACACAGUG C CACUCAC         533         GCTGATGG GGCTAGCTACAACGA TGTGTGAT         2236           2269         CAGUGGCC A UCAGCAGU         534         ACTGCTG GGCTACAACGA TGTGTGAT         2236           2277         CACUAGACA G UUCCAC         535         TGGAACTG GGCTACAACGA TGTGTACA         2236           2281         GCAGUUCA C CACUUUA         537         TAAAGTG GGCTACAACGA GGAACCA TGCATCA         2239           2284         GUUCACAC A CUUUAGAC         538         GTTAAAG GGCTACAACGA CTAAACGA CTAAACGA         2241           2294         CUUUAGAU A UCGUCAA         539         CATGACA GGCTACAACGA ATGCAACAA         2241		<del></del>			
2252         AAACCUCA G UGAUCACA         528         TGTGATCA GGCTACAACAG TGAGGTT         2230           2255         CCUCAGUG A UCACACAG         529         CTGTGTGA GGTAGCTACAACGA CACTGAGG         2231           2256         CAGUGAUC A CACAGUGG         530         CCACTGTG GGCTAGCTACAACGA GATCACTCA         2232           2260         GUGAUCAC A CAGUGGC         531         GGCCACTG GGCTAGCTACAACGA GTGTTCAC         2233           2263         AUCACACA G UGGCCAUC         532         GATGGCA GGCTAGCTACAACGA TGTGTGT         2234           2266         ACACAGUG G CAUCAGC         533         GGTGAGGTACAACGA GCACCAGA GCACTACACACGA CACTGTGT         2232           2266         ACAGGAG G UUCCACCA         534         AGGGCAG GGCTAGCTACAACGA TGATGGC         2237           2277         GGCAUCA G CACUUUA         535         TGGAGAG GGCTAGCTACAACGA TGCTGATGC         2237           2281         GCAGUUCA C ACCUUUA         537         TAAAGTGG GGCTAGCTACAACGA TGCTGAACGA         2223           2284         GUUCAGCC A CUCUUAGA         536         TGGTGAAG GGCTAGCTACAACGA TGCTACAACGA         2240           2291         CACUUUAG A CUGAUGU         539         CATGACAG GGCTAGCTACAACGA ATGACCA         2241           2292         ACAGUGUCA U AUCGUAGU         540         TAGCATGA GGCTAGCTACAACGA ATGACATGA	H	<del></del>			
2255         CCUCAGUG A UCACACAG         529         CTGTGTGA GGCTACAACAA CACTGAGG         2231           2256         CAGUGAUC A CACAGUGG         530         CCACTGTG GGCTACCAACGA GATCACTG         2232           2260         GUGAUCAC A CAGUGGC         531         GGCCACTG GGCTAGCTACAACGA GTGATCAC         2233           2263         AUCACACA G UGGCCAU         532         GATGGCA GGCTAGCTACAACGA CACTGTGT         2236           2266         ACAGUGG C A UCAGCAGU         534         ACTGCTGA GGCTACAACGA GCCACTG         2235           2267         CAGUGGCA UCAGCAU         534         ACTGCTGA GGCTACAACGA GCCACTGATGA         2235           2276         CAUCAGCA G CAGUUCCA         535         TGGAACTG GGCTACAACGA TGCTGACC         2236           2281         GCAGUUCC A CACUUUA         537         TAAAGTGG GGCTACCTACAACGA TGCTGACC         2236           2284         GUUCACC A CUUUAGA         536         GTCTAAAG GGCTACACACGA GGTAGCTACAACGA CACAAACGA         2240           2291         CACUUAGA C UCAUGCUA         539         CATGACAG GCTACACACGA ACGA ACGACACAACGA         2241           2292         AGACUGUC A UCAUGCUA         540         TAGCATGA GCCTACAACGA ACGATCAACAA         2242           2293         ACUGUCAU A UGCUAAUG         541         CACATTAGA GCTACAACGA ATGCAACAA         2245			<del></del>		
2258         CAGUGAUC A CACAGUGG         530         CCACTGTG GGCTAGCTACAACGA GATCACTG         2232           2260         GUGAUCAC A CAGUGGCC         531         GGCCACTG GGCTAGCTACAACGA GTGATCAC         2233           2263         AUCACACA G UGGCCAUC         532         GATGGCCA GGCTACCAACGA TGTGTAC         2234           2266         ACACAGUG G CCAUCAGC         533         GCTGATGG GGCTACCAACGA TGTGTGT         2235           2269         CAGUGGCC A UCAGCAGU         534         ACTGCTGA GGCTACCAACGA TGCTGACACGA TGCTGACACGA TGCTGACACGA TGCTGACACGA GCCACCA         535         TGGAGACTGCACACACA GGCTAGCTACAACGA TGCTGACACGA TGCTGACACGA GCCACCACCA         536         TGGTGGAA GGCTAGCTACAACGA TGCTGACACGA CTAAAGTG         2239           2281         GCAGUUCCA C CCACUUUA         537         TAAAGTG GGCTAGCTACAACGA GGTGAACTC         2239           2284         GUUCACCA C CUUUAGAC         538         GTCTAAAG GGCTAGCTACAACGA GGTGAACTC         2240           2291         CACUUUAG A CUGUCAUG         539         CATGACAG GGCTAGCTACAACGA CTAAAGTA         2241           2297         AGACUGUC A UGCUAAUG         541         CATTAGCA GGCTAGCTACAACGA AGACGATCAAACGA CACGATCAACGA         2243           2297         AGCUCAU A UGGUGUC         543         GGACACCA GCTACAACGA ATGCACTA         2244           2306         UGCUCAUG         542				TGTGATCA GGCTAGCTACAACGA TGAGGTTT	2230
2260         GUGAUCAC A CAGUGGCC         531         GGCCACTG GGCTAGCTACAAGGA GTGATCAC         2233           2263         AUCACACA G UGGCCAUC         532         GATGGCA GGCTAGCTACAACGA TGTGTGAT         2234           2266         ACACAGUG G CCAUCAGC         533         GCTGATGG GGCTAGCTACAACGA CACTGTGT         2235           2269         CAGUGGCC A UCAGCA         535         TGGAACTG GGCTACCAACGA TGATGGC         2237           2273         GGCCAUCA G CAGUUCA         535         TGGAACTG GGCTACCAACGA TGATGGC         2237           2276         CAUCAGCA G UUCCACCA         536         TGGTGGAA GGCTAGCTACAACGA TGATGGAC         2239           2284         GUUCCACC A CUUUUAG         537         TAAAGTGG GGCTAGCTACAACGA GGAACTGC         2239           2291         CACUUUAG A CUGUCAUG         539         CATGACAG GGCTAGCTACAACGA CTAAAGTG         2241           2291         CACUUUAG A UGCUAAUG         540         TAGCATGA GGCTAGCTACAACGA ACTCTAAA         2242           2297         AGACUGUC A UGCUCAGA         541         CATTAGCA GGCTAGCTACAACGA ACTCTAAA         2242           2299         ACUSUCAU G UGCCCCG         544         CGGGGAC GGCTAGCTACAACGA ACATTGAC         2246           2306         UGCUCABU G UCCCCGG         544         CGGGGAC GGCTAGCTACAACGA ACCATTAGA         2247 </td <td></td> <td></td> <td></td> <td></td> <td></td>					
2263         AUCACACA G UGGCCAUC         532         GATGGCCA GGCTAGCTACAACGA TGTGTGAT         2234           2266         ACACAGUG G CCAUCAGC         533         GCTGATGG GGCTAGCTACAACGA CACTGTGT         2235           2269         CAGUGGCC A UCAGCAGU         534         ACTGCTGA GGCTACTACAACGA GGCCACTG         2236           2273         GGCCAUCA G CAGUUCCA         535         TGGAGTGC GGCTACTACAACGA TGCTGATG         2237           2276         CAUCAGCA C UUCACCA         536         TGGTGGAG GGCTACTACAACGA TGCTGATG         2238           2281         GCAGUUCC A CACUUUA         537         TAAAGTG GGCTAGCTACAACGA GTGGAAC         2239           2284         GUUCACC A CUUUAGAC         538         GTCTAAAG GGCTAGCTACAACGA GTGGAAC         2240           2294         CACUUUAGA C UGUCAUG         539         CATGACAG GGCTAGCTACAACGA AGTCTAAA         2241           2294         UUUAGACU G UCAUGUU         540         TAGCATTAG GGCTAGCTACAACGA AGTCACATAA         2242           2297         ACUGUCAU G CUAAUGGU         541         CACTTAG GGCTAGCTACAACGA ATGACATT         2243           2299         ACUGUCAU G UUAUGGU         542         ACCATTAG GGCTACCTACAACGA ATGACATT         2245           2300         UCALGUU G UUACAAGA         544         CGGGGACA GGCTACCTACAACGA ACCATTAG 2246 <tr< td=""><td>2258</td><td>CAGUGAUC A CACAGUGG</td><td>530</td><td></td><td>2232</td></tr<>	2258	CAGUGAUC A CACAGUGG	530		2232
2266         ACACAGUG G CCAUCAGC         533         GCTGATGG GGCTAGCTACAACGA CACTGTGT         2235           2269         CAGUGGC A UCAGCAGU         534         ACTGCTGA GGCTAGCTACAACGA GGCCACTG         2236           2273         GGCCAUCA G CAGUUCCA         535         TGGARACTG GGCTAGCTACAACGA TGATGACG         2236           2275         CAUCAGCA G UUCCACCA         536         TGGATGAGA GGCTAGCTACAACGA TGCTGATG         2238           2281         GCAGUUCC A CCUUUA         537         TAAAGTG GGCTAGCTACAACGA GGACTGAC         2239           2284         GUUCCACC A CUUUAGAC         538         GTCTAAAG GGCTAGCTACAACGA GGTGACA         2240           2294         UUUAGACU G UCAUGCUA         540         TAGCATGA GGCTAGCTACAACGA AGTCTAAA         2242           2297         AGACUGUC A UCCUAGU         541         CATTAGCA GGCTAGCTACAACGA AGTCACAC         2242           2299         ACUGUCAU G UCUAGUU         542         ACCATTAG GGCTAGCTACAACGA ATGCATCA         2244           2300         UCAUGUCAU G UGUCCCG         543         GGACACCA GGCTAGCTACAACGA CATTAGCA         2246           2306         UGUCAUGA G UGUCAGGA         545         CCTGGGGA GCTAGCTACAACGA CATTAGCA         2247           2316         GUCCCCGA G CCUCAGAU         546         ATCTGAGG GCTAGCTACAACGA CACATTAGCA         2247<	2260	GUGAUCAC A CAGUGGCC	531	GGCCACTG GGCTAGCTACAACGA GTGATCAC	2233
2269         CAGUGGCC A UCAGCAGU         534         ACTGCTGA GGCTAGCTACAACGA GGCCACTG         2236           2273         GGCCAUCA G CAGUUCCA         535         TGGAACTG GGCTAGCTACAACGA TGATGGCC         2237           2276         CAUCAGCA G UUCCACCA         536         TGGTGGAA GGCTAGCTACAACGA TGATGGCC         2239           2281         GCAGUUCC A CCACUUA         537         TAAAGTGG GGCTAGCTACAACGA GGTGGAC         2239           2284         GUUCACC A CUJUAGAC         538         GTCTAAAG GGCTAGCTACAACGA GGTGGAC         2240           2291         CACUUUAG A CUGUCAUG         539         CATGACAG GGCTAGCTACAACGA ATGACTAA         2241           2297         AGACUGUC A UGCUAAUG         541         CATTAGCA GGCTAGCTACAACGA ATGACAT         2242           2297         AGACUGUC A UGCUAAUG         541         CATTAGCA GGCTAGCTACAACGA ATGACAT         2242           2299         ACUGUCAU G UGALUGU         543         GGACACCA GGCTAGCTACAACGA ATGACAT         2242           2300         UGUAGUCA A UGGUUCC         543         GGACACCA GGCTAGCTACAACGA CATTAGCA         2246           2301         GUCCCAGA G CCUCAGAU         546         CCGGGGA GGCTAGCTACAACGA ACCATTAG         2247           2316         GUCCCGA G CCUGAGAU         546         ATCTGAGG GGCTAGCTACAACGA CTGAGGT         2249	2263	AUCACACA G UGGCCAUC			2234
2273         GGCCAUCA G CAGUUCA         535         TGGAACTG GGCTAGCTACAACGA TGATGGCC         2237           2276         CAUCAGCA G UUCCACCA         536         TGGTGGAA GGCTAGCTACAACGA TGCTGATG         2238           2281         GCAGUUCA A CACUUUA         537         TAAAGTGG GGCTAGCTACAACGA GGAACTCC         2239           2284         GUUCACC A CUUUAGAC         538         GTCTAAAG GGCTAGCTACAACGA GGTGGAAC         2240           2291         CACUUUAG A CUGUCAUG         539         CATGACAG GGCTAGCTACAACGA GGTCAAACTA         2241           2294         UUUAGACU G UCAUGCUA         540         TAGCATGA GGCTAGCTACAACGA AGTCTAAA         2242           2297         AGCUGUCA A UGCUAAUGG         541         CATTAGCA GGCTAGCTACAACGA ATGACATC         2243           2299         ACUGUCAU G CUAAUGGU         542         ACCATTAG GGCTAGCTACAACGA ATGACATC         2245           2303         UGCUAAUG G UGCCCCG         544         CGGGGAC GGCTAGCTACAACGA ATGACATA         2246           2306         UGCUAAUG G UCCCCAGAU         546         ATCTGAGG GGCTAGCTACAACGA ACATTAGC         2247           2316         GUCCCCAG G CCUCAGAU         546         ATCTGAGG GGCTAGCTACAACGA ACATTAGG         2247           2323         AGCCUCAG A UCACUUGG         547         CCAAGACA ACAGACACA TAGACAACAA TAGACAACAA TAGACAACAA	2266	ACACAGUG G CCAUCAGC	533	GCTGATGG GGCTAGCTACAACGA CACTGTGT	2235
2276         CAUCAGCA G UUCCACCA         536         TGGTGGAA GGCTAGCTACAACGA TGCTGATG         2238           2281         GCAGUUCC A CCACUUUA         537         TAAAGTGG GGCTAGCTACAACGA GGAACTGC         2239           2284         GUCCACC A CUUUAGAC         538         GTCTAAAAG GGCTAGCAACGA GGAGCAAC         2240           2291         CACUUUAG A CUGUCAUG         539         CATGACAG GGCTAGCTACAACGA CTAAACGA         2241           2294         UUUAGACU G UCAUGUA         540         TAGCATGA GGCTAGCTACAACGA AGTCTAAA         2242           2297         AGACUGUC A UGCUAAUG         541         CATTAGCA GGCTAGCTACAACGA AGTCTACAACGT         2244           2303         UCAUGUCAU G CUAAUGGU         542         ACCATTAG GGCTACCAACGA ATGCATGA         2245           2306         UGCUCAUG G UGUCCCCG         543         GGGACACCA GGCTAGCTACAACGA ATGCATGA         2245           2306         UGCUCAUG G UGUCCCCG         545         CTCGGGGA GGCTAGCTACAACGA CACTATCA         2247           2316         GUCCCGAG         545         CTCGGGGA GGCTAGCTACAACGA CTGAGCT         2249           2323         AGCCUCAG A UCACUUGG         547         CCAAGTGA GGCTACAACGA CTGAGCT         2249           2323         AGCCUCAG A UCACUUGG         547         CCAAGTGA GGCTACCAACGA CTTACAACGA CTGAGTACTACACGA CTGATCTACAACGA CTACT	2269	CAGUGGCC A UCAGCAGU	534	ACTGCTGA GGCTAGCTACAACGA GGCCACTG	2236
2281         GCAGUUCC A CCACUUUA         537         TAAAGTGG GGCTAGCTACAACGA GGAACTGC         2239           2284         GUUCCACC A CUUUAGAC         538         GTCTAAAG GGCTAGCTACAACGA GGTGGAAC         2240           2291         CACUUUAG A CUGUCAU         539         CATGACAG GGCTAGCTACAACGA CTAAAGTG         2241           2294         UUUAGACU G UCAUGCUA         540         TAGCATGA GGCTAGCTACAACGA AGTACAACGA         ACTATAAA         2242           2297         AGACUGUC A UGCUAAUG         541         CATTAGCA GGCTAGCTACAACGA ATGACAGT         2243           2299         ACUGUCAU G CUAAUGGU         542         ACCATTAG GGCTAGCTACAACGA ATGACAT         2245           2303         UCAUGCUA A UGGUGUCC         543         GGACACCA GGCTAGCTACAACGA ATGACAT         2245           2306         UGCUAAUGGU G UCCCCGAG         544         CGGGGACA GGCTAGCTACAACGA ACTATACC         2246           2308         CUAAUGGU G UCCCCGAG         546         ATCTGAGGA GGCTAGCTACAACGA ACGA TCGGGGAC         2247           2316         GUCCCAGA G CCUCCAGAU         546         ATCTGAGG GGCTAGCTACAACGA CTGAGGCT         2248           2323         AGCCUCAG A UCACUUGG         547         CCAAGTGA GGCTACCAACGA CTGAGGTAC         2249           2326         CUCAGAUA A CAACAAA         548         AAACCAAG GGCTACCAACG	2273	GGCCAUCA G CAGUUCCA	535	TGGAACTG GGCTAGCTACAACGA TGATGGCC	2237
2284         GUUCCACC A CUUUAGAC         538         GTCTAAAG GGCTAGCTACAACGA GGTGGAAC         2240           2291         CACUUUAG A CUGUCAUG         539         CATGACAG GGCTAGCTACAACGA CTAAAGTG         2241           2294         UUUAGACU G UCAUGCUA         540         TAGCATGA GGCTAGCTACAACGA AGTCTAAA         2242           2297         AGACUGUC A UGCUAAUG         541         CATTAGCA GGCTAGCTACAACGA AGTCACACT         2243           2299         ACUGUCAU A UGGUGUCC         543         GGACACCA GGCTAGCTACAACGA ATGACAGT         2244           2306         UGCUAAUG G UGUCCCG         544         CGGGGAC GGCTAGCTACAACGA CATTAGCA         2246           2306         CUCAUAUG G UCCCCGAG         545         CTCGGGGA GCTACACACGA ACCATTAG         2247           2316         GUCCCCGA G CCUCAGAU         546         ATCTGAGG GGCTAGCTACAACGA ACCATTAG         2247           2323         AGCCUCAG A UCACUUG         547         CAAAGTGA GGCTAGCTACAACGA ACGACGA CTAGAGCA         2249           2323         AGCCUCAGA UCACUUG         548         AAACCAAG GGCTAGCTACAACGA CAAGTGAT         2249           2324         CUCAGAUC A CUUGGUU         548         AAACCAAG GGCTAGCTACAACGA CAAGTGAT         2251           2331         AUCACUAA         CAACACAA         550         TTTTTTTTTTAGAGCTACAACGA TTTTTAAC	2276	CAUCAGCA G UUCCACCA	536	TGGTGGAA GGCTAGCTACAACGA TGCTGATG	2238
2291         CACUUUAG A CUGUCAUG         539         CATGACAG GGCTAGCTACAACGA CTAAAGTG         2241           2294         UUUAGACU G UCAUGCUA         540         TAGCATGA GGCTAGCTACAACGA AGTCTAAA         2242           2297         AGACUGUC A UGCUAAUG         541         CATTAGCA GGCTAGCTACAACGA AGCACTCT         2243           2299         ACUGUCAU G CUAAUGGU         542         ACCATTAG GGCTAGCTACAACGA ATGACAGT         2244           2303         UCAUGUA A UGGUGUCC         543         AGCACCA GGCTAGCTACAACGA ATGACTAG         2245           2306         UGCUAAUG G UGUCCCCG         544         CGGGGACA GGCTAGCTACAACGA ACCATTAGCA         2246           2308         CUAAUGGU G UCCCCCAGG         545         CTCGGGGA GGCTACCAACGA ACCATTAGCA         2247           2316         GUCCCCGA G CCUCAGAU         546         ATCTGAGG GGCTAGCTACAACGA ACCATTAGCA         2248           2323         AGCCUCAG A UCACUUGG         547         CCAAGTGA GGCTACAACAGA CTACACAGA         CTGAGGCT           2331         AUCACUUG G UUAAAAA         549         TTTTTAAAC         2251           2332         AUCACUUG G UUAAAAA         550         TTTTTGTAG GGCTACAACGA TATTAAACCA         2251           2334         AUCACUAA         551         TTTTTGTAG GGCTACAACGA TTTTAAAC         2252	2281	GCAGUUCC A CCACUUUA	537	TAAAGTGG GGCTAGCTACAACGA GGAACTGC	2239
2294         UUUAGACU G UCAUGCUA         540         TAGCATGA GGCTAGCTACAACGA AGTCTAAA         2242           2297         AGACUGUC A UGCUAAUG         541         CATTAGCA GGCTAGCTACAACGA GACAGTCT         2243           2299         ACUGUCAU G CUAAUGGU         542         ACCATTAG GGCTAGCTACAACGA ATGACAGT         2244           2303         UCAUGCUA A UGGUGUCC         543         GGACACCA GGCTAGCTACAACGA CATTAGCA         2245           2306         UGCUAAUG G UGUCCCCG         544         CGGGGAC GGCTAGCTACAACGA ACCATTAG         2247           2308         CUAAUGG G UCCCCAGAG         545         CTCGGGGA GGCTAGCTACAACGA ACCATTAG         2247           2316         GUCCCCAG G CCUCAGAU         546         ATCTGAGG GGCTAGCTACAACGA TCGGGCT         2249           2323         AGCCUCAG A UCACUUGG         547         CCAAGTGA GGCTAGCTACAACGA CTGAGCT         2250           2331         AUCACUUG G UUUAAAAA         549         TTTTTAAA GGCTAGCAACGA TTTTAAC         2251           2332         GUUUAAAAA         549         TTTTTTAAA GGCTAGCAACGA TTTTTAA         2252           2331         AUCACUUG G UUUAAAAA         549         TTTTTTAAA GGCTAGCAACGA TTTTTAA         2251           2332         AGUUUAAAAA         550         TTTTTTTAA GGCTAGCTACAACGA TTTTTTA         2252	2284	GUUCCACC A CUUUAGAC	538	GTCTAAAG GGCTAGCTACAACGA GGTGGAAC	2240
2297         AGACUGUC A UGCUAAUG         541         CATTAGCA GGCTAGCTACAACGA GACAGTCT         2243           2299         ACUGUCAU G CUAAUGGU         542         ACCATTAG GGCTAGCTACAACGA ATGACAGT         2244           2303         UCAUGCUA A UGGUGUCC         543         GGACACCA GGCTAGCTACAACGA TAGCATGA         2245           2306         UGCUAAUG G UGUCCCG         544         CGGGGACA GGCTAGCTACAACGA CATTAGCA         2246           2308         CUAAAUGGU G UCCCCGAG         545         CTCGGGGA GGCTAGCTACAACGA TCGAGGACA         2247           2316         GUCCCCGA G CCUCAGAU         546         ATCTGAG GGCTAGCTACAACGA TCGAGGAC         2248           2323         AGCCUCAG A UCACUUGG         547         CCAAGTGA GGCTAGCAACGA TCGAGCA         2249           2326         CUCAGAUC A CUUGGUUU         548         AAACCAAG GGCTAGCTACAACGA TCGACGA         2250           2331         AUCACUUG G UUUAAAAA         549         TTTTTAAA GGCTAGCTACAACGA TTTTAAC         2251           2339         GUUUAAAA A CACCACA         550         TGTGGTTG GGCTACAACGA TTTTTAAC         2252           2342         UAAAAACA A CACAACAA         551         TTTTTGTG GGCTACAACGA TTTGTGT         2255           2345         AACCACAA A UACAACAA         551         TTTTGTTG GGCTACAACGA ATTTGTGT         2255	2291	CACUUUAG A CUGUCAUG	539	CATGACAG GGCTAGCTACAACGA CTAAAGTG	2241
2299         ACUGUCAU G CUAAUGGU         542         ACCATTAG GGCTAGCTACAACGA ATGACAT         2244           2303         UCAUGCUA A UGGUGUC         543         GGACACCA GGCTAGCTACAACGA TAGCATGA         2245           2306         UGCUAAUG G UGUCCCG         544         CGGGGACA GGCTAGCTACAACGA CATTAGCA         2246           2308         CUAAUGGU G UCCCCGAG         545         CTCGGGGA GGCTAGCTACAACGA ACCATTAG         2247           2316         GUCCCCGA G CCUCAGAU         546         ATCTGAGG GGCTAGCTACAACGA TCGGGGCC         2248           2323         AGCCUCAG A UCACUUGG         547         CCAAGTGA GGCTACAACGA CTGAGGCT         2249           2326         CUCAGAUC A CUUGGUU         548         AAACCAAG GGCTACCAACGA GATCTGAG         2250           2331         AUCACUUG G UUJAAAAA         549         TTTTTAAA GGCTACAACGA GATCTTAAA         2251           2339         GUUUAAAA A CAACCACA         550         TGTGGTTG GGCTACCAACGA TTTTAAAC         2252           2342         UAAAACA A CCACAAAA         551         TTTTGTGG GGCTAGCTACAACGA TTTTTTAA         2253           2355         ACCACAAA A UACAACAA         553         TTTTTGTG GGCTACCAACGA TTTTTTGTGT         2254           2355         ACAAAAU A CAACAAGA         554         TCTTGTGT GGCTACCAACGA ATTTTGTG         2256	2294	UUUAGACU G UCAUGCUA	540	TAGCATGA GGCTAGCTACAACGA AGTCTAAA	2242
2303         UCAUGCUA A UGGUGUCC         543         GGACACCA GGCTAGCTACAACGA TAGCATCA         2245           2306         UGCUAAUG G UGUCCCCG         544         CGGGGACA GGCTAGCTACAACGA CATTAGCA         2246           2308         CUAAUGGU G UCCCCGAG         545         CTCGGGGA GGCTAGCTACAACGA ACCATTAG         2247           2316         GUCCCCGA G CCUCAGAU         546         ATCTGAGG GGCTAGCTACAACGA TCGGGGAC         2248           2323         AGCCUCAG A UCACUUGG         547         CCAAGTGA GGCTAGCTACAACGA ATCTGAGC         2249           2326         CUCAGAUC A CUUGGUUU         548         AAACCAAG GGCTAGCTACAACGA ATCTGAG         2250           2331         AUCACUUG G UUUAAAAA         549         TTTTTAAA GGCTAGCTACAACGA ATCTTAAAC         2251           2332         GUUUAAAAA A CAACCACA         550         TGTGGTTG GGCTAGCTACAACGA TTTTAAAC         2252           2342         UAAAAACA A CCACAAAA         551         TTTTGTGG GGCTAGCTACAACGA TGTTTTTA         2253           2342         UAAAAACA A CACAAAA         552         GTATTTTG GGCTACCTACAACGA TTTTGTGT         2254           2350         ACCACAAA A UACAACAA         553         TTGTGTTA GGCTACCAACGA TTTTGTGT         2255           2351         CACAAAAU A CAACAAGA         554         TCTTGTTG GGCTACCAACGA ATTTTGTTG         2256<	2297	AGACUGUC A UGCUAAUG	541	CATTAGCA GGCTAGCTACAACGA GACAGTCT	2243
2306         UGCUANUG G UGUCCCG         544         CGGGGACA GGCTAGCTACAACGA CATTAGCA         2246           2308         CUAAUGGU G UCCCCGAG         545         CTCGGGGA GCTAGCTACAACGA ACCATTAG         2247           2316         GUCCCGA G CCUCAGAU         546         ATCTGAGG GGCTAGCTACAACGA TCGGGGAC         2248           2323         AGCCUCAG A UCACUUGG         547         CCAAGTGA GGCTAGCTACAACGA CTGAGGCT         2249           2326         CUCAGAUC A CUUGGUUU         548         AAACCAAG GGCTAGCTACAACGA GATCTGAG         2250           2331         AUCACUUG G UUUAAAAA         549         TTTTTAAA GGCTAGCAACGA CAAGGA TTTTAAAC         2251           2339         GUUUAAAA         A CAACCACA         550         TGTGGTTG GGCTAGCAACGA TTTTAAAC         2252           2342         UAAAAACA A CCACAAAAA         551         TTTTGTGG GGCTAGCAACGA TGTTTTTA         2253           2345         AAACAACA A UACAACAA         552         GTATTTTG GGCTAGCAACGA TTTTGTGT         2254           2350         ACCACAAAA UACAACAA         553         TTGTTGTA GGCTAGCAACGA TTTTGTGT         2255           2352         CACAAAAUA A CAACAAGA         554         TCTTGTTG GGCTAGCTACAACGA ATTTTGTG         2255           2352         CACAAAAUA A CAACAAGA         554         TCTTGTTG GGCTAGCTACAACGA TCTTTTTT	2299	ACUGUCAU G CUAAUGGU	542	ACCATTAG GGCTAGCTACAACGA ATGACAGT	2244
2308         CUAAUGGU G UCCCCGAG         545         CTCGGGGA GGCTAGCTACAACGA ACCATTAG         2247           2316         GUCCCCGA G CCUCAGAU         546         ATCTGAGG GGCTAGCTACAACGA TCGGGGAC         2248           2323         AGCCUCAG A UCACUUGG         547         CCAAGTGA GGCTAGCTACAACGA CTGAGGCT         2249           2326         CUCAGAUC A CUUGGUUU         548         AAACCAAG GGCTAGCTACAACGA GATCTGAG         2250           2331         AUCACUUG G UUUAAAAA         549         TTTTTAAA GGCTAGCTACAACGA CAAGTGAT         2251           2339         GUUUAAAA A CAACCACA         550         TGTGGTTG GGCTAGCAACGA TTTTAAAC         2252           2342         UAAAAACCA A CCACAAAA         551         TTTTGTGG GGCTAGCAACGA TGTTTTTA         2253           2345         AAACAACC A CAAAAUAC         552         GTATTTTG GGCTAGCAACGA TTTTGTGT         2254           2350         ACCACAAA A UACAACAA         553         TTGTTGTA GGCTACAACGA TTTTGTGT         2255           2352         CACAAAAUA C CAACAAGA         554         TCTTGTTG GGCTAGCAACGA ATTTTGTG         2255           2352         CACAAAAUA C CAACAAGA         554         TCTTGTTG GGCTAGCAACGA ATTTTTTT         2257           2351         CAACAAGA G CCUGGAAU         556         ATTCCAGG GGCTAGCTACAACGA TCTTTTTT         2258 </td <td>2303</td> <td>UCAUGCUA A UGGUGUCC</td> <td>543</td> <td>GGACACCA GGCTAGCTACAACGA TAGCATGA</td> <td>2245</td>	2303	UCAUGCUA A UGGUGUCC	543	GGACACCA GGCTAGCTACAACGA TAGCATGA	2245
2316 GUCCCGA G CCUCAGAU 546 ATCTGAGG GGCTAGCTACAACGA TCGGGGAC 2248 2323 AGCCUCAG A UCACUUGG 547 CCAAGTGA GGCTAGCTACAACGA CTGAGGCT 2249 2326 CUCAGAUC A CUUGGUUU 548 AAACCAAG GGCTAGCTACAACGA GATCTGAG 2250 2331 AUCACUUG G UUUAAAAA 549 TTTTTAAA GGCTAGCTACAACGA CAAGTGAT 2251 2339 GUUUAAAA A CAACCACA 550 TGTGGTTG GGCTAGCTACAACGA TTTTAAAC 2252 2342 UAAAAACA A CCACAAAA 551 TTTTGTGG GGCTAGCTACAACGA TGTTTTTA 2253 2345 AAACAACC A CAAAAUAC 552 GTATTTTG GGCTAGCTACAACGA GGTTGTTT 2254 2350 ACCACAAA A UACAACAA 553 TTGTTGTA GGCTAGCTACAACGA TTTTGTGGT 2255 2352 CACAAAAU A CAACAAGA 554 TCTTGTTG GGCTAGCTACAACGA TTTTGTGG 2256 2355 AAAAUACA A CAAGAGAC 555 GGCTCTTG GGCTAGCTACAACGA ATTTTGTG 2256 2355 AAAAUACA A CAAGAAGC 555 GGCTCTTG GGCTAGCTACAACGA TCTTGTTG 2257 2361 CAACAAGA G CCUGGAAU 556 ATTCCAGG GGCTAGCTACAACGA TCTTGTTG 2258 2368 AGCCUGGA A UUAUUUUA 557 TAAAATAA GGCTAGCTACAACGA TCTTGTTG 2259 2371 CUGGAAUU A UUUUAGGA 558 TCCTAAAA GGCTAGCTACAACGA ATTCCAG 2260 2379 AUUUUAGG A CCAGGAAG 559 CTTCCTGG GGCTAGCTACAACGA TCCCAGGCT 2259 2371 ACCAGGAA G CACGCUGU 561 ACAGCGTG GGCTAGCTACAACGA TCCCTGGT 2262 2390 AGGAAGCA G CACGCUGU 561 ACAGCGTG GGCTAGCTACAACGA TCCCTGGT 2262 2391 AGCAGCAC G CUGUUUU 562 AAACAGCG GGCTAGCTACAACGA TCCCTTCC 2263 2392 GAAGCAGC A CGCUGUUU 562 AAACAGCG GGCTAGCTACAACGA GCTGCTTC 2264 2394 AGCAGCAC G CUGUUUAU 563 ATAAACAG GGCTAGCTACAACGA AGCGTGCT 2265 2397 AGCACGCU G UUUAUUGA 564 TCAATAAA GGCTAGCTACAACGA AGCGTGCT 2266 2401 CGCUGUUU A UUGAAAGA 565 TCTTTCAA GGCTAGCTACAACGA AACAGCG 2267 2410 UUGAAAGA G UCACAGAA 566 TTCTTGTA GGCTAGCTACAACGA AACAGCG 2267 2410 UUGAAAGA G UCACAGAA 566 TTCTTCTG GGCTAGCTACAACGA GACTCTTT 2269	2306	UGCUAAUG G UGUCCCCG	544	CGGGGACA GGCTAGCTACAACGA CATTAGCA	2246
2323         AGCCUCAG A UCACUUGG         547         CCAAGTGA GGCTAGCTACAACGA CTGAGGCT         2249           2326         CUCAGAUC A CUUGGUUU         548         AAACCAAG GGCTAGCTACAACGA GATCTGAG         2250           2331         AUCACUUG G UUUAAAAA         549         TTTTTAAA GGCTAGCTACAACGA CAAGTGAT         2251           2339         GUUUAAAAA A CAACCACA         550         TGTGGTTG GGCTAGCTACAACGA TTTTTAAC         2252           2342         UAAAAACA A CCACAAAA         551         TTTTGTGG GGCTAGCTACAACGA TGTTTTTA         2253           2345         AAACAACC A CAAAAUAC         552         GTATTTTG GGCTAGCTACAACGA TTTTGTGT         2255           2350         ACCACAAA A UACAACAA         553         TTGTTGTA GGCTACAACGA TTTTGTGT         2256           2352         CACAAAAU A CAACAAGA         554         TCTTGTTG GGCTAGCTACAACGA ATTTTGTG         2256           2355         AAAAUACA A CAAGAGC         555         GGCTCTTG GGCTACCAACGA ATTTTTTT         2257           2361         CAACAAGA G CCUGGAAU         556         ATTCCAGG GGCTACCAACGA TCTTGTTG         2258           2371         CUGGAAUU A UUUUAGGA         558         TCCTAAAA GGCTACCAACGA ATTCCAG         2260           2379         AUUUUAGG A CAGCACG         560         GCGTGCTG GGCTACCAACGA TCCTACAACGA TCCTGCTCCT         2262	2308	CUAAUGGU G UCCCCGAG	545	CTCGGGGA GGCTAGCTACAACGA ACCATTAG	2247
2326 CUCAGAUC A CUUGGUUU 548 AAACCAAG GGCTAGCTACAACGA GATCTGAG 2250 2331 AUCACUUG G UUUAAAAA 549 TTTTTAAA GGCTAGCTACAACGA CAAGTGAT 2251 2339 GUUUAAAA A CAACCACA 550 TGTGGTTG GGCTAGCTACAACGA TTTTAAAC 2252 2342 UAAAAACA A CCACAAAA 551 TTTTGTGG GGCTAGCTACAACGA TGTTTTTA 2253 2345 AAACAACC A CAAAAUAC 552 GTATTTG GGCTAGCTACAACGA TGTTTTTA 2254 2350 ACCACAAA A UACAACAA 553 TTGTTGTA GGCTAGCTACAACGA TTTGTGGT 2254 2352 CACAAAAU A CAACAAGA 553 TTGTTGTG GGCTAGCTACAACGA ATTTTGTG 2256 2352 CACAAAAU A CAACAAGA 554 TCTTGTTG GGCTAGCTACAACGA ATTTTGTG 2256 2355 AAAAUACA A CAAGAGCC 555 GGCTCTTG GGCTAGCTACAACGA TGTTTTTT 2257 2361 CAACAAGA G CCUGGAAU 556 ATTCCAGG GGCTAGCTACAACGA TCTTGTTG 2258 2368 AGCCUGGA UUAUUUUA 557 TAAAATAA GGCTAGCTACAACGA TCCAGGCT 2259 2371 CUGGAAUU A UUUUAGGA 558 TCCTAAAA GGCTAGCTACAACGA AATTCCAG 2260 2379 AUUUUAGG A CCAGGAAG 559 CTTCCTGG GGCTAGCTACAACGA TCCTAGAT 2261 2387 ACCAGGAA G CAGCACGC 560 GCGTGCTAGCAACGA TCCTGGT 2262 2390 AGGAAGCA G CACGCUGU 561 ACAGCGTG GGCTAGCTACAACGA TCCTGGT 2262 2391 AGCAGCAC G CUGUUUU 562 AAACAGCG GGCTAGCTACAACGA TCCTGCT 2263 2392 GAAGCAGC A CGCUGUUU 562 AAACAGCG GGCTAGCTACAACGA TCCTTCT 2263 2394 AGCAGCAC G CUGUUUAU 563 ATAAACAG GGCTAGCTACAACGA AGCGTCTT 2264 2397 AGCACGCU G UUUAAUUGA 564 TCAATAAA GGCTAGCTACAACGA AGCGTCTT 2265 2397 AGCACGCU G UUUAAUUGA 564 TCAATAAA GGCTAGCTACAACGA AGCGTCTT 2266 2401 CGCUGUUU A UUGAAAGA 565 TCTTTCAA GGCTAGCTACAACGA AACAGCG 2267 2410 UUGAAAGA G UCACAGAA 566 TTCTGTGA GGCTAGCTACAACGA AACAGCG 2267 2410 UUGAAAGA G UCACAGAA 566 TTCTGTGA GGCTAGCTACAACGA AACAGCG 2267 2411 AAAGAGUC A CAGAAGAG 567 CTCTTCTG GGCTAGCTACAACGA GCCTCTT 2268	2316	GUCCCCGA G CCUCAGAU	546	ATCTGAGG GGCTAGCTACAACGA TCGGGGAC	2248
2331 AUCACUUG G UUUAAAAA 549 TTTTTAAA GGCTAGCTACAACGA CAAGTGAT 2251 2339 GUUUAAAA A CAACCACA 550 TGTGGTTG GGCTAGCTACAACGA TTTTAAAC 2252 2342 UAAAAACA A CCACAAAA 551 TTTTGTGG GGCTAGCTACAACGA TGTTTTTA 2253 2345 AAACAACC A CAAAAUAC 552 GTATTTG GGCTAGCTACAACGA GGTTGTTT 2254 2350 ACCACAAA A UACAACAA 553 TTGTTGTA GGCTAGCTACAACGA TTTGTGGT 2255 2352 CACAAAAU A CAACAAGA 553 TTGTTGTG GGCTAGCTACAACGA ATTTTGTG 2256 2355 AAAAUACA A CAACAAGA 554 TCTTGTTG GGCTAGCTACAACGA ATTTTGTG 2256 2355 AAAAUACA A CAACAAGA 555 GGCTCTTG GGCTAGCTACAACGA TGTATTTT 2257 2361 CAACAAGA G CCUGGAAU 556 ATTCCAGG GGCTAGCTACAACGA TCTTGTTG 2258 2368 AGCCUGGA A UUAUUUUA 557 TAAAATAA GGCTAGCTACAACGA TCCAGGCT 2259 2371 CUGGAAUU A UUUUAGGA 558 TCCTAAAA GGCTAGCTACAACGA AATTCCAG 2260 2379 AUUUUAGG A CCAGGAAG 559 CTTCCTGG GGCTAGCTACAACGA ATTCCAG 2260 2387 ACCAGGAA G CACGCUGU 561 ACAGCGT GGCTAGCTACAACGA TCCTGGT 2262 2390 AGGAAGCA G CACGCUGU 561 ACAGCGT GGCTAGCTACAACGA TCCTGGT 2262 2392 GAAGCAGC A CGCUGUUU 562 AAACAGCG GGCTAGCTACAACGA TGCTTCCT 2263 2394 AGCAGCAC G CUGUUUAU 563 ATAAACAG GGCTAGCTACAACGA GCTGCTTC 2264 2397 AGCACGCU G UUUAAUUGA 564 TCAATAAA GGCTAGCTACAACGA AGCGTCTT 2265 2397 AGCACGCU G UUUAAUUGA 564 TCAATAAA GGCTAGCTACAACGA AGCGTCT 2266 2401 CGCUGUUU A UUGAAAGA 565 TCTTTCAA GGCTAGCTACAACGA AACAGCG 2267 2410 UUGAAAGA G UCACAGAA 566 TTCTGTGA GGCTAGCTACAACGA TCTTTCAA 2268 2413 AAAGAGUC A CAGAAGAG 567 CTCTTCTG GGCTAGCTACAACGA GCCTCTT 2269	2323	AGCCUCAG A UCACUUGG	547	CCAAGTGA GGCTAGCTACAACGA CTGAGGCT	2249
2339 GUUUAAAA A CAACCACA 550 TGTGGTTG GGCTAGCTACAACGA TTTTAAAC 2252 2342 UAAAAACA A CCACAAAA 551 TTTTGTGG GGCTAGCTACAACGA TGTTTTTA 2253 2345 AAACAACC A CAAAAUAC 552 GTATTTG GGCTAGCTACAACGA GGTTGTTT 2254 2350 ACCACAAA A UACAACAA 553 TTGTTGTA GGCTAGCTACAACGA TTTGTGGT 2255 2352 CACAAAAU A CAACAAGA 554 TCTTGTTG GGCTAGCTACAACGA ATTTTGTG 2256 2355 AAAAUACA A CAAGAGCC 555 GGCTCTTG GGCTAGCTACAACGA TGTATTTT 2257 2361 CAACAAGA G CCUGGAAU 556 ATTCCAGG GGCTAGCTACAACGA TCTTGTTG 2258 2368 AGCCUGGA A UUAUUUUA 557 TAAAATAA GGCTAGCTACAACGA TCCAGGCT 2259 2371 CUGGAAUU A UUUUAGGA 558 TCCTAAAA GGCTAGCTACAACGA AATTCCAG 2260 2379 AUUUUAGG A CCAGGAAG 559 CTTCCTGG GGCTAGCTACAACGA CCTAAAAT 2261 2387 ACCAGGAA G CAGCACGC 560 GCGTGCTG GGCTAGCTACAACGA TCCTGGT 2262 2390 AGGAAGCA G CACGCUGU 561 ACAGCGTG GGCTAGCTACAACGA TCCTGGT 2262 2392 GAAGCAGC A CGCUGUUU 562 AAACAGCG GGCTAGCTACAACGA GCTGCTTC 2264 2394 AGCAGCAC G CUGUUUAU 563 ATAAACAG GGCTAGCTACAACGA GCTGCTTC 2264 2397 AGCACGCU G UUUAUUGA 564 TCAATAAA GGCTAGCTACAACGA AGCGTGCT 2265 2397 AGCACGCU G UUUAUUGA 564 TCAATAAA GGCTAGCTACAACGA AGCGTGCT 2266 2401 CGCUGUUU A UUGAAAGA 566 TCCTTCTAA GGCTAGCTACAACGA AAACACGC 2267 2410 UUGAAAGA G UCACAGAA 566 TCCTTCTG GGCTAGCTACAACGA TCTTTCAA 2268 2413 AAAGAGUC A CAGAAGAG 567 CTCTTCTG GGCTAGCTACAACGA GACTCTTT 2269	2326	CUCAGAUC A CUUGGUUU	548	AAACCAAG GGCTAGCTACAACGA GATCTGAG	2250
2342 UAAAAACA A CCACAAAA 551 TTTTGTGG GGCTAGCTACAACGA TGTTTTTA 2253 2345 AAACAACC A CAAAAUAC 552 GTATTTTG GGCTAGCTACAACGA GGTTGTTT 2254 2350 ACCACAAA A UACAACAA 553 TTGTTGTA GGCTAGCTACAACGA TTTGTGGT 2255 2352 CACAAAAU A CAACAAGA 554 TCTTGTTG GGCTAGCTACAACGA ATTTTGTG 2256 2355 AAAAUACA A CAAGAGCC 555 GGCTCTTG GGCTAGCTACAACGA TGTATTTT 2257 2361 CAACAAGA G CCUGGAAU 556 ATTCCAGG GGCTAGCTACAACGA TCTTGTTG 2258 2368 AGCCUGGA A UUAUUUUA 557 TAAAATAA GGCTAGCTACAACGA TCCAGGCT 2259 2371 CUGGAAUU A UUUUAGGA 558 TCCTAAAA GGCTAGCTACAACGA AATTCCAG 2260 2379 AUUUUAGG A CCAGGAAG 559 CTTCCTGG GGCTAGCTACAACGA CCTAAAAT 2261 2387 ACCAGGAA G CAGCACGC 560 GCGTGCTG GGCTAGCTACAACGA TTCCTGGT 2262 2390 AGGAAGCA G CACGCUGU 561 ACAGCGTG GGCTAGCTACAACGA TGCTTCCT 2263 2392 GAAGCAGC A CGCUGUUU 562 AAACAGCG GGCTAGCTACAACGA GCTGCTTC 2264 2394 AGCAGCAC G CUGUUUAU 563 ATAAACAG GGCTAGCTACAACGA GCTGCTTC 2264 2397 AGCACGCU G UUUAUUGA 564 TCAATAAA GGCTAGCTACAACGA AGCGTGCT 2265 2397 AGCACGCU G UUUAUUGA 564 TCAATAAA GGCTAGCTACAACGA AGCGTGCT 2266 2401 CGCUGUUU A UUGAAAGA 565 TCTTTCAA GGCTAGCTACAACGA AACAGCG 2267 2410 UUGAAAGA G UCACAGAA 566 TTCTTGTG GGCTAGCTACAACGA GACTCTTT 2269 2413 AAAGAGUC A CAGAAGAG 567 CTCTTCTG GGCTAGCTACAACGA GACTCTTT 2269	2331	AUCACUUG G UUUAAAAA	549	TTTTTAAA GGCTAGCTACAACGA CAAGTGAT	2251
2345 AAACAACC A CAAAAUAC 552 GTATTTTG GGCTAGCTACAACGA GGTTGTTT 2254 2350 ACCACAAA A UACAACAA 553 TTGTTGTA GGCTAGCTACAACGA TTTGTGGT 2255 2352 CACAAAAU A CAACAAGA 554 TCTTGTTG GGCTAGCTACAACGA ATTTTGTG 2256 2355 AAAAUACA A CAAGAGCC 555 GGCTCTTG GGCTAGCTACAACGA TGTATTTT 2257 2361 CAACAAGA G CCUGGAAU 556 ATTCCAGG GGCTAGCTACAACGA TCTTGTTG 2258 2368 AGCCUGGA A UUAUUUUA 557 TAAAATAA GGCTAGCTACAACGA TCCAGGCT 2259 2371 CUGGAAUU A UUUUAGGA 558 TCCTAAAA GGCTAGCTACAACGA AATTCCAG 2260 2379 AUUUUAGG A CCAGGAAG 559 CTTCCTGG GGCTAGCTACAACGA CCTAAAAT 2261 2387 ACCAGGAA G CAGCACGC 560 GCGTGCTG GGCTAGCTACAACGA TCCTGGT 2262 2390 AGGAAGCA G CACGCUGU 561 ACAGCGTG GGCTAGCTACAACGA TGCTTCCT 2263 2392 GAAGCAGC A CGCUGUU 562 AAACAGCG GGCTAGCTACAACGA TGCTTCCT 2264 2394 AGCAGCAC G CUGUUUAU 563 ATAAACAG GGCTAGCTACAACGA GTGCTTC 2264 2397 AGCACGCU G UUUAUUGA 564 TCAATAAA GGCTAGCTACAACGA AGCGTGCT 2265 2401 CGCUGUUU A UUGAAAGA 566 TCTTTCAA GGCTAGCTACAACGA AAACAGCG 2267 2410 UUGAAAGA G UCACAGAA 566 TCCTTCTG GGCTAGCTACAACGA GACTCTTT 2268 2413 AAAGAGUC A CAGAAGAG 567 CTCTTCTG GGCTAGCTACAACGA GACTCTTT 2269	2339	GUUUAAAA A CAACCACA	550	TGTGGTTG GGCTAGCTACAACGA TTTTAAAC	2252
2350 ACCACAAA A UACAACAA 553 TTGTTGTA GGCTAGCTACAACGA TTTGTGGT 2255 2352 CACAAAAU A CAACAAGA 554 TCTTGTTG GGCTAGCTACAACGA ATTTTGTG 2256 2355 AAAAUACA A CAAGAGCC 555 GGCTCTTG GGCTAGCTACAACGA ATTTTGTG 2257 2361 CAACAAGA G CCUGGAAU 556 ATTCCAGG GGCTAGCTACAACGA TCTTGTTG 2258 2368 AGCCUGGA A UUAUUUUA 557 TAAAATAA GGCTAGCTACAACGA TCCAGGCT 2259 2371 CUGGAAUU A UUUUAGGA 558 TCCTAAAA GGCTAGCTACAACGA AATTCCAG 2260 2379 AUUUUAGG A CCAGGAAG 559 CTTCCTGG GGCTAGCTACAACGA CCTAAAAT 2261 2387 ACCAGGAA G CAGCACGC 560 GCGTGCTG GGCTAGCTACAACGA TCCTGGT 2262 2390 AGGAAGCA G CACGCUGU 561 ACAGCGTG GGCTAGCTACAACGA TCCTTGCT 2263 2392 GAAGCAGC A CGCUGUUU 562 AAACAGCG GGCTAGCTACAACGA GCTGCTTC 2264 2394 AGCAGCAC G CUGUUUAU 563 ATAAACAG GGCTAGCTACAACGA GTGCTGCT 2265 2397 AGCACGCU G UUUAUUGA 564 TCAATAAA GGCTAGCTACAACGA AGCGTGCT 2266 2401 CGCUGUUU A UUGAAAGA 566 TCCTTCTAA GGCTAGCTACAACGA AAACAGCG 2267 2410 UUGAAAGA G UCACAGAA 566 TCCTTCTG GGCTAGCTACAACGA GACTCTTT 2268 2413 AAAGAGUC A CAGAAGAG 567 CTCTTCTG GGCTAGCTACAACGA GACTCTTT 2269	2342	UAAAAACA A CCACAAAA	551	TTTTGTGG GGCTAGCTACAACGA TGTTTTTA	2253
2352 CACAAAAU A CAACAAGA 554 TCTTGTTG GGCTAGCTACAACGA ATTTTGTG 2256 2355 AAAAUACA A CAAGAGCC 555 GGCTCTTG GGCTAGCTACAACGA TGTATTTT 2257 2361 CAACAAGA G CCUGGAAU 556 ATTCCAGG GGCTAGCTACAACGA TCTTGTTG 2258 2368 AGCCUGGA A UUAUUUUA 557 TAAAATAA GGCTAGCTACAACGA TCCAGGCT 2259 2371 CUGGAAUU A UUUUAGGA 558 TCCTAAAA GGCTAGCTACAACGA AATTCCAG 2260 2379 AUUUUAGG A CCAGGAAG 559 CTTCCTGG GGCTAGCTACAACGA CCTAAAAT 2261 2387 ACCAGGAA G CAGCACGC 560 GCGTGCTG GGCTAGCTACAACGA TTCCTGGT 2262 2390 AGGAAGCA G CACGCUGU 561 ACAGCCTG GGCTAGCTACAACGA TGCTTCCT 2263 2392 GAAGCAGC A CGCUGUUU 562 AAACAGCG GGCTAGCTACAACGA GTGCTTCC 2264 2394 AGCAGCAC G CUGUUUAU 563 ATAAACAG GGCTAGCTACAACGA GTGCTGCT 2265 2397 AGCACGCU G UUUAUUGA 564 TCAATAAA GGCTAGCTACAACGA AGCGTGCT 2266 2401 CGCUGUUU A UUGAAAGA 566 TCCTTCTAA GGCTAGCTACAACGA AACAGCG 2267 2410 UUGAAAGA G UCACAGAA 566 TCCTTCTG GGCTAGCTACAACGA GACTCTTT 2268 2413 AAAGAGUC A CAGAAGAG 567 CTCTTCTG GGCTAGCTACAACGA GACTCTTT 2269	2345	AAACAACC A CAAAAUAC	552	GTATTTTG GGCTAGCTACAACGA GGTTGTTT	2254
2355 AAAAUACA A CAAGAGCC 555 GGCTCTTG GGCTAGCTACAACGA TGTATTTT 2257 2361 CAACAAGA G CCUGGAAU 556 ATTCCAGG GGCTAGCTACAACGA TCTTGTTG 2258 2368 AGCCUGGA A UUAUUUUA 557 TAAAATAA GGCTAGCTACAACGA TCCAGGCT 2259 2371 CUGGAAUU A UUUUAGGA 558 TCCTAAAA GGCTAGCTACAACGA AATTCCAG 2260 2379 AUUUUAGG A CCAGGAAG 559 CTTCCTGG GGCTAGCTACAACGA CCTAAAAT 2261 2387 ACCAGGAA G CAGCACGC 560 GCGTGCTG GGCTAGCTACAACGA TTCCTGGT 2262 2390 AGGAAGCA G CACGCUGU 561 ACAGCGTG GGCTAGCTACAACGA TGCTTCCT 2263 2392 GAAGCAGC A CGCUGUUU 562 AAACAGCG GGCTAGCTACAACGA GCTGCTTC 2264 2394 AGCAGCAC G CUGUUUAU 563 ATAAACAG GGCTAGCTACAACGA GTGCTGCT 2265 2397 AGCACGCU G UUUAUUGA 564 TCAATAAA GGCTAGCTACAACGA AGCGTGCT 2266 2401 CGCUGUUU A UUGAAAGA 566 TCCTTCAA GGCTAGCTACAACGA AACAGCG 2267 2410 UUGAAAGA G UCACAGAA 566 TCCTTCTG GGCTAGCTACAACGA GACTCTTT 2269	2350	ACCACAAA A UACAACAA	553	TTGTTGTA GGCTAGCTACAACGA TTTGTGGT	2255
2361 CAACAAGA G CCUGGAAU 556 ATTCCAGG GGCTAGCTACAACGA TCTTGTTG 2258 2368 AGCCUGGA A UUAUUUUA 557 TAAAATAA GGCTAGCTACAACGA TCCAGGCT 2259 2371 CUGGAAUU A UUUUAGGA 558 TCCTAAAA GGCTAGCTACAACGA AATTCCAG 2260 2379 AUUUUAGG A CCAGGAAG 559 CTTCCTGG GGCTAGCTACAACGA CCTAAAAT 2261 2387 ACCAGGAA G CAGCACGC 560 GCGTGCTG GGCTAGCTACAACGA TTCCTGGT 2262 2390 AGGAAGCA G CACGCUGU 561 ACAGCGTG GGCTAGCTACAACGA TGCTTCCT 2263 2392 GAAGCAGC A CGCUGUUU 562 AAACAGCG GGCTAGCTACAACGA GCTGCTTC 2264 2394 AGCAGCAC G CUGUUUAU 563 ATAAACAG GGCTAGCTACAACGA GTGCTGCT 2265 2397 AGCACGCU G UUUAUUGA 564 TCAATAAA GGCTAGCTACAACGA AGCGTGCT 2266 2401 CGCUGUUU A UUGAAAGA 566 TCCTTCAA GGCTAGCTACAACGA AAACAGCG 2267 2410 UUGAAAGA G UCACAGAA 566 TTCTGTGA GGCTAGCTACAACGA GACTCTTT 2269	2352	CACAAAAU A CAACAAGA	554	TCTTGTTG GGCTAGCTACAACGA ATTTTGTG	2256
2368 AGCCUGGA A UUAUUUUA 557 TAAAATAA GGCTAGCTACAACGA TCCAGGCT 2259 2371 CUGGAAUU A UUUUAGGA 558 TCCTAAAA GGCTAGCTACAACGA AATTCCAG 2260 2379 AUUUUAGG A CCAGGAAG 559 CTTCCTGG GGCTAGCTACAACGA CCTAAAAT 2261 2387 ACCAGGAA G CAGCACGC 560 GCGTGCTG GGCTAGCTACAACGA TTCCTGGT 2262 2390 AGGAAGCA G CACGCUGU 561 ACAGCGTG GGCTAGCTACAACGA TGCTTCCT 2263 2392 GAAGCAGC A CGCUGUUU 562 AAACAGCG GGCTAGCTACAACGA GCTGCTTC 2264 2394 AGCAGCAC G CUGUUUAU 563 ATAAACAG GGCTAGCTACAACGA GTGCTGCT 2265 2397 AGCACGCU G UUUAUUGA 564 TCAATAAA GGCTAGCTACAACGA AGCGTGCT 2266 2401 CGCUGUUU A UUGAAAGA 565 TCTTTCAA GGCTAGCTACAACGA AAACAGCG 2267 2410 UUGAAAGA G UCACAGAA 566 TTCTGTGA GGCTAGCTACAACGA GACTCTTT 2269	2355	AAAAUACA A CAAGAGCC	555	GGCTCTTG GGCTAGCTACAACGA TGTATTTT	2257
2371 CUGGAAUU A UUUUAGGA 558 TCCTAAAA GGCTAGCTACAACGA AATTCCAG 2260 2379 AUUUUAGG A CCAGGAAG 559 CTTCCTGG GGCTAGCTACAACGA CCTAAAAT 2261 2387 ACCAGGAA G CAGCACGC 560 GCGTGCTG GGCTAGCTACAACGA TTCCTGGT 2262 2390 AGGAAGCA G CACGCUGU 561 ACAGCGTG GGCTAGCTACAACGA TGCTTCCT 2263 2392 GAAGCAGC A CGCUGUUU 562 AAACAGCG GGCTAGCTACAACGA GCTGCTTC 2264 2394 AGCAGCAC G CUGUUUAU 563 ATAAACAG GGCTAGCTACAACGA GTGCTGCT 2265 2397 AGCACGCU G UUUAUUGA 564 TCAATAAA GGCTAGCTACAACGA AGCGTGCT 2266 2401 CGCUGUUU A UUGAAAGA 565 TCTTTCAA GGCTAGCTACAACGA AAACAGCG 2267 2410 UUGAAAGA G UCACAGAA 566 TTCTGTGA GGCTAGCTACAACGA TCTTTCAA 2268 2413 AAAGAGUC A CAGAAGAG 567 CTCTTCTG GGCTAGCTACAACGA GACTCTTT 2269	2361	CAACAAGA G CCUGGAAU	556	ATTCCAGG GGCTAGCTACAACGA TCTTGTTG	2258
2379 AUUUUAGG A CCAGGAAG 559 CTTCCTGG GGCTAGCTACAACGA CCTAAAAT 2261 2387 ACCAGGAA G CAGCACGC 560 GCGTGCTG GGCTAGCTACAACGA TTCCTGGT 2262 2390 AGGAAGCA G CACGCUGU 561 ACAGCGTG GGCTAGCTACAACGA TGCTTCCT 2263 2392 GAAGCAGC A CGCUGUUU 562 AAACAGCG GGCTAGCTACAACGA GCTGCTTC 2264 2394 AGCAGCAC G CUGUUUAU 563 ATAAACAG GGCTAGCTACAACGA GTGCTGCT 2265 2397 AGCACGCU G UUUAUUGA 564 TCAATAAA GGCTAGCTACAACGA AGCGTGCT 2266 2401 CGCUGUUU A UUGAAAGA 565 TCTTTCAA GGCTAGCTACAACGA AAACAGCG 2267 2410 UUGAAAGA G UCACAGAA 566 TTCTGTGA GGCTAGCTACAACGA TCTTTCAA 2268 2413 AAAGAGUC A CAGAAGAG 567 CTCTTCTG GGCTAGCTACAACGA GACTCTTT 2269	2368	AGCCUGGA A UUAUUUUA	557	TAAAATAA GGCTAGCTACAACGA TCCAGGCT	2259
2387 ACCAGGAA G CAGCACGC 560 GCGTGCTG GGCTAGCTACAACGA TTCCTGGT 2262 2390 AGGAAGCA G CACGCUGU 561 ACAGCGTG GGCTAGCTACAACGA TGCTTCCT 2263 2392 GAAGCAGC A CGCUGUUU 562 AAACAGCG GGCTAGCTACAACGA GCTGCTTC 2264 2394 AGCAGCAC G CUGUUUAU 563 ATAAACAG GGCTAGCTACAACGA GTGCTGCT 2265 2397 AGCACGCU G UUUAUUGA 564 TCAATAAA GGCTAGCTACAACGA AGCGTGCT 2266 2401 CGCUGUUU A UUGAAAGA 565 TCTTTCAA GGCTAGCTACAACGA AAACAGCG 2267 2410 UUGAAAGA G UCACAGAA 566 TTCTGTGA GGCTAGCTACAACGA TCTTTCAA 2268 2413 AAAGAGUC A CAGAAGAG 567 CTCTTCTG GGCTAGCTACAACGA GACTCTTT 2269	2371	CUGGAAUU A UUUUAGGA	558	TCCTAAAA GGCTAGCTACAACGA AATTCCAG	2260
2390 AGGAAGCA G CACGCUGU 561 ACAGCGTG GGCTAGCTACAACGA TGCTTCCT 2263 2392 GAAGCAGC A CGCUGUUU 562 AAACAGCG GGCTAGCTACAACGA GCTGCTTC 2264 2394 AGCAGCAC G CUGUUUAU 563 ATAAACAG GGCTAGCTACAACGA GTGCTGCT 2265 2397 AGCACGCU G UUUAUUGA 564 TCAATAAA GGCTAGCTACAACGA AGCGTGCT 2266 2401 CGCUGUUU A UUGAAAGA 565 TCTTTCAA GGCTAGCTACAACGA AAACAGCG 2267 2410 UUGAAAGA G UCACAGAA 566 TTCTGTGA GGCTAGCTACAACGA TCTTTCAA 2268 2413 AAAGAGUC A CAGAAGAG 567 CTCTTCTG GGCTAGCTACAACGA GACTCTTT 2269	2379	AUUUUAGG A CCAGGAAG	559	CTTCCTGG GGCTAGCTACAACGA CCTAAAAT	2261
2392 GAAGCAGC A CGCUGUUU 562 AAACAGCG GGCTAGCTACAACGA GCTGCTTC 2264 2394 AGCAGCAC G CUGUUUAU 563 ATAAACAG GGCTAGCTACAACGA GTGCTGCT 2265 2397 AGCACGCU G UUUAUUGA 564 TCAATAAA GGCTAGCTACAACGA AGCGTGCT 2266 2401 CGCUGUUU A UUGAAAGA 565 TCTTTCAA GGCTAGCTACAACGA AAACAGCG 2267 2410 UUGAAAGA G UCACAGAA 566 TTCTGTGA GGCTAGCTACAACGA TCTTTCAA 2268 2413 AAAGAGUC A CAGAAGAG 567 CTCTTCTG GGCTAGCTACAACGA GACTCTTT 2269	2387	ACCAGGAA G CAGCACGC	560	GCGTGCTG GGCTAGCTACAACGA TTCCTGGT	2262
2392 GAAGCAGC A CGCUGUUU 562 AAACAGCG GGCTAGCTACAACGA GCTGCTTC 2264 2394 AGCAGCAC G CUGUUUAU 563 ATAAACAG GGCTAGCTACAACGA GTGCTGCT 2265 2397 AGCACGCU G UUUAUUGA 564 TCAATAAA GGCTAGCTACAACGA AGCGTGCT 2266 2401 CGCUGUUU A UUGAAAGA 565 TCTTTCAA GGCTAGCTACAACGA AAACAGCG 2267 2410 UUGAAAGA G UCACAGAA 566 TTCTGTGA GGCTAGCTACAACGA TCTTTCAA 2268 2413 AAAGAGUC A CAGAAGAG 567 CTCTTCTG GGCTAGCTACAACGA GACTCTTT 2269	2390	AGGAAGCA G CACGCUGU	561		
2394 AGCAGCAC G CUGUUUAU 563 ATAAACAG GGCTAGCTACAACGA GTGCTGCT 2265 2397 AGCACGCU G UUUAUUGA 564 TCAATAAA GGCTAGCTACAACGA AGCGTGCT 2266 2401 CGCUGUUU A UUGAAAGA 565 TCTTTCAA GGCTAGCTACAACGA AAACAGCG 2267 2410 UUGAAAGA G UCACAGAA 566 TTCTGTGA GGCTAGCTACAACGA TCTTTCAA 2268 2413 AAAGAGUC A CAGAAGAG 567 CTCTTCTG GGCTAGCTACAACGA GACTCTTT 2269	2392	GAAGCAGC A CGCUGUUU	562		
2397 AGCACGCU G UUUAUUGA 564 TCAATAAA GGCTAGCTACAACGA AGCGTGCT 2266 2401 CGCUGUUU A UUGAAAGA 565 TCTTTCAA GGCTAGCTACAACGA AAACAGCG 2267 2410 UUGAAAGA G UCACAGAA 566 TTCTGTGA GGCTAGCTACAACGA TCTTTCAA 2268 2413 AAAGAGUC A CAGAAGAG 567 CTCTTCTG GGCTAGCTACAACGA GACTCTTT 2269	2394	AGCAGCAC G CUGUUUAU	563	ATAAACAG GGCTAGCTACAACGA GTGCTGCT	
2401 CGCUGUUU A UUGAAAGA 565 TCTTTCAA GGCTAGCTACAACGA AAACAGCG 2267 2410 UUGAAAGA G UCACAGAA 566 TTCTGTGA GGCTAGCTACAACGA TCTTTCAA 2268 2413 AAAGAGUC A CAGAAGAG 567 CTCTTCTG GGCTAGCTACAACGA GACTCTTT 2269	2397	AGCACGCU G UUUAUUGA	564		
2410 UUGAAAGA G UCACAGAA 566 TTCTGTGA GGCTAGCTACAACGA TCTTTCAA 2268 2413 AAAGAGUC A CAGAAGAG 567 CTCTTCTG GGCTAGCTACAACGA GACTCTTT 2269	2401	CGCUGUUU A UUGAAAQA			
2413 AAAGAGUC A CAGAAGAG 567 CTCTTCTG GGCTAGCTACAACGA GACTCTTT 2269	2410				
Germanded   Did   Amandelms Addesmotwown Priviliti VV/A	2423	AGAAGAGG A UGAAGGUG	568	CACCTTCA GGCTAGCTACAACGA CCTCTTCT	2270

2429	GGAUGAAG G UGUCUAUC	569	GATAGACA GGCTAGCTACAACGA CTTCATCC	2271
2431	AUGAAGGU G UCUAUCAC	570	GTGATAGA GGCTAGCTACAACGA ACCTTCAT	2272
2435	AGGUGUCU A UCACUGCA	571	TGCAGTGA GGCTAGCTACAACGA AGACACCT	2273
2438	UGUCUAUC A CUGCAAAG	572	CTTTGCAG GGCTAGCTACAACGA GATAGACA	2274
2441	CUAUCACU G CAAAGCCA	573	TGGCTTTG GGCTAGCTACAACGA AGTGATAG	2275
2446	ACUGCAAA G CCACCAAC	574	GTTGGTGG GGCTAGCTACAACGA TTTGCAGT	2276
2449	GCAAAGCC A CCAACCAG	575	CTGGTTGG GGCTAGCTACAACGA GGCTTTGC	2277
2453	AGCCACCA A CCAGAAGG	576	CCTTCTGG GGCTAGCTACAACGA TGGTGGCT	2278
2462	CCAGAAGG G CUCUGUGG	577	CCACAGAG GGCTAGCTACAACGA CCTTCTGG	2279
2467	AGGGCUCU G UGGAAAGU	578	ACTITCCA GGCTAGCTACAACGA AGAGCCCT	2280
2474	UGUGGAAA G UUCAGCAU	579	ATGCTGAA GGCTAGCTACAACGA TTTCCACA	2281
2479	AAAGUUCA G CAUACCUC	580	GAGGTATG GGCTAGCTACAACGA TGAACTTT	2282
2481	AGUUCAGC A UACCUCAC	581	GTGAGGTA GGCTAGCTACAACGA GCTGAACT	2283
2483	UUCAGCAU A CCUCACUG	582	CAGTGAGG GGCTAGCTACAACGA ATGCTGAA	2284
2488	CAUACCUC A CUGUUCAA	583	TTGAACAG GGCTAGCTACAACGA GAGGTATG	2285
2491	ACCUCACU G UUCAAGGA	584	TCCTTGAA GGCTAGCTACAACGA AGTGAGGT	2286
2500	UUCAAGGA A CCUCGGAC	585	GTCCGAGG GGCTAGCTACAACGA TCCTTGAA	2287
2507	AACCUCGG A CAAGUCUA	586	TAGACTTG GGCTAGCTACAACGA CCGAGGTT	2288
2511	UCGGACAA G UCUAAUCU	587	AGATTAGA GGCTAGCTACAACGA TTGTCCGA	2289
2516	CAAGUCUA A UCUGGAGC	588	GCTCCAGA GGCTAGCTACAACGA TAGACTTG	2290
2523	AAUCUGGA G CUGAUCAC	589	GTGATCAG GGCTAGCTACAACGA TCCAGATT	2291
2527	UGGAGCUG A UCACUCUA	590	TAGAGTGA GGCTAGCTACAACGA CAGCTCCA	2292
2530	AGCUGAUC A CUCUAACA	591	TGTTAGAG GGCTAGCTACAACGA GATCAGCT	2293
2536	UCACUCUA A CAUGCACC	592	GGTGCATG GGCTAGCTACAACGA TAGAGTGA	2294
2538	ACUCUAAC A UGCACCUG	593	CAGGTGCA GGCTAGCTACAACGA GTTAGAGT	2295
2540	UCUAACAU G CACCUGUG	594	CACAGGTG GGCTAGCTACAACGA ATGTTAGA	2296
2542	UAACAUGC A CCUGUGUG	595	CACACAGG GGCTAGCTACAACGA GCATGTTA	2297
2546	AUGCACCU G UGUGGCUG	596	CAGCCACA GGCTAGCTACAACGA AGGTGCAT	2298
2548	GCACCUGU G UGGCUGCG	597	CGCAGCCA GGCTAGCTACAACGA ACAGGTGC	2299
2551	CCUGUGUG G CUGCGACU	598	AGTCGCAG GGCTAGCTACAACGA CACACAGG	2300
2554	GUGUGGCU G CGACUCUC	599	GAGAGTCG GGCTAGCTACAACGA AGCCACAC	2301
2557	UGGCUGCG A CUCUCUUC	600	GAAGAGAG GGCTAGCTACAACGA CGCAGCCA	2302
2568	CUCUUCUG G CUCCUAUU	601	AATAGGAG GGCTAGCTACAACGA CAGAAGAG	2303
2574	UGGCUCCU A UUAACCCU	602	AGGGTTAA GGCTAGCTACAACGA AGGAGCCA	2304
2578	UCCUAUUA A CCCUCCUU	603	AAGGAGGG GGCTAGCTACAACGA TAATAGGA	2305
2587	CCCUCCUU A UCCGAAAA	604	TTTTCGGA GGCTAGCTACAACGA AAGGAGGG	2306
2596	UCCGAAAA A UGAAAAGG	605	CCTTTTCA GGCTAGCTACAACGA TTTTCGGA	2307
2604	AUGAAAAG G UCUUCUUC	606	GAAGAAGA GGCTAGCTACAACGA CTTTTCAT	2308
2617	CUUCUGAA A UAAAGACU	607	AGTCTTTA GGCTAGCTACAACGA TTCAGAAG	2309
2623	AAAUAAAG A CUGACUAC	608	GTAGTCAG GGCTAGCTACAACGA CTTTATTT	
2627	AAAGACUG A CUACCUAU	609	ATAGGTAG GGCTAGCTACAACGA CAGTCTTT	
2630	GACUGACU A CCUAUCAA	610	TTGATAGG GGCTAGCTACAACGA AGTCAGTC	2312
2634	GACUACCU A UCAAUUAU	611	ATAATTGA GGCTAGCTACAACGA AGGTAGTC	2313
2638	ACCUAUCA A UUAUAAUG	612	CATTATAA GGCTAGCTACAACGA TGATAGGT	2314
2641	UAUCAAUU A UAAUGGAC	613	GTCCATTA GGCTAGCTACAACGA AATTGATA	2315
2644	CAAUUAUA A UGGACCCA	614	TGGGTCCA GGCTAGCTACAACGA TATAATTG	
2648	UAUAAUGG A CCCAGAUG	615	CATCTGGG GGCTAGCTACAACGA CCATTATA	2317
2654	GGACCCAG A UGAAGUUC	616	GAACTTCA GGCTAGCTACAACGA CTGGGTCC	
2659	CAGAUGAA G UUCCUUUG	617	CAAAGGAA GGCTAGCTACAACGA CTGAGTCC	
2669	UCCUUUGG A UGAGCAGU		ACTGCTCA GGCTAGCTACAACGA CCAAAGGA	2319
<del></del>		618		2320
2673	UUGGAUGA G CAGUGUGA	619	TCACACTG GGCTAGCTACAACGA TCATCCAA	2321
2676	GAUGAGCA G UGUGAGCG	620	CGCTCACA GGCTAGCTACAACGA TGCTCATC	2322

2670	HOLOGRAM C TOTAGOTO	625	laggamas agams are see	
2678	UGAGCAGU G UGAGCGGC	621	GCCGCTCA GGCTAGCTACAACGA ACTGCTCA	
2682	CAGUGUGA G CGGCUCCC	622	GGGAGCCG GGCTAGCTACAACGA TCACACTG	2324
2685	UGUGAGCG G CUCCCUUA	623	TAAGGGAG GGCTAGCTACAACGA CGCTCACA	2325
2693	GCUCCCUU A UGAUGCCA	624	TGGCATCA GGCTAGCTACAACGA AAGGGAGC	2326
2696	CCCUUAUG A UGCCAGCA	625	TGCTGGCA GGCTAGCTACAACGA CATAAGGG	2327
2698	CUUAUGAU G CCAGCAAG	626	CTTGCTGG GGCTAGCTACAACGA ATCATAAG	2328
2702	UGAUGCCA G CAAGUGGG	627	CCCACTTG GGCTAGCTACAACGA TGGCATCA	2329
2706	GCCAGCAA G UGGGAGUU	628	AACTCCCA GGCTAGCTACAACGA TTGCTGGC	2330
2712	AAGUGGGA G UUUGCCCG	629	CGGGCAAA GGCTAGCTACAACGA TCCCACTT	2331
2716	GGGAGUUU G CCCGGGAG	630	CTCCCGGG GGCTAGCTACAACGA AAACTCCC	2332
2727	CGGGAGAG A CUUAAACU	631	AGTTTAAG GGCTAGCTACAACGA CTCTCCCG	2333
2733	AGACUUAA A CUGGGCAA	632	TTGCCCAG GGCTAGCTACAACGA TTAAGTCT	2334
2738	UAAACUGG G CAAAUCAC	633	GTGATTTG GGCTAGCTACAACGA CCAGTTTA	2335
2742	CUGGGCAA A UCACUUGG	634	CCAAGTGA GGCTAGCTACAACGA TTGCCCAG	2336
2745	GGCAAAUC A CUUGGAAG	635	CTTCCAAG GGCTAGCTACAACGA GATTTGCC	2337
2758	GAAGAGGG G CUUUUGGA	636	TCCAAAAG GGCTAGCTACAACGA CCCTCTTC	2338
2770	UUGGAAAA G UGGUUCAA	637	TTGAACCA GGCTAGCTACAACGA TTTTCCAA	2339
2773	GAAAAGUG G UUCAAGCA	638	TGCTTGAA GGCTAGCTACAACGA CACTTTTC	2340
2779	UGGUUCAA G CAUCAGCA	639	TGCTGATG GGCTAGCTACAACGA TTGAACCA	2341
2781	GUUCAAGC A UCAGCAUU	640	AATGCTGA GGCTAGCTACAACGA GCTTGAAC	2342
2785	AAGCAUCA G CAUUUGGC	641	GCCAAATG GGCTAGCTACAACGA TGATGCTT	2343
2787	GCAUCAGC A UUUGGCAU	642	ATGCCAAA GGCTAGCTACAACGA GCTGATGC	2344
2792	AGCAUUUG G CAUUAAGA	643	TCTTAATG GGCTAGCTACAACGA CAAATGCT	2345
2794	CAUUUGGC A UUAAGAAA	644	TTTCTTAA GGCTAGCTACAACGA GCCAAATG	2346
2802	AUUAAGAA A UCACCUAC	645	GTAGGTGA GGCTAGCTACAACGA TTCTTAAT	2347
2805	AAGAAAUC A CCUACGUG	646	CACGTAGG GGCTAGCTACAACGA GATTTCTT	2348
2809	AAUCACCU A CGUGCCGG	647	CCGGCACG GGCTAGCTACAACGA AGGTGATT	2349
2811	UCACCUAC G UGCCGGAC	648	GTCCGGCA GGCTAGCTACAACGA GTAGGTGA	2350
2813	ACCUACGU G CCGGACUG	649	CAGTCCGG GGCTAGCTACAACGA ACGTAGGT	2351
2818	CGUGCCGG A CUGUGGCU	650	AGCCACAG GGCTAGCTACAACGA CCGGCACG	2352
2821	GCCGGACU G UGGCUGUG	651	CACAGCCA GGCTAGCTACAACGA AGTCCGGC	2353
2824	GGACUGUG G CUGUGAAA	652	TTTCACAG GGCTAGCTACAACGA CACAGTCC	2354
2827	CUGUGGCU G UGAAAAUG	653	CATTTTCA GGCTAGCTACAACGA AGCCACAG	2355
2833	CUGUGAAA A UGCUGAAA	654	TTTCAGCA GGCTAGCTACAACGA TTTCACAG	2356
2848	GUGAAAAU G CUGAAAGA	655	TCTTTCAG GGCTAGCTACAACGA ATTTTCAC	2357
	AAGAGGGG G CCACGGCC	656	GGCCGTGG GGCTAGCTACAACGA CCCCTCTT	2358
2851	AGGGGGCC A CGGCCAGC GGGCCACG G CCAGCGAG	657	GCTGGCCG GGCTAGCTACAACGA GGCCCCCT	2359
2858	CACGGCCA G CGAGUACA	658	CTCGCTGG GGCTAGCTACAACGA CGTGGCCC	2360
2862		659	TGTACTCG GGCTAGCTACAACGA TGGCCGTG	2361
2864	GCCAGCGA G UACAAAGC CAGCGAGU A CAAAGCUC	660	GCTTTGTA GGCTAGCTACAACGA TCGCTGGC	2362
2869	AGUACAAA G CUCUGAUG	661	GAGCTTTG GGCTAGCTACAACGA ACTCGCTG	2363
2875	AAGCUCUG A UGACUGAG	662	CATCAGAG GGCTAGCTACAACGA TTTGTACT	2364
2878	CUCUGAUG A CUGAGCUA	663	CTCAGTCA GGCTAGCTACAACGA CAGAGCTT	2365
2883	AUGACUGA G CUAAAAAU	664	TAGCTCAG GGCTAGCTACAACGA CATCAGAG	2366
2890	AGCUAAAA A UCUUGACC	665	ATTITTAG GGCTAGCTACAACGA TCAGTCAT	2367
2896	····	666	GGTCAAGA GGCTAGCTACAACGA TTTTAGCT	2368
2900	CUIGACCC A CAUDIGGCC	667	AATGTGGG GGCTAGCTACAACGA CAAGATTT	2369
2900	CUUGACCC A CAUUGGCC	668	GGCCAATG GGCTAGCTACAACGA GGGTCAAG	2370
2906	UGACCCAC A UUGGCCAC	669	GTGGCCAA GGCTAGCTACAACGA GTGGGTCA	2371
2909	CACAUUG G CCACCAUC	670	GATGGTGG GGCTAGCTACAACGA CAATGTGG	2372
	CAUUGGCC A CCAUCUGA	671	TCAGATGG GGCTAGCTACAACGA GGCCAATG	2373
2912	UGGCCACC A UCUGAACG	672	CGTTCAGA GGCTAGCTACAACGA GGTGGCCA	2374

2920 AUCUGANA G GUGGUUNAC 674 GTTARCCA GOCTRACTRICANCAG GTTCAGATT 2375 2923 UGANCGUG G UUNACCUG 675 CAGGTTAN GGCTRACTRICANCAGA GTTCAGATT 2377 2927 GUGGUUNA C CUGGGUGG 676 CAGGTTAN GGCTRACTRICANCAGA ACGGTTCA 2377 2928 UGCUGGAG G CUGGCACC 678 GCTCCCCAG GGCTRACTRICANCAGA AGGTTANA 2379 29292 GUGANCCU G CUGGGAGC 677 GCTCCCAG GGCTRACTRICANCAGA AGGTTANA 2379 29292 GGGAGCCU G CACARACCA 679 GCTCCCAG GGCTRACTRICANCAGA AGGTTCAC 2380 2942 GGGAGCCU G ACCARACC 679 GCTCGTG GGCTRACTRICANCAGA AGGTCC 2381 2942 GGGAGCCU G A CCARACCAA 680 TTGCTTG GGCTRACTRICANCAGA AGGTCC 2382 2942 GGGAGCCU G A CCARACCAA 680 TTGCTTG GGCTRACTRICANCAGA AGGTCC 2382 2949 UGCACCAA G CARAGCAA 680 TTGCTTG GGCTRACTRICANCAGA GCAGGCTC 2382 2949 UGCACCAA G CARAGCAA 680 TTGCTTG GGCTRACTRICANCAGA TTGGTGC 2383 2958 CARAGARG G CCUCUGAU 682 ATCAGRAG GGCTRACTRICANCA CACAGGCC 2385 2958 GGCUUUU A UGGUGAUU 683 ANTONCAG GGCTRACTRICANCAGA CACAGGCC 2385 2958 CUGURAUS G UGARUUGUU 683 ANTONCAG GGCTRACTRICANCAGA CACAGGCC 2386 2958 UGCUCUU A UGGUGAUA 685 TTCAACAA GGCTRACTRACAGA CACAGGCC 2387 2979 AUGUGAUA U GUGAAUAC 686 TTTCAACA GGCTRACTRACAGA CACAGCC 2387 2979 AUGUGAUA A UGUCUCAA 687 TTGCAGTA GGCTRACTRACAGA ATCACCA 2387 2981 UGUUGAAU A CUCCAAA 687 TTGCAGTA GGCTRACTRACAGA ATCACCA 2388 2981 UGAUNACU G CRANUNUG 689 ATTTGCAG GGCTRACTRACAGA ATCACCA 2389 2982 UUCUCCAA A UAUGGAAAA 690 TTTCCATA GGCTRACTRACAGA ATCACCA 2381 2983 AUCUCCAA A CUACCUCA 693 TUACCTATA GGCTRACTRACAGA ATCACCA 2381 2984 UACUUCCAA CUCCACA 691 TTTCCATA GGCTRACTRACAGA ATCACCA 2381 2985 AUCUCCAAA CUACCUCA 693 TUACGTT GGCTRACTRACAGA ATCACCA 2381 2986 UACUCCAAA CUACCUCA 693 TUACGTT GGCTRACTRACAGA ATCACCA 2381 2986 UACUCCAAA CUACCUCA 693 TUACGTT GGCTRACTRACAGA ATCTCATT 2394 2987 AUGUGAAAU A UGGAAAU 686 ATTTTCAG GGCTRACTRACAGA ATTTCCAG 2393 2003 CUCCAAGA A CUACCUCA 693 TUACGTT GGCTRACTRACAGA ATTTCCAG 2393 2004 CUCCAAGA CUACCUCA 693 TUACGTT GGCTRACTRACAGA ATTTCCAG 2393 2005 UCUCCAAA CUACCUCA 693 TUACGTT GGCTRACTRACAGA ATTTCCAG 2393 2007 CUCCAAGA A CUACCUCA 699 TUACGTT GGCTRACTRACAGA ATTTCCAT 2398 2007 CUCCAAGA COCACAC	2918	CCAUCUGA A CGUGGUUA	673	TAACCACG GGCTAGCTACAACGA TCAGATGG	2375
2923         UBARCGUG G UURACCUG         675         CAGGTTAA GGCTAGCTACAACGA CACGTTCA         2377           2927         CGUGGUUA A CCUGCUGG         676         CCAGGAGG GGCTAGCTACAACGA TAACCAAC         2378           2931         GUURACCU G CAGGGAGC         678         GCTCCAGG GGCTAGCTACAACGA AGGTTACC         2380           2942         GGGGAGCU G CACCAGC         679         GCTTGGTG GGCTAGCTACAACGA AGGTTACC         2381           2944         GAGCUGC A CCAGAGCA         680         TGCTGTGG GGCTAGCTACAACGA CAGGGCC         2381           29494         GAGCUGC A CAGGAGA         681         CTCCTTG GGCTAGCTACAACGA CAGGGCC         2381           29494         GAGCUCG A GCAUGUGU         682         ATCAGAGG GGCTAGCTACAACGA TGTGGTACA         2383           2958         CAAGGAGG         G CUCUUGAU         682         ATCAGAGG GGCTAGCTACAACGA CACCACTC         2384           2956         GCCUCUG A UGAUUGU         684         AACAATCA GGCTAGCTACAACGA CACCATCA         2386           2971         UGAUGGUG A UGAUGAU         686         GTATTCAA GCCTAGCTACAACGA CACCATCA         2387           2979         AUUUUGAAU A CUGCAAAU         688         ATTGCAGG GCTAGCTACAACGA CACCATCA         2389           2984         UGAUGAAU A CUGCAAAU         688         ATTGCAG GCCTAGCTACAACGA ACTACACA					
2927         CGUGGUUA A CCUGCUGG         676         CCAGCAGG         GGTCCCAG         GATTACTAAACGA         TAACCAG         2378           2931         GUUAACCU         GUGGGAGC         677         GCTCCCAG         GGTTAGCTACAAGGA         AAGTTAAA         2379           2942         GGGAGCU         GACCAAGC         678         GGTGAGG         GGTTAGCTACAACGA         AAGGCUGC         2381           2944         GAGCCUCC         ACAAGCAA         680         TTGCTTG         GGCTAGCTACAACGA         AGGCUGC         2382           2949         GACCACA         680         TTGCTTG         GGCTAGCTACAACGA         AGGCUGC         2382           2949         GACCACA         680         TTGCTTG         GGCTAGCTACAACGA         CCTCCTTC         2382           2958         CUCUGAU         681         ACTCACTCT         GGCTAGCTACAACGA         CCTCCTTC         2384           2956         GUCUGAU         AUGUAGAA         681         TTCAACAA         GGCTAGCTACAACGA         AACCACCA         2387           2971         UGUGGAU         GUGAAAU         686         ATTTCAA         GGCTAGCTACAACGA         AACCACCA         2387           2974         UGUGUGAA         CGCAAAUAU         688         ATTTGCAG			<del></del>		
2931         GUUAACCU G CUGGAGC         677         GCTCCCAG GGCTAGCTACAACGA AGGTTAAC         2379           2938         UGCUGGAG G CUGCACC         678         GGTGAGG GGCTAGCTACAAGGA TCCCAGGA         2380           2942         GGAGGCU G CACCAAGC         679         GCTTGAGG GGCTACACAGAGA GAGGTCC         2382           2944         GAGCCUGC A CCACAGC         680         TTGCTTGG GGCTACCAACGA GCAGGTCC         2382           2959         UGCACCAA G CAAGGAGG         681         CCTCCTTG         GGCTAGCTACAACGA CCTCCTCTTG         2383           2958         CAAGGAGG         682         ATCAAGAG GGCTACCAACGA CCTCCTCTT         2382           2958         CAAGGAGG         681         ATCAACCA GGCTACCAACGA CACCACCA         2385           2966         CUCUGAUG         684         AACAATCA GGCTACCAACGA CACCACA         2386           2971         UGUGGAU         GUAAUAUC         685         GTACACAAA         GGCTAGCTACAACGA ATCACACA         2388           2971         UGUGGAU         GUAAUAUG         686         ATTTTCAA         GGCTAGCTACAACGA ATCACACA         2389           2981         UGUGAAUA         GGB         ATTTTCAA         GGCTAGCTACAACGA ATTTCACA         2392           2981         UGUGAAUA         GGB         ATTTTCAA         G					
2938         UGCUGGGA G CCUGCACC         678         GGTSCAGG GGCTAGCTACAACGA TCCCAGCA         2380           2942         GGGAGCCU G CACCAAGC         679         GCTTSGTG GGCTAGCTACAACGA AGGACCC         2381           2944         GAGCUGCA C CACAGCAA         680         TGCTTGTG GGCTAGCTACAACGA GCAGGCT         2383           2949         UGCACCAA G CAAGGAGG         681         CCTCCTTG GGCTAGCTACAACGA TTGGTGCA         2383           2956         GCACUCUGA U GGUGAUU         682         ARCAGAGG GGCTAGCTACAACGA CTCAGAGG         2384           2956         GCUCUGAU G UGGUAUU         684         AACAATCA GGCTAGCTACAACGA CACGAGGC         2386           2956         CUCUGAUG G UGAUUGUU         684         AACAATCA GGCTAGCTACAACGA CACCATCA         2386           2971         UGUGGAU G UUGAUUAC         685         TTCAACAA GCCTAGCTACAACGA CACCATCA         2386           2971         UGUGAU G UUGAAUC         686         GTATTCAA GGCTAGCTACAACGA ATCCACA         2389           2991         UGUGAAU A UGCAAAU G 688         ATTTGCAG GCCTACCACACGA ATCCACAC         2392           2991         UGAAUACU G CAAAUAUG         689         CATTCTTG GGCTAGCACACA ATCCATA         2392           2996         LUGCAAU A UUGCAA         691         TATTCCA GCCTACACAGA ATTTCCATA         2391           <					
2942 GGGAGCCU G CACCAAGC 679 GCTTGGTG GCTAGCTACAACGA AGGCTCC 2381 2944 GAGCCUGC A CCAAGCAA 680 TTGGTTGG GGCTAGCTACAACGA GCAGGCTC 2382 2958 CAAGGAGG G CAAGCAAC 681 CTCCTTG GGCTAGCTACAACGA CTGGTGC 2382 2958 CAAGGAGG G CCUCUGAU 682 ATCAGAGG GGCTAGCTACAACGA CTCCCTTG 2384 2958 CAAGGAGG G CCUCUGAU 682 ATCAGAGG GGTAGCTACAACGA CTCCCTTG 2384 2958 CAAGGAGG G CCUCUGAU 682 ATCAGAGG GGTAGCTACAACGA CTCCCTTG 2384 2958 CUCUGAUG G UGAUUGUU 684 AACAATCA GGCTAGCTACAACGA CATCAGAG 2385 2958 CUCUGAUG G UGAUUGUU 684 AACAATCA GGCTAGCTACAACGA CATCAGAG 2385 2971 UGAUGGUG U UUGAAUAC 686 GTATCAA GGCTAGCTACAACGA CATCAGAG 2387 2974 UGGUGAUU G UUGAAUAC 686 GTATCAA GGCTAGCTACAACGA CACCATCA 2387 2979 AUUGUGAA U CUCCAAA 687 TTGCACA GGCTAGCTACAACGA ATCACCA 2389 2981 UGAUGAAA A UAUGGAAA 687 TTGCACA GGCTAGCTACAACGA ATCACAC 2390 2988 UACUGCAA A UAUGGAAA 689 CATATTTG GGCTAGCTACAACGA ATTCACA 2390 2989 CUCCAAAU A UGGAAAA 690 CATATTG GGCTAGCTACAACGA ATTTGCAC 2390 2990 CUGCAAAU A UGGAAAA 690 CATATTCCA GGCTAGCTACAACGA ATTTGCAC 2393 3005 UCUCCAA A UAUGGAAA 691 GATTTCCA GGCTAGCTACAACGA ATTTGCAC 2393 3006 CUCCAACU A CUCCAAGA 692 TGAAGAGA GGCTAGCTACAACGA ATTTGCAC 2393 3017 CCUCAAGA G CAAACGUG 692 TGAAGAGA GGCTAGCTACAACGA ATTTGCAC 2397 3021 AAGGCAA A CUUCACAC 692 TGAAGAGA GGCTAGCTACAACGA TTCCATAT 2394 3022 GAGCAAC G CUCCAAGA 694 TCTTGAGG GGCTAGCTACAACGA TTCTTGAGG 2397 3021 AAGGCAA A CUUCAAGA 694 TCTTGAGG GGCTAGCTACAACGA TTCTTGAGG 2397 3022 GAGCAAC G GACCUUA 699 AGAAAAA AGGCTAGCTACAACGA TTCTTGTCTT 2398 3023 GAGCAAC G GACCUUA 699 AGAAAAA GGCTAGCTACAACGA TTCTTCTT 2398 3024 CAAACGUG A CUUCAAGA 697 TATATCAC GGCTAGCTACAACGA TTCTCTTT 2398 3025 CAAACGUG A CUUCAAGA 697 TATATCAC GGCTAGCTACAACGA TTCTCTTT 2398 3026 CAAACGUG A CUUCAAGA 700 CACCTCTTG GGCTAGCTACAACGA TTCTCTTT 2404 3047 CAACAAGA A CGGACCU 701 GTGCTGC GGCTAGCTACAACGA TTCTCTTT 2404 3047 CAACAAGA A CGGACCU 702 CACCTCTTTC GGCTAGCTACAACGA TTCTCTTT 2404 3049 ACAAGGAG A CUUCACAC 701 GTGCTCC GGCTAGCTACAACGA TCTCTCTT 2405 3054 GAGCACA CAAGGACA 702 GTGCTCCAACGA TCCATCTTC 2405 3054 GAGCACA A CGAGCAC 701 GTGCTCCA GGCTAG			<del></del>		
2944         GAGCCUGC A CCAAGCAA         680         TTGCTTGG GGCTAGCTACAACGA GCAGGCTC         2382           2949         UGCACCAA G CAAGGAG         681         CCTCCTTG GGCTAGCTACACGA TTGGTCA         2383           2958         CAAGGAGG         GCUCUGUA         682         ATCAACGA GCTACTTG         2384           2965         GGCCUCUG A UGGUGAUU         683         AATCACCA GGCTAGCTACAACGA CCTCCTTG         2386           2966         CUCUGAUG G UGAUUGUU         684         AACAACA GGCTAGCTACAACGA CACCATCA         2387           2971         UGGUGAUU G UUGAAUAC         685         GTATCAA GGCTAGCTACAACGA AACCACA         2387           2974         UGGUGAUU A UGCUCCA         687         TTGCAGTA GGCTAGCTACAACGA AATCACA         2388           2979         AUUGUGAA         AUCUGCAA         687         TTGCAGTA GGCTAGCTACACGA ATTCAACA         2392           2981         UGUUGAAU A UGGAAAU         688         ATTGCAG GGCTAGCTACAACGA ATTCAACA         2392           2996         CUGCAAAU A UGGAAAU         689         CATTCCA GGCTAGCTACAACGA ATTCCAACA         2392           2996         CUGCAAUA A UGGAAAU         691         GATTCCA GGCTAGCTACAACGA TTCCAACA         2393           3008         CUCCAACU A CUCCACA         692         TGGAGAG GGCTAGCTACAACGA TTCCAACA         23					
2949         UGCACCAA G CAAGGAGG         681         CCTCCTTG GGCTAGCTACACGA TTGGTGC         2383           2958         CAAGGAGG G CCUCUGAU         692         ATCAGAGG GGCTAGCTACACGA CCTCCTTG         2384           2968         CGCUCUGA D UGGUGAU         683         AACACCA GGCTAGCTACAACGA CACGACGA         2385           2968         CUCUGAUG G UGAUUGUU         684         AACAATCA GGCTAGCTACAACGA CACCATCA         2386           2971         UGGUGAUU G UUGAUAC         685         TTCAACAA GGCTAGCTACAACGA CACCAACA         2387           2979         AUGUGAUA         686         GTATTCAA GGCTAGCTACAACGA CATCAACA         2389           2981         UGUUGAUA         688         ATTTGCAG GGCTAGCTACAACGA TCAACACA         2390           2984         UGAUACU G CAAAUUG         689         CATATTTG GGCTAGCTACAACGA ATTCAACA         2392           2980         LUCUCCAA         AUGUGAA         691         TTTCCATTA GGCTAGCTACAACGA TTCCATCA         2393           2996         CUCGAAAU         10GAAACAC         692         TGAAGAGA ACTTCAACGA TTCCATCA         2393           2996         LUCGAAA         AUCUCCAA         692         TGAGAGAA         ATCTTGAG         GGCTAGCTACAACGA TTGCATCA         2393           3005         LUCUCCAA         CULCCCAA         CULC					
2958         CAAGGAGG G CCUCUGAU         682         ATCAGAGG GGCTAGCTACAACGA CCTCCTTG         2384           2956         GGCCUCUG A UGGUGAUU         683         AATCACCA GGCTAGCTACAACGA CAGAGGC         2385           2968         CUCUGAUG G UGAUUGUU         684         AACAATCA GGCTAGCTACAACGA CATCAGA         2386           2971         UGAUGAUU G UUGAALAC         685         TTCAACAA GGCTAGCTACAACGA CACCATCA         2387           2974         UGGUGAUU G UUGAALAC         686         GTATTCAA GGCTAGCTACAACGA TACACAC         2388           2979         AUUGUGAA         A CUGCAAA         687         TTGCAGTA GGCTAGCTACACGA TACACACA         2389           2984         UGUGAALA A UGUGCAAA         688         ATTTCCATA GGCTAGCTACAACGA ATTCACA         2391           2988         UACUCCAA A UAUGGAAA         691         CTTCCATA         GGCTAGCTACAACGA ATTCCACA         2392           2996         AUAUGGAA         691         CTTCCATA         GGCTAGCTACAACGA ATTCCACATA         2392           2996         AUAUGGAA         691         CTTCAGG         GGCTAGCTACAACGA TTCCACATA         2393           3008         CUCCACACA         ACUACUCCA         692         TGGAGCTACAACGA TTCCAACGA TTCCACAGA         2395           3017         CCUCAAGA         694         T			<b> </b>		
2965         GGCCUCUG A UGGUGAU         683         AATCACCA GGCTAGCTACAACGA CACAGGCC         2385           2966         CUCUGAUG G UGAUUGUU         684         AACAATCA GGCTAGCTACAACGA CACAGAGA         2386           2971         UGAUGGUG A UUGUUGAA         685         TTCAACAA GGCTAGCTACAACGA CACCATCA         2387           2974         UGGUGAUU G UUGAAUAC         686         GTATTCAA GGCTAGCTACAACGA AATCACA         2389           2981         UGGUGAAU A CUGCAAAU         687         TTGCAGTA GGCTAGCTACAACGA ATCAACA         2339           2984         UGAAUACU G CAAAUAUG         689         CATATTTG GGCTAGCTACAACGA ATCAACA         2391           2986         UACUGCAA A UAUGGAAA         690         CATATTTG GGCTAGCTACAACGA ATTCAACA         2392           2996         CUGCAAAU A UGGAAAA         691         GATTTCCA GGCTAGCAACGA ATTCAACA         2392           2996         CUGAAAU A UGUCUCCA         692         TTGAGAGA GGCTAGCTACAACGA ATTCGACA         2392           3005         UCUCUACA A CUACCUCA         693         TGAGAGAG GCTAGCTACAACGA ATTCGACA         2395           3017         CCUCAAGA G CAAACGUU         695         CACGTTTG GGCTACAACGA ATTCGACA         2397           3021         AAGACAA G UGACUUAU         697         ATAAGTCA GGCTACAACGA TTCTTGAG         2397					
2968         CUCUGAUG G UGAUUGUU         684         AACAATCA GGCTAGCTACAACGA CATCAGAG         2386           2971         UGAUGGUG A UUGAUGAA         685         TTCAACAA GGCTAGCTACAACGA CACCATCA         2387           2979         AUUGUUGA A UACUGCAA         685         GTATTCAA GGCTAGCTACAACGA AATCACCA         2388           2981         UGUUGAAU A CUGCAAAU         688         ATTTGCAGTA GGCTAGCTACAACGA ATTCACAC         2390           2984         UGADAUC G CAAAUAUG         689         CATATTTG GGCTAGCTACAACGA ATTCACAC         2390           2984         UACUGCAA A UAUGGAAA         690         CATTTTG GGCTAGCTACAACGA ATTCACAC         2392           2990         CUGCAAAU A UAGGAAAC         691         GATTCCA GGCTAGCTACAACGA ATTCCAAC         2393           3005         UCUCUCCA A CUACCUCA         692         TGGAGTAG GGCTAGCTACAACGA TTCCAATT         2394           3006         CUCCAACA A CUCCACACA         694         TCTTGAGG GGCTAGCTACAACGA TTCCATCAT         2395           3017         CCUCAAGA G CAAACGUG         695         CACGTTTG GGCTAGCTACAACGA TTCCTTT         2398           3022         AAGACAAA A CUGACUU         696         AAGTCACG GGCTACCTACAACGA TTCCTTT         2398           3022         AAGACAGA A CUUAUUUU         697         AAAATAGA GGCTAGCTACAACGA CACGTTTGCTCAACGA					
2971         UGAUGGUG A UUGUUGAA         685         TTCAACAA GGCTAGCTACAACGA CACCATCA         2387           2974         UGGUGAUU G UUGAANAC         686         GTATTCAA GGCTAGCTACAACGA AATCACCA         2388           2979         AUUGUUGA A UACUGCAA         687         TTGCAGTA GGCTAGCTACAACGA ATCACCA         2389           2981         UGUUGAAD A CUGCCAAU         688         ATTTGCAG GGCTAGCTACAACGA ATCACAC         2390           2984         UGAULACU G CAAAURUG         689         CATATTTG GGCTAGCTACAACGA AGTATCAC         2390           2986         UACUGCAA A UAUGGAAA         690         TTTCATG GGCTAGCTACAACGA TTCACACGA         2391           2996         CUGCAAAU A UGGAAAU         691         GATTTCCA GGCTAGCTACAACGA TTCCATT         2394           3005         UCUCUCCA A CUACACGA         691         TGAGGTAG         GGCTAGCTACAACGA TTCCATT         2394           3006         CUCCAACU A CUUCACA         692         TGGAGGAG GGCTAGCTACAACGA TTCCATT         2394           3017         CCUCAAGA G CAAACGUG         694         CATTGGGCTACAACGA TTCCTTT         2398           3023         GAGCAAC G UGACUUAU         697         ATAAGTCA GGCTACAACGA TTCCTTT         2398           3026         CAAACGUG A CUUAUUUU         698         AAAATAGG GGCTACAACGA TACGATTCAACGA CTCCTTTC		<del></del>			
2974         UGGUGAUU G UUGAAUAC         686         GTATTCAA GGCTAGCTACAGGA ARTCACCAA         2388           2979         AUUGUUGA A UACUGCAA         687         TTGCAGTA GGCTAGCTACAACGA TCAACAAT         2389           2981         UUGUUGAAU A CUGCAAAU         688         ATTGCAG GGCTAGCTACAACGA ATTCAACA         2390           2984         UGAAUACU G CAAAUAUG         689         CATATTG GGCTAGCTACAACGA ATTCAACA         2391           2986         UACUGCAA A UAUGGAAA         690         TTTCCATA GGCTAGCTACAACGA ATTCCAACA         2392           2996         CUGCAAAU A UGUCUCCA         692         TGGAGAGA GGCTAGCTACAACGA ATTCCAACA         2393           3005         DCUCUCCA A CUACCACA         692         TGGAGAGA GGCTAGCTACAACGA ATTCGAGA         2395           3008         DCUCCAACU A CCUCAAGA         694         TCTTGAGG GGCTAGCTACAACGA AGTTGGAC         2397           3021         AAGAGCAA A CGUGACUU         695         CACGTTTG GGCTAGCTACAACGA AGTTGACACGA         2397           3022         AGAGCAAA C GUGACUU         695         CACGTTTG GGCTAGCTACAACGA TCTTGAGA         2397           3023         GAGCAACG G UUAUUUUU         697         ATAAGTCA GGCTAGCTACAACGA CACGTTTG         2399           3040         CUUUAUUUUU         698         AAAATTACA GGCTACAACGA CACGATTGCAACGA CACGTTTG					
2979         AUUGUUGA A UACUGCAA         687         TTGCAGTA GGCTAGCTACAAGA TCAACAAT         2389           2981         UGUUGAAU A CUGCAAAU         688         ATTTGCAG GGCTAGCTACAAGA ATTCAACA         2390           2984         UGAGUAGA A GUACCAAU         689         CATATTG GGCTAGCTACAAGA AGTATTCA         2391           2988         UACUGCAA A LAUGGAAA         699         CATATTG GGCTAGCAACGA AGTATTCA         2392           2990         CUGCAAGU A UGGAAAUC         691         GATTTCCA GGCTAGCAACGA TTTCCATT         2393           3005         UCUCUCCA A CUACCUCA         692         TGAGGTAG GGCTACCAACGA TTCCATT         2394           3006         CUCCAACU A CUCCAAGA         694         TCTTGAGG GGCTAGCTACAACGA TTCTGAGG         2396           3017         CCUCAAGA G CAAACGUG         695         CACGTTTG GGCTAGCTACAACGA TCTTGAGG         2397           3021         AAGACAA G UGACUUAU         696         AAGTCACG GGCTAGCTACAACGA TTCTCTT         2398           3026         CAAACGUG A CUUAUUU         699         AGAAAAAA GGCTAACAACGA CACGTTTC         2400           3030         CGUGACUU A UUUUUUCU         699         AGAAAAAA GGCTACAACGA AGTCCACGA         2401           3041         CUACACGAU         700         CATCCTTG GGCTAGCTACAACGA ACCTTGTT         2403		- <del></del>			
2981         UGUUGAAU         CUGCAAU         688         ATTIGCAG         GGCTAGCTACAAGA         ATTICACA         2390           2984         UGAAUACU         G CAAAUAUG         699         CATATTTG         GGCTAGCTACAACGA         ATTATCA         2391           2988         UACUGCAA         A UAUGGAAA         690         CATATTCA         GGCTAGCTACAACGA         ATTACCA         2392           2990         CUGCAAAU         A UACUCCA         692         TGGAGAGA         GGCTAGCTACAACGA         ATTACCA         3394           3005         UCUCUCCA         A CUACACUA         692         TGGAGAGA         GGCTAGCTACAACGA         AGTTGCAGA         2395           3008         CUCCAACU         A CUACACUA         694         TCTGAGG         GGCTAGCTACAACGA         AGTTGAGG         2397           3021         AAGAGCAA         A CUGAUUAU         696         AAGTCAC         GGCTAGCTACAACGA         ATTTGCTT         2398           3021         AAGACGAA         A CUUAUUUU         697         ATAAATAG         GGCTAGCTACAACGA         ATTTCTTT         2399           3026         CAAACGUG         A CUUAUUUU         698         AAAATAG         GGCTAGCTACAACGA         ATTGCTTT         2401           3030         CGGA					
2984         UGANUACU G CAAAUAUG         689         CATATTTG GGCTAGCTACAACGA AGTATTCA 2391           2988         UACUGCAA A UAUGGAAA         690         TTCCATA GGCTAGCTACAACGA ATTGCAGTA 2392           2990         CUGCAAAU A UGGAAAUC         691         GATTTCCA GGCTAGCTACAACGA ATTGCAGTA 2393           2996         AUXUGGAA A UCUCUCCA         692         TGGAGGA GGCTAGCTACAACGA ATTGCAGTA 2394           3005         UCUCUCCA A CUACAGA         694         TCTGAGG GGCTAGCTACAACGA AGTTGGAG 2397           3017         CCUCAAGA G CAAACGUG         695         CACGTTTG GGCTAGCTACAACGA ATTGCTCTT         2398           3021         AAGGCAAA C GUGACUUAU         697         ATAAGTCA GGCTAGCTACAACGA TTGCTCTT         2398           3023         GAGCAAC G UGACUUAU         697         ATAAGTCA GGCTAGCTACAACGA CACGTTTG         2400           3030         CGUGACUU A UUUUUUUU         698         AAAATAAG GGCTAGCTACAACGA AGTCACGA 2401           3041         UUUUCUCA A CAAGGAUG         700         CATCCTTG GGCTAGCTACAACGA ATGCACGA 2402           3047         CAACAAGG A UGCACCAC         701         GTGTGACGACGACACACAACAA CACACAUACACA 702         TAGTGCTG GGCTAGCTACAACGA ATCCTTGT 2404           3054         ACGAUGCAC C CUACACAC         703         GTGTAGTCACAACGA TGCACACAACAACAACAACAACAACAACAACAACAACAACA					
2988         UACUGCAA A UAUGGAAA         690         TTTCCATA GGCTAGCTACAACGA TTGCAGTA         2392           2990         CUGCAAAU A UGGAAAUC         691         GATTTCCA GGCTAGCTACAACGA ATTTGCAG         2393           2996         AUAUGGAA A UCUCUCCA         692         TGGAGAGA GGCTAGCTACAACGA TTGCAGTA         2395           3005         UCUCUCCA C CUCAAGA         694         TGTGAGG GGCTAGCTACAACGA TGTGAGG         2395           3017         CCUCAAGA G CAAACGUG         695         CACGTTTG GGCTAGCTACAACGA TCTTGAGG         2397           3021         AAGAGCAA A CGUGACUU         696         AAGTCAC GGCTAGCTACAACGA TTGCTCT         2398           3022         CAAACGUG A CUUAUUU         697         ATAAGTCA GGCTAGCTACAACGA CACGTTTG         2399           3030         CGUGACUU A UUUUUUUU         699         AGAAAAAA GGCTAGCTACAACGA CACGTTTG         2400           3041         UUUUCUCA A CAAGGAUG         700         CATCCTTG GGCTAGCTACAACGA TGAGAAAA         2402           3047         CAACAGGA U UACACCC         701         GTGCTAGCTACAACGA ATCCTTGT         2403           3047         CACAGAGC A CUACACC         703         GTGTAGTACAACGA ATCCTTGT         2405           3052         AGGAUGCA G CACUACAC         703         GTGTAGTGCTACAACGA ATCCTTGT         2405				<del></del>	
2990         CUGCAAAU A UGGAAAUC         691         GATTTCCA GGCTAGCTACAACGA ATTTGCAG         2393           2996         AUAUGGAA A UCUCUCCA         692         TGGAGGAG GGCTAGCTACAACGA TTCCATAT         2394           3005         UCUCUCCA A CUACCUCA         693         TGAGGTAG GGCTAGCTACAACGA TCCAGAGA         2395           3008         CUCCAACGA G CAAACGUG         694         TCTTGAGG GGCTAGCTACAACGA TCTTGAGG         2396           3017         CCUCAAGA G CAAACGUG         695         CACGTTTG GGCTAGCTACAACGA TCTTGAGG         2397           3021         AAGAGCAA A CGUGACUU         696         AAGTCACG GGCTAGCTACAACGA TTGCTCT         2398           3023         GAGCAAAC G UGACUUAU         697         ATAAGTCA GGCTAGCTACAACGA CACGTTTG         2409           3030         CGUGACUU A UUUUUUUU         698         AGAAAAAA GGCTAGCTACAACGA CACGTTTG         2401           3041         UUUUCUCA A CAAGGAUG         700         CATCCTTG GGCTAGCTACAACGA TGAGAAAA         2402           3047         ACAAGGAU G GCACUA         701         GTGTGCTACAACGA TGACAACGA TCCTTTGT         2403           3049         ACAAGGAU G CACUACAC         703         GTGTAGTACAACGA TCCAACGA TCCATCTT         2405           3052         AGAGACACA TACACAU         704         ATGTTGAG GGCTAGCTACAACGA TCCATCTT         2406<				<del></del>	
2996         AUAUGGAA         A UCUCUCCA         692         TGGAGAGA         GGCTAGCTACAACGA         TTCCATAT         2394           3005         UCUCUCCA         A CUCACAGA         693         TGAGGTAG         GGCTAGCTACAACGA         TGGAGAGA         2395           3008         CUCCAACU         A CUCACAGA         694         TCTTGAGG         GGCTAGCTACAACGA         AGTTGGAG         2396           3017         CCUCAAGA         A CUCACUU         695         ACCGTTTG         GGCTAGCTACAACGA         ATCTTTGAGG         2397           3021         AAGAGCAA         A GUGACUU         696         AAATCACG         GGCTAGCTACAACGA         ATGTTGCTC         2399           3026         CAAACGUG         A UUUUUUU         698         AAAATAAG         GGCTAGCTAACAGA         ACCGTTTG         2400           3041         UUUUCUCA         A CAAGGAUC         700         CATCCTTG         GGCTAGCTACAACGA         AAATCACG         2401           3049         ACAACAGA         J UGCAGCAC         701         GTGCTGCTACAACGA         ATCCTTGT         2404           3052         AGGAUGCA         G CACCACAU         704         ATGTGTG         GGCTAGCTACAACGA         ATCCTTGT         2405           3057         GCAGCACU					
3005         UCUCUCCA A CUACCUCA         693         TGAGGTAG GGCTAGCTACAACGA TGGAGAGA         2395           3008         CUCCAACU A CCUCAAGA         694         TCTTGAGG GGCTAGCTACAACGA AGTTGGAG         2396           3017         CCUCAAGA G CAAACGUG         695         CACGTTTG GGCTAGCTACAACGA TCTCTGAGG         2397           3021         AAGAGCAA A CGUGACUU         696         AAGTCACG GGCTAGCTACAACGA TTGCTCT         2398           3023         GAGCAAAC G UGACUUAU         697         ATAAGTCA GGCTAGCTACAACGA CTTGCTTC         2399           3026         CAAACGUG A CUUAUUUU         698         AAAATAAG GGCTAGCTACAACGA CACGTTTG         2400           3030         CGUGACUU A UUUUUUCU         699         AGAAAAAA GGCTAGCTACAACGA TGAGAAAA         2401           3047         CAACAAGG A UGCAGCAC         701         GTGCTGC AGCTACCAACGA AGGA CCTTGTT 2403           3049         ACAAGGAU G CACUACAC         702         TAGTGCTG GGCTACCAACGA TGCATCCT         2405           3052         AGGAUGCA G CACUACAC         703         GTGTAGT         GGCTAGCTACAACGA ATCCTTCT         2406           3054         GAUGCAGC A CUACACAU         704         ATGTGTG GGCTACCAACGA ATGTGCTCC         2406           3057         GCAGCACU A CACUAGAA         705         TCCATGTG GGCTACCAACGA ATGTGCTCC         2406					
3008         CUCCAACU A CCUCAAGA         694         TCTTGAGG GGCTAGCTACAACGA AGTTGAGG         2396           3017         CCUCAAGA G CAAACGUG         695         CACGTTTG GGCTAGCTACAACGA TCTTGAGG         2397           3021         AAGAGCAA A CGUGACUU         696         AAGTCACG GGCTAGCTACAACGA TCTGCTCT         2398           3023         GAGCAAAC G UGACUUAU         697         ATAAGTCA GGCTAGCTACAACGA GTTTGCTC         2399           3026         CAAACGUG A CUUAUUUU         698         AAAATAAG GGCTAGCTACAACGA AGTTGCTTG         2400           3030         CGUGACUU A UUUUUUCU         699         AGAAAAAA GGCTAGCTACAACGA AGTGACACG         2401           3041         UUUUCUCA A CAAGGAUG         700         CATCCTTG GGCTAGCTACAACGA AGTGACACG         2402           3047         CAACAAGG A UGCAGCAC         701         GTGCTGCA GGCTAGCTACAACGA ATCCTTGT         2403           3049         ACAAGGAU G CACUACAC         702         TAGTGCTG GGCTAGCTACAACGA ATCCTTCT         2405           3052         AGGAUGCA G ACCUACAC         703         GTGTAGTACAACGA AGTGCTACAACGA CTCCATC         2405           3057         GCAGCACU A CACAUGAA         705         TCCATTG GGCTAGCTACAACGA TGTACTC         2406           3061         CACUACACA C AUGGAGCCU         707         AGGCTCAACGACACAACGA TCCATTTTCTC					
3017         CCUCAAGA G CAAACGUG         695         CACGTTTG GGCTAGCTACAACGA TCTTGAGG         2397           3021         AAGAGCAA A CGUGACUU         696         AAGTCACG GGCTAGCTACAACGA TTGCTCT         2398           3023         GAGCAAAC G UGACUUAU         697         ATAAGTCA GGCTAGCTACAACGA GTTTGCTC         2399           3026         CARACGUG A CUUAUUUU         698         AAAATAAG GGCTAGCTACAACGA CACGTTTG         2400           3030         CGUGACUU A UUUUUUCUC 699         AGAAAAAA GGCTAGCTACAACGA TGAGAAAA         2402           3041         UUUUCUCA A CAAGGAUG         700         CATCCTTG GGCTACAACGA TGAGAAAA         2402           3047         CAACAAGG A UGCAGCAC         701         GTGCTGCA GGCTACAACGA TCCTTGTT         2403           3049         ACAAGGAU G CACUACAC         703         GTGTAGTG GGCTAGCTACAACGA ACCTTCTGT         2404           3052         AGGAUCA G CACUACAC         703         GTGTAGTG GGCTAGCTACAACGA ACCTCTTCT         2405           3054         GAUGCACU A CACAUGGA         705         TCCATGTG GGCTAGCTACAACGA ACTGCTCC         2406           3057         GCAGCACU A CACAUGGA         705         TCCATGTG GGCTAGCTACAACGA GTGTAGTG         2407           3059         AGCACUGCA A UGGAGCCU         707         AGGCTCCA GGCTAGCTACAACGA TCCATGTG         2410					
3021         AAGAGCAA A CGUGACUU         696         AAGTCACG GGCTAGCTACAACGA TTGCTCT         2398           3023         GAGCAAAC G UGACUUAU         697         ATAAGTCA GGCTAGCTACAACGA GTTTGCTC         2399           3026         CAAACGUG A CUUAUUUU         698         AAAATAAG GGCTAGCTACAACGA CACGTTTG         2400           3030         CGUGACUU A UUUUUUCU         699         AGAAAAAA GGCTAGCTACAACGA AAGTCACC         2401           3041         UUUUCUCA A CAAGGAUG         700         CATCCTTG GGCTAGCTACAACGA TGAAACGA TGAACGA CTTGTTG         2403           3047         CAACAAGA UGCAGCAC         701         GTGTGTG GGCTAGCTACAACGA ACCTTGTTG         2404           3052         AGGAUGCA G CACUACAC         703         GTGTAGTG GGCTAGCTACAACGA TGCATCCT         2405           3054         GAUGCAGC A CUACACAU         704         ATGTGTAG GGCTAGCTACAACGA GCTGCATC         2406           3057         GCAGCACU A CACAUGGA         705         TCCATGTG GGCTAGCTACAACGA GTGATGTC         2406           3059         AGCACUACA C A CUAGAGA         705         TCCATGTG GGCTAGCTACAACGA GTGATGTC         2407           3061         CACAUGGA G CUAAGAA         708         TTCTTAGG GGCTAGCTACAACGA TTTTCTT         2410           3082         AAGAAAAA A UGGAGCCA         709         TGGCTCCA GGCTAGCTACAACGA TCCATTTT					
3023         GAGCANAC G UGACUUAU         697         ATAAGTCA GGCTAGCTACAACGA GTTTGCTC         2399           3026         CAAACGUG A CUUAUUUU         698         AAAATAAG GGCTAGCTACAACGA CACGTTTG         2400           3030         CGUGACUU A UUUUUUCU         699         AGAAAAAA GGCTAGCTACAACGA AAGTCACG         2401           3041         UUUUUCUCA A CAAGGAUG         700         CATCCTTG GGCTAGCTACAACGA TGAGAAAA         2402           3047         CAACAAGG A UGCAGCAC         701         GTGCTGC AGGCTACAACGA TCCTTGTTG         2403           3049         ACAAGGAU G CACUACAC         703         GTGTAGTG GGCTAGCTACAACGA TCCTTGTTG         2405           3052         AGGAUGCA G CACUACAC         703         GTGTAGTG GGCTAGCTACAACGA TCCTCTC         2405           3054         GAUGCAGC A CUCACACU         704         ATGTTGTG GGCTAGCTACAACGA GTGCTCCT         2406           3057         GCAGCACU A CACAUGGA         705         TCCATGTG GGCTAGCTACAACGA GTGTAGTC         2407           3061         CACUACAC A UGGAGCCU         707         AGGCTCCA GGCTAGCTACAACGA GTGTAGTG         2409           3066         CACAUGGA G CCUGGAC         709         TGGCTCCA GGCTAGCTACAACGA TCCATGTG         2410           3087         AAAAUGGA G CCAGGCCU         710         AGGCCTGG GGCTAGCTACAACGA TCCATTCTT         24					
3026         CAAACGUG A CUUAUUUU         698         AAAATAAG GGCTAGCTACAACGA CACGTTTG         2400           3030         CGUGACUU A UUUUUUCU         699         AGAAAAAA GGCTAGCTACAACGA AAGTCACG         2401           3041         UUUUCUCA A CAAGGAUG         700         CATCCTTG GGCTAGCTACAACGA TGAGAAAA         2402           3047         CAACAAGGA U GCAGCACU         701         GTGCTGCG GGCTAGCTACAACGA CCTTGTTG         2403           3049         ACAAGGAU G CACUACAC         703         GTGTAGTG GGCTAGCTACAACGA TGCATCCT         2404           3052         AGGAUGCA G CACUACAC         703         GTGTAGTG GGCTACACACAGA TGCATCCT         2405           3054         GAUGCAGC A CUACACAU         704         ATGTGTG GGCTACCACACA GCTGCTACCAACGA TGCTACCACACA         2406           3057         GCAGCACU A CACAUGGA         705         TCCATGTG GGCTACCAACGA AGTGGTCC         2407           3059         AGCACUAC A CAUGGAGC         706         GCTCCATG GGCTACCAACGA GTGTAGTG         2409           3066         CACAUGGA G CCUAGGAA         708         TTCTTAGG GGCTACCAACGA TCCATGTG         2410           3082         AAGAAAAA A UGGAGCCA         709         TGGCTCCA GGCTACCAACGA TTTTTCTT         2411           3099         GGACCUGGA A CAAGGCAA         711         GTTCCAGG GGCTACCAACGA TCCATTTT					
3030         CGUGACUU A UUUUUUCU         699         AGAAAAAA GGCTAGCTACAACGA AAGTCACG         2401           3041         UUUUCUCA A CAAGGAUG         700         CATCCTTG GGCTAGCTACAACGA TGAGAAAA         2402           3047         CAACAAGG A UGCAGCAC         701         GTGCTGCA GGCTAGCTACAACGA CCTTGTTG         2403           3049         ACAAGGAU G CAGCACUA         702         TAGTGCTG GGCTAGCTACAACGA ATCCTTGT         2404           3052         AGGAUGCA G CACUACAC         703         GTGTAGTG GGCTAGCTACAACGA TGCATCCT         2405           3054         GAUGCAGC A CUACACAU         704         ATGTGTAG GGCTAGCTACAACGA GCTGCACC         2406           3057         GCAGCACU A CACAUGGA         705         TCCATGTG GGCTAGCTACAACGA GTGTGCT         2406           3059         AGCACUAC A CAUGGAGC         706         GCTCCATG GGCTAGCTACAACGA GTGTAGTG         2409           3066         CACAUGGA G CCUAGGAA         707         AGGCTCCA GGCTAGCTACAACGA TTCCATGTG         2410           3082         AAGAAAAA A UGGAGCCA         709         TGGCTCCA GGCTACCAACGA TCCATTTT         2412           3092         GGAGCCAG G CCUGGAAC         711         GTTCCATG GGCTACCAACGA TTCCATGTC         2413           3104         GGAACAAG G CAAGGAAA         712         TTGCCTTG GGCTACCAACGA TTCCTTGCC         2414 <td></td> <td></td> <td></td> <td></td> <td></td>					
3041         UUUUCUCA A CAAGGAUG         700         CATCCTTG GGCTAGCTACAACGA TGAGAAAA         2402           3047         CAACAAGG A UGCAGCAC         701         GTGCTGCA GGCTAGCTACAACGA CCTTGTTG         2403           3049         ACAAGGAU G CAGCACAC         702         TAGTGCTG GGCTAGCACACGA ACCACACACACACACACACACACACACACA					
3047         CAACAAGG A UGCAGCAC         701         GTGCTGCA GGCTAGCTACAACGA CCTTGTTG         2403           3049         ACAAGGAU G CAGCACUA         702         TAGTGCTG GGCTAGCTACAACGA ATCCTTGT         2404           3052         AGGAUGCA G CACUACAC         703         GTGTAGTG GGCTAGCTACAACGA TGCATCCT         2405           3054         GAUGCAGC A CUACACAU         704         ATGTGTAG GGCTAGCTACAACGA GCTGCATC         2406           3057         GCAGCACU A CACAUGGA         705         TCCATGTG GGCTAGCTACAACGA AGTGTGCTC         2407           3059         AGCACUAC A CAUGGAGC         706         GCTCCATG GGCTAGCTACAACGA GTGTAGTG         2408           3061         CACUACAC A UGGAGCCU         707         AGGCTCCA GGCTAGCTACAACGA GTGTAGTG         2410           3082         AAGAAAAA A UGGAGCCA         709         TGGCTCCA GGCTAGCTACAACGA TCCATGTG         2411           3087         AAAAUGGA G CCAGGCCU         710         AGGCCTGG GGCTAGCTACAACGA TCCATGTT         2412           3099         GGCCUGGA A CAAGGCAA         711         GTTCCATG GGCTAGCTACAACGA TCCAGGCC         2414           3104         GGAACAAG G CAAGAAAC         712         TTGCCTTG GGCTAGCTACAACGA TCTTGTCC         2415           3111         GGCAAGAA A CCAAGACU         714         AGTTTGG GGCTAGCTACAACGA TTCTTCCC				······································	
3049 ACAAGGAU G CAGCACUA 702 TAGTGCTG GGCTAGCTACAACGA ATCCTTGT 2404 3052 AGGAUGCA G CACUACAC 703 GTGTAGTG GGCTAGCTACAACGA TGCATCCT 2405 3054 GAUGCAGC A CUACACAU 704 ATGTGTAG GGCTAGCTACAACGA GGTGCATC 2406 3057 GCAGCACU A CACAUGGA 705 TCCATGTG GGCTAGCTACAACGA AGTGCTGC 2407 3059 AGCACUAC A CAUGGAGC 706 GCTCCATG GGCTAGCTACAACGA AGTGCTGC 2408 3061 CACUACAC A UGGAGCCU 707 AGGCTCCA GGCTAGCTACAACGA GTGTAGTG 2409 3066 CACAUGGA G CCUAAGAA 708 TTCTTAGG GGCTAGCTACAACGA TCCATGTG 2410 3082 AAGAAAAA A UGGAGCCA 709 TGGCTCCA GGCTAGCTACAACGA TCCATGTG 2410 3087 AAAAUGGA G CCUGGAAC 710 AGGCCTGG GGCTAGCTACAACGA TCCATTTT 2411 3087 AAAAUGGA G CCUGGAAC 711 GTTCCAGG GGCTAGCTACAACGA TCCATTTT 2412 3092 GGAGCCAG G CCUGGAAC 711 GTTCCAGG GGCTAGCTACAACGA TCCATTTT 2412 3099 GGCCUGGA A CAAGGCAA 712 TTGCCTTG GGCTAGCTACAACGA TCCAGCCC 2414 3104 GGAACAAG G CAAGAAAC 713 GTTTCTTG GGCTAGCTACAACGA TCCAGGCC 2414 3104 GGAACAAG G CAAGAAAC 713 GTTTCTTG GGCTAGCTACAACGA TCCTGGCC 2415 3111 GGCAAGAA A CCAAGACU 714 AGTCTTGG GGCTAGCTACAACGA TTCTTGCC 2416 3117 AAACCAAG A CUAGAUAG 715 CTATCTAG GGCTAGCTACAACGA TTCTTGCC 2416 3117 AAACCAAG A CUAGAUAG 715 CTATCTAG GGCTAGCTACAACGA CTAGTCTT 2418 3122 AAGACUAG A UAGCGUCA 716 TGACGCTA GGCTAGCTACAACGA CTAGTCTT 2418 3123 ACUAGAUA G CGUCACCA 717 TGGTGACG GGCTAGCTACAACGA CTAGTCTT 2419 3124 UAGAUAGC G UCACCAGC 718 GCTGGTGA GGCTAGCTACAACGA CTAGTCTT 2420 3130 AUAGCGUC A CCAGCAGC 719 GCTGCTGG GGCTAGCTACAACGA GCTATCTAA 2420 3131 AUAGCGUC A CCAGCAGC 719 GCTGCTGG GGCTAGCTACAACGA TGCTGTGT 2421 3134 CGUCACCA G CAGCGAAA 720 TTTCGCTG GGCTAGCTACAACGA TGCTGTGT 2422 3137 CACCAGCA G CGAAAGCU 721 AGCTTTCG GGCTAGCTACAACGA TGCTGGTG 2422 3137 CACCAGCA G CGAAAGCU 721 AGCTTTCG GGCTAGCTACAACGA TGCTGGTG 2422 3137 CACCAGCA G CGAAAGCU 721 AGCTTTCG GGCTAGCTACAACGA TGCTGGTG 2422 3137 CACCAGCA G CGAAGCU 721 AGCTTTCG GGCTAGCTACAACGA TGCTGGTG 2422 3134 CAGCCAAA G CUUUGCGA 722 TCCCAAAG GGCTAGCTACAACGA TTTCGCTG 2424 3148 AAAGCUUU G CGAGCUCC 723 GGGGCTGG GGCTAGCTACAACGA TTTCCGTG 2424					
AGGAUGCA G CACUACAC 703 GTGTAGTG GGCTAGCTACAACGA TGCATCCT 2405 3054 GAUGCAGC A CUACACAU 704 ATGTGTAG GGCTAGCTACAACGA GCTGCATC 2406 3057 GCAGCACU A CACAUGGA 705 TCCATGTG GGCTAGCTACAACGA AGTGCTGC 2407 3059 AGCACUAC A CAUGGAGC 706 GCTCCATG GGCTAGCTACAACGA GTAGTGCT 2408 3061 CACUACAC A UGGAGCCU 707 AGGCTCCA GGCTAGCTACAACGA GTGTAGTG 2409 3066 CACAUGGA G CCUAAGAA 708 TTCTTAGG GGCTAGCTACAACGA TCCATGTG 2410 3082 AAGAAAAA A UGGAGCCA 709 TGGCTCCA GGCTAGCTACAACGA TCCATGTG 2410 3087 AAAAUGGA G CCAGGCCU 710 AGGCCTGG GGCTAGCTACAACGA TCCATTTT 2411 3099 GGAGCCAG G CCUGGAAC 711 GTTCCAGG GGCTAGCTACAACGA TCCATTTT 2412 3099 GGCCUGGA A CAAGGCAA 712 TTGCCTTG GGCTAGCTACAACGA TCCAGGCC 2414 3104 GGAACAAG G CAAGAAAC 713 GTTTCTTG GGCTAGCTACAACGA TCCAGGCC 2415 3111 GGCAAGAA A CCAAGACCU 714 AGTCTTG GGCTAGCTACAACGA TTCTTGCC 2416 3117 AAACCAAG A CUAGAUAG 715 CTATCTAG GGCTAGCTACAACGA TTCTTGCC 2416 3117 AAACCAAG A CUAGAUAG 715 CTATCTAG GGCTAGCTACAACGA CTAGTCTT 2417 3122 AAGACUAG A UAGCGUCA 716 TGACGCTA GGCTAGCTACAACGA CTAGTCTT 2418 3125 ACUAGAUA G CGUCACCA 717 TGGTGACG GGCTAGCTACAACGA CTAGTCTT 2418 3126 ACUAGAUA G CGUCACCA 717 TGGTGACG GGCTAGCTACAACGA TTCTAGT 2419 3127 UAGAUAGC G UCACCAGC 718 GCTGGTG GGCTAGCTACAACGA GCTATCTA 2420 3130 AUAGCGUC A CCAGCAGC 719 GCTGCTG GGCTAGCTACAACGA GCTATCTA 2420 3131 CACCAGCA G CAGAGACU 721 AGCTTCTG GGCTAGCTACAACGA TGGTGACG 3131 CACCAGCA G CAGAGACU 721 AGCTTCTG GGCTAGCTACAACGA TGGTGACG 3131 CACCAGCA G CAGAGACU 721 AGCTTCTG GGCTAGCTACAACGA TGGTGACG 3134 CAGCGAAA G CUUUGCGA 722 TCGCAAAG GGCTAGCTACAACGA TGCTGGTG 2423 3143 CAGCGAAA G CUUUGCGA 722 TCGCAAAG GGCTAGCTACAACGA TTCTCGTG 2424 3148 AAAGCUUU G CGAGCUCC 723 GGAGCTCG GGCTAGCTACAACGA AAAGCTTT 2425					
3054 GAUGCAGC A CUACACAU 704 ATGTGTAG GGCTAGCTACAACGA GCTGCATC 2406 3057 GCAGCACU A CACAUGGA 705 TCCATGTG GGCTAGCTACAACGA AGTGCTGC 2407 3059 AGCACUAC A CAUGGAGC 706 GCTCCATG GGCTAGCTACAACGA GTGTGGCT 2408 3061 CACUACAC A UGGAGCCU 707 AGGCTCCA GGCTAGCTACAACGA GTGTAGTG 2409 3066 CACAUGGA G CCUAAGAA 708 TTCTTAGG GGCTAGCTACAACGA TCCATGTG 2410 3082 AAGAAAAA A UGGAGCCA 709 TGGCTCCA GGCTAGCTACAACGA TCCATGTG 2411 3087 AAAAUGGA G CCAGGCCU 710 AGGCCTGG GGCTAGCTACAACGA TCCATTTT 2411 3092 GGAGCCAG G CCUGGAAC 711 GTTCCAGG GGCTAGCTACAACGA TCCATTTT 2412 3099 GGCCUGGA A CAAGGCAA 712 TTGCCTTG GGCTAGCTACAACGA TCCAGTCC 2413 3104 GGAACAAG G CAAGAAAC 713 GTTTCTTG GGCTAGCTACAACGA TCCAGGCC 2414 3104 GGAACAAG G CAAGAAAC 713 GTTTCTTG GGCTAGCTACAACGA TTCTTGCC 2415 3111 GGCAAGAA A CCAAGACU 714 AGTCTTG GGCTAGCTACAACGA TTCTTGCC 2416 3117 AAACCAAG A CUAGAUAG 715 CTATCTAG GGCTAGCTACAACGA TTCTTGCC 2416 3122 AAGACUAG A UAGCGUCA 716 TGACGCTA GGCTAGCTACAACGA CTTGGTTT 2418 3125 ACUAGAUA G CGUCACCA 717 TGGTGAC GGCTAGCTACAACGA TATCTAGT 2419 3127 UAGAUAGC G UCACCAGC 718 GCTGGTGA GGCTAGCTACAACGA TATCTAGT 2419 3127 UAGAUAGC G UCACCAGC 719 GCTGGTGA GGCTAGCTACAACGA GCTATCTA 2420 3130 AUAGCGUC A CCAGCAGC 719 GCTGCTGG GGCTAGCTACAACGA GCTATCTA 2421 3134 CGUCACCA G CAGCGAAA 720 TTTCGCTG GGCTAGCTACAACGA TGGTGCC 2422 3137 CACCAGCA G CGAAAGCU 721 AGCTTTCG GGCTAGCTACAACGA TGCTGGTG 2423 3143 CAGCGAAA G CUUUGCGA 722 TCGCAAAG GGCTAGCTACAACGA TTTCGCTG 2424 3148 AAAGCUUU G CGAGCUCC 723 GGAGCTCG GGCTAGCTACAACGA AAAGCTTT 2425	3052				
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3143 CAGCGAAA G CUUUGCGA 722 TCGCAAAG GGCTAGCTACAACGA TTTCGCTG 2424 3148 AAAGCUUU G CGAGCUCC 723 GGAGCTCG GGCTAGCTACAACGA AAAGCTTT 2425	3137	CACCAGCA G CGAAAGCU	721		
3148 AAAGCUUU G CGAGCUCC 723 GGAGCTCG GGCTAGCTACAACGA AAAGCTTT 2425	3143	CAGCGAAA G CUUUGCGA	722		
	3148	AAAGCUUU G CGAGCUCC	723		2425
	3152	CUUUGCGA G CUCCGGCU	724		

3158	GAGCUCCG G CUUUCAGG	725	CCTGAAAG GGCTAGCTACAACGA CGGAGCTC	2427
3170	UCAGGAAG A UAAAAGUC	726	GACTTTTA GGCTAGCTACAACGA CTTCCTGA	2428
3176	AGAUAAAA G UCUGAGUG	727	CACTCAGA GGCTAGCTACAACGA TTTTATCT	2429
3182	AAGUCUGA G UGAUGUUG	728	CAACATCA GGCTAGCTACAACGA TCAGACTT	2430
3185	UCUGAGUG A UGUUGAGG	729	CCTCAACA GGCTAGCTACAACGA CACTCAGA	2431
3187	UGAGUGAU G UUGAGGAA	730	TTCCTCAA GGCTAGCTACAACGA ATCACTCA	2432
3203	AGAGGAGG A UUCUGACG	731	CGTCAGAA GGCTAGCTACAACGA CCTCCTCT	2433
3209	GGAUUCUG A CGGUUUCU	732	AGAAACCG GGCTAGCTACAACGA CAGAATCC	2434
3212	UUCUGACG G UUUCUACA	733	TGTAGAAA GGCTAGCTACAACGA CGTCAGAA	2435
3218	CGGUUUCU A CAAGGAGC	734	GCTCCTTG GGCTAGCTACAACGA AGAAACCG	2436
3225	UACAAGGA G CCCAUCAC	735	GTGATGGG GGCTAGCTACAACGA TCCTTGTA	2437
3229	AGGAGCCC A UCACUAUG	736	CATAGTGA GGCTAGCTACAACGA GGGCTCCT	2438
3232	AGCCCAUC A CUAUGGAA	737	TTCCATAG GGCTAGCTACAACGA GATGGGCT	2439
3235	CCAUCACU A UGGAAGAU	738	ATCTTCCA GGCTAGCTACAACGA AGTGATGG	2440
3242	UAUGGAAG A UCUGAUUU	739	AAATCAGA GGCTAGCTACAACGA CTTCCATA	2441
3247	AAGAUCUG A UUUCUUAC	740	GTAAGAAA GGCTAGCTACAACGA CAGATCTT	2442
3254	GAUUUCUU A CAGUUUUC	741	GAAAACTG GGCTAGCTACAACGA AAGAAATC	2443
3257	UUCUUACA G UUUUCAAG	742	CTTGAAAA GGCTAGCTACAACGA TGTAAGAA	2444
3265	GUUUUCAA G UGGCCAGA	743	TCTGGCCA GGCTAGCTACAACGA TTGAAAAC	2445
3268	UUCAAGUG G CCAGAGGC	744	GCCTCTGG GGCTAGCTACAACGA CACTTGAA	2446
3275	GGCCAGAG G CAUGGAGU	745	ACTCCATG GGCTAGCTACAACGA CTCTGGCC	2447
3277	CCAGAGGC A UGGAGUUC	746	GAACTCCA GGCTAGCTACAACGA GCCTCTGG	2448
3282	GGCAUGGA G UUCCUGUC	747	GACAGGAA GGCTAGCTACAACGA TCCATGCC	2449
3288	GAGUUCCU G UCUUCCAG	748	CTGGAAGA GGCTAGCTACAACGA AGGAACTC	2450
3300	UCCAGAAA G UGCAUUCA	749	TGAATGCA GGCTAGCTACAACGA TTTCTGGA	2451
3302	CAGAAAGU G CAUUCAUC	750	GATGAATG GGCTAGCTACAACGA ACTTTCTG	2452
3304	GAAAGUGC A UUCAUCGG	751	CCGATGAA GGCTAGCTACAACGA GCACTTTC	2453
3308	GUGCAUUC A UCGGGACC	752	GGTCCCGA GGCTAGCTACAACGA GAATGCAC	2454
3314	UCAUCGGG A CCUGGCAG	753	CTGCCAGG GGCTAGCTACAACGA CCCGATGA	2455
3319	GGGACCUG G CAGCGAGA	754	TCTCGCTG GGCTAGCTACAACGA CAGGTCCC	2456
3322	ACCUGGCA G CGAGAAAC	755	GTTTCTCG GGCTAGCTACAACGA TGCCAGGT	2457
3329	AGCGAGAA A CAUUCUUU	756	AAAGAATG GGCTAGCTACAACGA TTCTCGCT	2458
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3355	ACAACGUG G UGAAGAUU	762	AATCTTCA GGCTAGCTACAACGA CACGTTGT	2464
3361	UGGUGAAG A UUUGUGAU	763	ATCACAAA GGCTAGCTACAACGA CTTCACCA	2465
3365	GAAGAUUU G UGAUUUUG	764	CAAAATCA GGCTAGCTACAACGA AAATCTTC	2466
3368	GAUUUGUG A UUUUUGGCC	765	GGCCAAAA GGCTAGCTACAACGA CACAAATC	
3374	UGAUUUUG G CCUUGCCC	766	GGGCAAGG GGCTAGCTACAACGA CAAAATCA	2468
3379	UUGGCCUU G CCCGGGAU	767	ATCCCGGG GGCTAGCTACAACGA AAGGCCAA	2469
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3398	UUAUAAGA A CCCCGAUU	771:	AATCGGGG GGCTAGCTACAACGA TCTTATAA	2473
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3407	CCCCGAUU A UGUGAGAA	773	TTCTCACA GGCTAGCTACAACGA AATCGGGG	2475
3409	CCGAUUAU G UGAGAAAA	774	TTTTCTCA GGCTAGCTACAACGA ATAATCGG	2476
3422	AAAAGGAG A UACUCGAC	775	GTCGAGTA GGCTAGCTACAACGA CTCCTTTT	2477
3424	AAGGAGAU A CUCGACUU	776	AAGTCGAG GGCTAGCTACAACGA ATCTCCTT	2478

3429	GAUACUCG A CUUCCUCU	777	AGAGGAAG GGCTAGCTACAACGA CGAGTATC	2479
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3448	AAUGGAUG G CUCCCGAA	780	TTCGGGAG GGCTAGCTACAACGA CATCCATT	2482
3456	GCUCCCGA A UCUAUCUU	781	AAGATAGA GGCTAGCTACAACGA TCGGGAGC	2483
3460	CCGAAUCU A UCUUUGAC	782	GTCAAAGA GGCTAGCTACAACGA AGATTCGG	2484
3467	UAUCUUUG A CAAAAUCU	783	AGATTTTG GGCTAGCTACAACGA CAAAGATA	2485
3472	UUGACAAA A UCUACAGC	784	GCTGTAGA GGCTAGCTACAACGA TTTGTCAA	2486
3476	CAAAAUCU A CAGCACCA	785	TGGTGCTG GGCTAGCTACAACGA AGATTTTG	
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3481	UCUACAGC A CCAAGAGC	787	GCTCTTGG GGCTAGCTACAACGA GCTGTAGA	
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		788	ACACGTCG GGCTAGCTACAACGA TCTTGGTG	2490
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3493	AGAGCGAC G UGUGGUCU	790	AGACCACA GGCTAGCTACAACGA GTCGCTCT	2492
3495	AGCGACGU G UGGUCUUA	791	TAAGACCA GGCTAGCTACAACGA ACGTCGCT	2493
3498	GACGUGUG G UCUUACGG	792	CCGTAAGA GGCTAGCTACAACGA CACACGTC	2494
3503	GUGGUCUU A CGGAGUAU	793	ATACTCCG GGCTAGCTACAACGA AAGACCAC	2495
3508	CUUACGGA G UAUUGCUG	794	CAGCAATA GGCTAGCTACAACGA TCCGTAAG	2496
3510	UACGGAGU A UUGCUGUG	795	CACAGCAA GGCTAGCTACAACGA ACTCCGTA	2497
3513	GGAGUAUU G CUGUGGGA	796	TCCCACAG GGCTAGCTACAACGA AATACTCC	2498
3516	GUAUUGCU G UGGGAAAU	797	ATTTCCCA GGCTAGCTACAACGA AGCAATAC	2499
3523	UGUGGGAA A UCUUCUCC	798	GGAGAAGA GGCTAGCTACAACGA TTCCCACA	2500
3536	CUCCUUAG G UGGGUCUC	799	GAGACCCA GGCTAGCTACAACGA CTAAGGAG	2501
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3546	GGGUCUCC A UACCCAGG	801	CCTGGGTA GGCTAGCTACAACGA GGAGACCC	2503
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3581	CUUUUGCA G UCGCCUGA	809	TCAGGCGA GGCTAGCTACAACGA TGCAAAAG	2511
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3598	GGGAAGGC A UGAGGAUG	812	CATCCTCA GGCTAGCTACAACGA GCCTTCCC	2514
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3648	CAGAUCAU G CUGGACUG	822	CAGTCCAG GGCTAGCTACAACGA ATGATCTG	2524
3653	CAUGCUGG A CUGCUGGC	823	GCCAGCAG GGCTAGCTACAACGA CCAGCATG	2525
3656	GCUGGACU G CUGGCACA	824	TGTGCCAG GGCTAGCTACAACGA AGTCCAGC	2526
3660	GACUGCUG G CACAGAGA	825	TCTCTGTG GGCTAGCTACAACGA CAGCAGTC	2527
3662	CUGCUGGC A CAGAGACC	826	GGTCTCTG GGCTAGCTACAACGA GCCAGCAG	2528
3668	GCACAGAG A CCCAAAAG	827	CTTTTGGG GGCTAGCTACAACGA CTCTGTGC	2529
3681	AAAGAAAG G CCAAGAUU	828	AATCTTGG GGCTAGCTACAACGA CTTTCTTT	2530

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3691	CAAGAUUU G CAGAACUU	830	AAGTTCTG GGCTAGCTACAACGA AAATCTTG	2532
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3700	CAGAACUU G UGGAAAAA	832	TTTTTCCA GGCTAGCTACAACGA AAGTTCTG	2534
3708	GUGGAAAA A CUAGGUGA	833	TCACCTAG GGCTAGCTACAACGA TTTTCCAC	2535
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3720	GGUGAUUU G CUUCAAGC	836	GCTTGAAG GGCTAGCTACAACGA AAATCACC	2538
3727	UGCUUCAA G CAAAUGUA	837	TACATTTG GGCTAGCTACAACGA TTGAAGCA	2539
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3738	AAUGUACA A CAGGAUGG	841	CCATCCTG GGCTAGCTACAACGA TGTACATT	2543
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4297	CUAGAAGC A CAUGUGUA	963	TACACATG GGCTAGCTACAACGA GCTTCTAG	2665
4299	AGAAGCAC A UGUGUAUU	964	AATACACA GGCTAGCTACAACGA GTGCTTCT	2666
4301	AAGCACAU G UGUAUUUA	965	TAAATACA GGCTAGCTACAACGA ATGTGCTT	2667
4303	GCACAUGU G UAUUUAUA	966	TATAAATA GGCTAGCTACAACGA ACATGTGC	2668
4305	ACAUGUGU A UUUAUACC	967	GGTATAAA GGCTAGCTACAACGA ACACATGT	2669
4309	GUGUAUUU A UACCCCCA	968	TGGGGGTA GGCTAGCTACAACGA AAATACAC	2670
4311	GUAUUUAU A CCCCCAGG	969	CCTGGGGG GGCTAGCTACAACGA ATAAATAC	2671
4322	CCCAGGAA A CUAGCUUU	970	AAAGCTAG GGCTAGCTACAACGA TTCCTGGG	
4326	GGAAACUA G CUUUUGCC	971	GGCAAAAG GGCTAGCTACAACGA TAGTTTCC	
4332	UAGCUUUU G CCAGUAUU	972	AATACTGG GGCTAGCTACAACGA AAAAGCTA	
4336	UUUUGCCA G UAUUAUGC	973	GCATAATA GGCTAGCTACAACGA TGGCAAAA	
4338	UUGCCAGU A UUAUGCAU	974	ATGCATAA GGCTAGCTACAACGA ACTGGCAA	
4341	CCAGUAUU A UGCAUAUA	975	TATATGCA GGCTAGCTACAACGA AATACTGG	
4343	AGUAUUAU G CAUAUAUA	976	TATATATG GGCTAGCTACAACGA ATAATACT	
4345	UAUUAUGC A UAUAUAAG	977	CTTATATA GGCTAGCTACAACGA GCATAATA	2679
4347	UUAUGCAU A UAUAAGUU	978	AACTTATA GGCTAGCTACAACGA ATGCATAA	
4349	AUGCAUAU A UAAGUUUA	979	TAAACTTA GGCTAGCTACAACGA ATATGCAT	
4353	AUAUAUAA G UUUACACC	980	GGTGTAAA GGCTAGCTACAACGA TTATATAT	
4357	AUAAGUUU A CACCUUUA	981	TAAAGGTG GGCTAGCTACAACGA AAACTTAT	
4359	AAGUUUAC A CCUUUAUC	982	GATAAAGG GGCTAGCTACAACGA GTAAACTT	
4365	ACACCUUU A UCUUUCCA	983	TGGAAAGA GGCTAGCTACAACGA AAAGGTGT	
	<del></del>			
4373	AUCUUUCC A UGGGAGCC	984	GGCTCCCA GGCTAGCTACAACGA GGAAAGAT	2686

4383 GGGRGCCA G CUGUUUUU 986 AAAAGCAG GGCTAGCTACAACGA TGGCTCCC 2688 4386 AGCCAGCU G CUUUUUGU 987 ACAAAAAG GGCTAGCTACAACGA AGCTGGCT 2689 4399 UGUUUUU GUUUUU 988 AAAAAATACA GGCTAGCTACAACGA AGCTGGCT 2689 4399 UUUUUUUU A UAGUUUUU 989 AAAAAAACA GGCTAGCTACAACGA CACAAAAA 2691 4405 UUUUUAADAG UUUUUUUU 991 AAAAAAACA GGCTAGCTACAACGA CACAAAAA 2691 4406 UUUUAADAG G CUUUUUUU 991 AAAAAAACA GGCTAGCTACAACGA CACAAAAA 2691 4410 UUUAAUAGU G CUUUUUU 991 AAAAAAAA GGCTAGCTACAACGA CACAAAAA 2693 4410 UUUUUUU A CAACAAG 993 CTTGTTAG GGCTAGCTACAACGA CACAAAAAA 2694 4424 UUUUUUU A CAACAAG 993 CTTGTTAG GGCTAGCTACAACGA CACAAAAAA 2694 4428 UUUUAACAAGA A UGUACACA 993 CTTGTTAG GGCTAGCTACAACGA CACAAAAAA 2695 4439 AGAAUGUA A CUACACAG 995 GAGTTACA GGCTAGCTACAACGA TATCTCTA 2698 4439 AGAAUGUA A CUCCAGAU 997 TACTGGAG GGCTAGCTACAACGA TATCTCTA 2698 4439 AGAAUGUA A CUCCAGAU 997 TACTGGAG GGCTAGCTACAACGA TATCTCTA 2698 4446 AACUCCAG A UAGAGAAA 999 TTCTCTCA GGCTAGCTACAACGA CTGGATT 2700 4446 AACUCCAG A UAGAGAAA 999 TTCTCTCA GGCTAGCTACAACGA CTGGATT 2701 4457 GAGAAAUA G UGACAAGU 1000 ACTTGTCA GGCTAGCTACAACGA CTGGATT 2701 4460 AAAUAGGAA A UAGUGACA 999 TTCTCTCA GGCTAGCTACAACGA CTGGATT 2701 4461 AAGUACAA UAGUGAA 999 TTCTCTCA GGCTAGCTACAACGA TATCTCTCT 2701 4460 AAAUAGGAA AUAGUGAA 1001 TTCACTTG GGCTAGCTACAACGA TATCTCTCT 2701 4461 AGUACACA G UGACAAGU 1000 ACTTGTCA GGCTAGCTACAACGA TATCTCTCT 2701 4460 AAAUAGGA A UAGUGAA 1001 TTCACTTG GGCTAGCTACAACGA TATCTCTCT 2704 4471 AGUACACA G UGAAGAAC 1002 GTTCTTCA GGCTAGCTACAACGA TATTCTCC 2704 4472 UAGAGAA AUAGUGA 1001 TTCACTTG GGCTAGCTACAACGA TATTCTCC 2704 4473 UAGAGAA AUAGUGA 1001 TTCACTTG GGCTAGCTACAACGA TATTCTCC 2704 4474 AGGAACU A CUCCUGUG 1003 CAGTAGGA GGCTAGCTACAACGA TATTCTCCT 2705 4479 ACACUACU G CUAAAUCC 1004 GGCAGAGGA GGCTAGCTACAACGA TATTCTCCT 2704 4479 ACACUACU G CUAAAUCC 1004 GGCAGAGGA GGCTAGCTACAACGA TATTCTCCT 2705 4479 ACACUACU G CUAAAUCC 1004 GGCAGGAGA GGCTAGCTACAACGA TATGCGAT 2704 4479 ACACUACU G CUAAAUCC 1004 GGCAGGAGA GGCTAGCTACAACGA TATGCGAT 2704 4479 ACACUACU G UUAAGAA 1001 TTCACTTG GGCTAGCTACAACGA TATGCGAT 27	4070	COLUMN C COLORS	005	CONCORDO COCHA COMA CA A COA MOCCAMOO	2697
4396 AGCCAGCU G CUUUUUUU 987 ACAAAAAG GGCTAGCTACAACQA AGCTGGCT 2689 4399 UUGUUUUU G UGAUUUUU 988 AAAAATCA GGCTAGCTACAACQA AAAAAGCA 2690 4405 UUUUUUUUA A UAGUGCUU 990 AAGCACTA GGCTAGCTACAACQA CACAAAAA 2691 4405 UUUUUUUA A UAGUGCUU 991 AAAAAGCA GGCTAGCTACAACQA CACAAAAA 2691 4406 UUUUAAAAA G UGCUUUUU 991 AAAAAGCA GGCTAGCTACAACQA TATAAAAA 2693 4410 UUAAAAAGU G CUUUUUU 992 AAAAAAGA GGCTAGCTACAACQA CACAAAAA 2694 4410 UUAAAAAGU G CUUUUUU 992 AAAAAAAG GGCTAGCTACAACQA CACAAAAA 2694 4421 UUUUAUUA A CAAGAAUG 993 CTTGTTAG GGCTAGCTACAACQA CACAAAAA 2694 4422 UUUUGACUA A CAAGAAUG 993 CTTGTTAG GGCTAGCTACAACQA CAAAAAAA 2695 4428 UUUGACUA A CAAGAAUG 995 CAGTTACA GGCTAGCTACAACQA CAAAAAAA 2696 4434 UAACCAAQA A UUAACUCC 995 GAGTTACA GGCTAGCTACAACQA ATTCTTAT 2697 4435 ACAAGAAU G UAACUCCA 996 TGGASTTAC GGCTAGCTACAACQA ATTCTTAT 2697 4446 AACUCCAG A UAGUGACA 997 ATCTGGAG GGCTAGCTACAACQA ATTCTTAT 2698 4446 AACUCCAG A UAGUGACA 999 TTCTCCTA GGCTAGCTACAACQA ATTCTTCT 2700 4446 AACUCCAG A UAGUGACA 999 TTCTCCTA GGCTAGCTACAACQA TACTTCT 2700 4446 AACUCCAG A UAGUGACA 999 TTCTCCTA GGCTAGCTACAACQA ATTCTTCT 2700 4446 AAGUGACAA G UGAACAACU 1000 ACTTCTCTA GGCTAGCTACAACGA TACTTCTC 2700 4446 AAGUGACAA G UGAAGAAU 1000 ACTTCTCTA GGCTAGCTACAACGA ATTCTCCT 2700 4446 AAGUGACAA G UGAAGAAC 1000 ACTTCTCTA GGCTAGCTACAACGA TACTTCTC 2700 44471 AGUGAAGAA CACUCCUG 1000 ACTTCTCA GGCTAGCTACAACGA TACTTCTC 2700 4446 AAGUGACAA G UGAAGAAC 1000 ACTTCTCA GGCTAGCTACAACGA TACTTCTC 2700 44471 AGUGAAGAA CACUACUG 1000 ACTTCTCA GGCTAGCTACAACGA TACTTCTCT 2705 4473 UGAAGAAC CUACUGUU 1001 AGCATGA GGCTAGCACACAC ATCTTCTCT 2705 4476 ACACACCC A CUACUGU 1001 AGCATGA GGCTAGCACACAC ATCTTCACT 2705 4479 ACACUACUG CUAAAUCC 1003 CAGTTAGT GGCTAGCACACAC ATCTTCACT 2705 4479 ACACUACUG CUAAAUCC 1003 CAGTTAGT GGCCTAGCTACAACGA ATCTTCAC 2706 4499 ACACUACUG AUCCACC 1003 AGGAAGA GGCTAGCTACAACCA ATGTTGTT 2701 4499 ACACUACUG AUCCACC 1003 AGGAAGA GGCTAGCTACAACCA ATGTTGTT 2701 4490 AAAUCCUC A UCCACACU 1000 AGGAGA GGCTAGCTACAACCA ATGTGGTT 2714 4590 CUACUCAU A UCCACACU 1000 AGGAGA GGCTAGCTACAACCA ATGTGGTT 271	4379	CCAUGGGA G CCAGCUGC	985	GCAGCTGG GGCTAGCTACAACGA TCCCATGG	2687
1939  UGUUUUU G UGAUUUUU 988					
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4454 AUAGAGAA A UAGUGACA 999 TETCACTA GGCTAGCTACAACGA TETCTAT 2701 4457 GAGAAAUA G UGACAAGU 1000 ACTTGTCA GGCTAGCTACAACGA TATTTCTC 2702 4460 AAAUAGUG A CAAGUGAA 1001 TETCACTTG GGCTAGCTACAACGA CACTATTT 2703 4464 AGUACAA G UGACAGAU 1001 TETCACTTG GGCTAGCTACAACGA CACTATTT 2703 4464 AGUACAA G UGAAGAAC 1002 GTTCTTCA GGCTAGCTACAACGA CACTATTT 2703 4471 AGUGACAA G UGACUGCU 1003 CAGTAGTG GGCTAGCTACAACGA TETTCACT 2705 4473 UGAAGAAC A CUACUGCU 1004 AGCAGTAG GGCTAGCTACAACGA GTTCTCA 2706 4476 AGAACACU A CUGCUAAA 1005 TETAGCAG GGCTAGCTACAACGA AGTGTCTC 2706 4477 ACACUACU G CUAAAUCC 1006 GGATTTAG GGCTAGCTACAACGA AGTGTGTT 2708 4484 ACUGCUAA A UCCUCAUG 1007 CATGAGGA GGCTAGCTACAACGA AGTGTGTT 2708 4489 AAAUCCUC A UGUUACUC 1008 GAGTTAAC GGCTAGCTACAACGA ATGAGTT 2710 4490 AAAUCCUC A UGUUACUC 1009 CTGAGTAA GGCTAGCTACAACGA ATGAGGT 2711 4491 AUACUCAU G UUACUCAG 1009 CTGAGTAA GGCTAGCTACAACGA ATGAGGA 2712 4500 GUUACUCA G UGUUAGAG 1011 CTCTAACA GGCTAGCTACAACGA ATGAGGA 2712 4500 GUUACUCA G UGUUAGAG 1011 CTCTAACA GGCTAGCTACAACGA ATGAGGA 2713 4501 UACUCAGU G UUAUAGAG 1011 CTCTAACA GGCTAGCTACAACGA ATGAGTA 2713 4511 UUACAGAGAA UCCUUCCU 1013 AGGAAGGA GGCTAGCTACAACGA ATGAGTA 2714 4522 CUUCCUAA A CCCAAUGA 1014 TCATTGGG GGCTAGCTACAACGA TTCATGAT 2716 4527 UAAACCCA A UGACUUCCU 1015 GGAAGTCA GGCTAGCTACAACGA TTCATGAG 2716 4528 CUUCCUAA A CCCAAUGA 1014 TCATTGGG GGCTAGCTACAACGA TTCATGAG 2716 4538 ACUUCCUC A CCCCACCC 1015 GGAAGTCA GGCTAGCTACAACGA CTTGAGTA 2717 4530 ACCCAAUG A CUUCCAACC 1017 GGTTGGAG GGCTAGCTACAACGA CTTGAGGA 2716 4538 ACUUCCUC A CCCCAGCG 1018 GGCGGGG GGCTAGCTACAACGA CTTGAGGA 2720 4550 CAACCCCC G CCACCCU 1019 TGAGGTGG GGCTAGCTACAACGA CTTGAGGA 2720 4551 CACGCAGC A CCCCAGCG 1021 CCTGAGG GGCTAGCTACAACGA GGGAGGGG 2720 4550 CAACCCCC G CCACCUCA 1019 TGAGGTGG GGCTAGCTACAACGA GGGAGGGG 2720 4551 ACCUCAGG C CACGCAGG 1022 CCTCAAG GGCTAGCTACAACGA GGGAGGGG 2720 4551 CACGCAGG A CCCCAGCG 1022 GTCCTGAG GGCTAGCTACAACGA GGGAGGGG 2722 4565 CAGGGCAC C CACCACC 1018 GGCTAGCTACAACGA GGGAGAGCT 2721 4565 CAGGGCAC C CACCAGG 1022 GTCCTGCG GGCTAGCTACAACGA GCGCTGCTG 27	4439	AGAAUGUA A CUCCAGAU	997	ATCTGGAG GGCTAGCTACAACGA TACATTCT	2699
4457 GAGAAAUA G UGACAAGU 1000 ACTTGTCA GGCTAGCTACAACGA TATTTCTC 2702 4466 AAUAGUG A CAAGUGAA 1001 TTCACTTG GGCTAGCTACAACGA CACTATTT 2703 4466 AGUGACAA G UGAAGAAC 1002 GTTCTTCA GGCTAGCTACAACGA CACTATTT 2703 4466 AGUGACAA G UGAAGAAC 1002 GTTCTTCA GGCTAGCTACAACGA TTGTCACT 2704 4471 AGUGAAGA A CACUACUG 1003 CAGTAGTG GGCTAGCTACAACGA TTGTCACT 2705 4473 UGAAGAAC A CUACUGCU 1004 AGCAGTAG GGCTAGCTACAACGA GTTCTTCA 2706 4476 AGAACACU A CUGCUAAA 1005 TTTAGCAG GGCTAGCTACAACGA AGTGTTCT 2707 4477 ACACUACU G CUAAAUCC 1006 GGATTTAG GGCTAGCTACAACGA AGTGTTC 2707 4486 ACUGCUAA A UCCUCAUG 1007 CATGAGGA GGCTAGCTACAACGA AGTAGTGT 2709 4490 AAAUCCUC A UGUUACUC 1008 GAGTAACA GGCTAGCTACAACGA AGTAGGTT 2710 4492 AUCCUCAU G UUACUCCG 1009 CTGAGTAA GGCTAGCTACAACGA ATGAGGT 2710 4492 AUCCUCAU G UUAGUGGU 1010 ACACTGAG GGCTAGCTACAACGA ACATGAG 2711 4590 CUCAUGUU A CUCAGUGU 1010 ACACTGAG GGCTAGCTACAACGA ACATGAG 2711 4500 GUUACUCA G UGUUAGAG 1011 CTCTAACA GGCTAGCTACAACGA ACATGAG 2712 4501 UACUCAGU G UUAGAGAA 1012 TTCTCTAA GGCTAGCTACAACGA ACATGAG 2713 4502 UACUCAUA A CCCAAUGA 1014 TCATTGGG GGCTAGCTACAACGA TCGAGTAC 2713 4511 UUAGAGAA A UCCUUCCU 1013 AGGAAGGA GGCTAGCTACAACGA TCGAGTAC 2714 4521 CUUCCUAA A CCCAAUGA 1014 TCATTGGG GGCTAGCTACAACGA TCGAGTA 2715 4522 CUUCCUAA A CCCAAUGA 1014 TCATTGGG GGCTAGCTACAACGA TTCGAGTA 2716 4521 UAAACCCA A UGACUUCC 1015 GGAAGTCA GGCTAGCTACAACGA TTGGGTT 2716 4530 ACCCAAUG A CUCCAACC 1016 GAGGGGG GGCTAGCTACAACGA TTGGGAT 2718 4531 ACUUCCUA A CCCCAGGG 1026 CAGGAGG GGCTAGCTACAACGA CATTGGGT 2718 4533 ACUUCCUA A CCCCAGGG 1026 GGGGGGG GGCTAGCTACAACGA CATTGGGA 272 4551 CCCCGCC A CCUCAACC 1017 GTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	4446	AACUCCAG A UAGAGAAA	998	TTTCTCTA GGCTAGCTACAACGA CTGGAGTT	2700
4460 AAAUAGUG A CAAGUGAA 4464 AGUGACAA G UGAAGAAC 4464 AGUGACAA G UGAAGAAC 4471 AGUGACAA G UGAAGAAC 4471 AGUGACAA G UGAAGAAC 4471 AGUGACAA G UGAAGAAC 4473 UGAAGAAC A CACUACUG 1003 CAGTAGTTAG CACTAGCTACAACGA TTGTCACT 4705 4473 UGAAGAAC A CUACUGCU 1004 AGCAGTAG GGCTAGCTACAACGA GTTCTTCA 4476 AGAACACU A CUGCUAAA 1005 TTTAGCAG GGCTAGCTACAACGA GTTCTTCA 4479 ACACUACU G CUAAAUCC 1006 GGATTTAG GGCTAGCTACAACGA AGTAGTTT 4479 ACACUACU G CUAAAUCC 1006 GGATTTAG GGCTAGCTACAACGA AGTAGTTT 2708 4484 ACUGCUAA A UCCUCAUG 1007 CATGAGGA GGCTAGCTACAACGA AGTAGTT 2709 4490 AAAUCCUC A UGUUACUC 1008 GAGTAACA GGCTAGCTACAACGA AGTAGTT 4491 AAUCCUC A UGUUACUC 1009 CTGAGTAA GGCTAGCTACAACGA AGTAGTT 4492 AUCCUCAUG UUACUC 1009 CTGAGTAA GGCTAGCTACAACGA ATGAGGAT 4590 GUUACUCA G UGUUACUC 1010 ACACTGAG GGCTAGCTACAACGA AACATGAG 4712 4590 GUUACUCA G UGUUAGAG 1011 CTCTAACA GGCTAGCTACAACGA AACATGAG 4712 4500 GUUACUCA G UGUUAGAG 1011 CTCTAACA GGCTAGCTACAACGA ACATGAG 4712 4501 UUACAGAA A UCCUUCCU 1013 AGGAAGGA GGCTAGCTACAACGA ACTGAGTA 4511 UUAGAGAA A UCCUUCCU 1013 AGGAAGGA GGCTAGCTACAACGA TTGGTAGTA 4522 CUUCCUAA A CCCAAUGA 1014 TCATTGGG GGCTAGCTACAACGA TTGGTAA 4521 UAAACCCA A UGACUUCC 1015 GGAAGTCA GGCTAGCTACAACGA TTGGTAA 4530 ACCCAAUGA 1014 TCATTGGG GGCTAGCTACAACGA TTGGTAA 4530 ACCCAAUGA 1016 CAGGGGAG GGCTAGCTACAACGA CATTGGGT 4527 UAAACCCA A UGACUUCC 1016 GAGGGAGG GGCTAGCTACAACGA CATTGGGT 4538 ACUUCCCU G CUCCAACC 1017 GGTTGGAG GGCTAGCTACAACGA CATTGGGT 4544 CUGCUCCA A CCCCCGCC 1018 GGCGGGGG GGCTAGCTACAACGA CATTGGGT 4553 CCCCGCC C CCCCCGC 1018 GGCGGGGG GGCTAGCTACAACGA GGGGGTG 4554 CUCAGGG C CACCUCA 1019 TGAGGTGG GGCTAGCTACAACGA GGGGGTG 4555 CAACCCC G CACCUCA 1019 TGAGGTGG GGCTAGCTACAACGA GGGGGTG 4556 CAGGCCC A CCUCAGG 1020 CCCTGAGG GGCTAGCTACAACGA GGGGGTG 4720 4557 CACCAGGG C CACGUUG 1021 CCTCTGAG GGCTAGCTACAACGA GGGGGTG 4721 4559 CACCAAUG C CUCAACC 1021 TGAGTGG GGCTAGCTACAACGA CCTGAGGT 4720 4559 CACCAAUG C CCCAGGG 1021 CCTCTGAG GGCTAGCTACAACGA CCTGAGGT 4720 4559 CAGGACUG C CUGAUCC 1028 GGCTAGCTACAACGA CAACCACA CTGGTCG 4579 CAGGACUG A CUGACCC 1029 GGCTAGCT	4454	AUAGAGAA A UAGUGACA	999	TGTCACTA GGCTAGCTACAACGA TTCTCTAT	2701
4464 AGUGACAA G UGAAGRAC 1002 GTTCTTCA GGCTAGCTACAACGA TTGTCACT 2704 4471 AGUGAAGA A CACUACUG 1003 CAGTAGTG GGCTAGCTACAACGA TCTTCACT 2705 4473 UGAAGACA A CUACUGCU 1004 AGCAGTAG GGCTAGCTACAACGA TCTTCACT 2705 4476 AGAACACU A CUGCUAAA 1005 TTTAGCAG GGCTAGCTACAACGA AGTGTTCT 2707 4477 ACACUACU G CUAAAUCC 1006 GGATTTAG GGCTAGCTACAACGA AGTGTTCT 2707 4484 ACUGCUAA A UCCUCAUG 1007 CATGAGGA GGCTAGCTACAACGA AGTGTTCT 2709 4489 AAAUCCU CA UGUUACUC 1008 GAGTTAG GGCTAGCTACAACGA GAGGATTT 2710 4490 AAAUCCU CA UGUUACUC 1008 GAGTAACA GGCTAGCTACAACGA GAGGATT 2710 4492 AUCCUCAUG UUACUCAG 1009 CTGAGTAA GGCTAGCTACAACGA ATGAGGAT 2711 4495 CUCAUGUU A CUCAUGU 1010 ACACTGAG GGCTAGCTACAACGA ATGAGGAT 2711 4500 GUUACUCA G UGUUAGAG 1011 CTCTAACA GGCTAGCTACAACGA ACATGAG 2712 4500 GUUACUCA G UGUUAGAG 1011 CTCTAACA GGCTAGCTACAACGA TGAGTAAC 2713 4501 UACQAGU G UUAGAGAA 1012 TTCTCTAA GGCTAGCTACAACGA TGAGTAAC 2713 4511 UUAGAGAA A UCCUUCCU 1013 AGGAAGGA GGCTAGCTACAACGA TCTGTATA 2715 4527 UAAACCCA A UGACUUCC 1015 GGAAGTCA GGCTAGCTACAACGA TCTCTTAA 2715 4530 ACCCAAUG A CUCCAUGA 1014 TCATTGGG GGCTAGCTACAACGA TTGTGTA 2716 4531 ACCUCCUAA C CUCCAACC 1016 GGAAGTCA GGCTAGCTACAACGA TGGGTTTA 2717 4530 ACCCAAUG A CUCCAGC 1017 GGTTGGAG GGCTAGCTACAACGA TGGGTTA 2718 4538 ACUUCCUA C CUCCAACC 1017 GGTTGGAG GGCTAGCTACAACGA TGGGTTA 2719 4544 CUGCUCCA C CCCCCGCC 1018 GGCAGGTGG GGCTAGCTACAACGA TGGGGTTG 2718 4550 CAACCCCC G CCACCUCA 1019 TGAGGTGG GGCTAGCTACAACGA TGGGGTTG 2720 4551 ACCUCAGG C CACGAGGA 1022 CCCTGAGG GGCTAGCTACAACGA GGCGGGG 2722 4561 ACCUCAGG C CACGAGGA 1022 CCCTGAGG GGCTAGCTACAACGA GGCGGGG 2722 4561 ACCUCAGG C CACGAGGAC 1022 GTCCTGCG GGCTAGCTACAACGA GGCGGGG 2722 4561 ACCUCAGG C CACGAGGAC 1022 GTCCTGCG GGCTAGCTACAACGA GGCGGGG 2722 4561 ACCUCAGG C CAGGACCA 1023 GGCTGG GGCTAGCTACAACGA GCCCTGAG 2725 4562 CAGGACCA C CUCAAGG 1022 GTCCTGC GGCTAGCTACAACGA CCTGAGGT 2725 4563 CCCCAGGA C CAGGACCA 1023 GGCTAGCTACAACGA GCCCTGAG 2725 4564 CAGGACCA C GAGGACCA 1023 GTGTCTG GGCTAGCTACAACGA CCCTCCTG 2725 45670 CACGAGGA C CAGGACCA 1023 GTGTCTG GGCTAGCTACAACGA CAGCTCC 2730 4	4457	GAGAAAUA G UGACAAGU	1000	ACTTGTCA GGCTAGCTACAACGA TATTTCTC	2702
4471 AGUGAAGA A CACUACUG 1003 CAGTAGTG GGCTAGCTACAACGA TCTTCACT 2705 4473 UGAAGACA A CUACUGCU 1004 AGCAGTAG GGCTAGCTACAACGA GTTCTCA 2706 4476 AGAACACU A CUGCUAAA 1005 TTTAGCAG GGCTAGCTACAACGA AGTGTTCT 2707 4479 ACACUACU G CUAAAUCC 1006 GGATTTAG GGCTAGCTACAACGA AGTGTTCT 2707 4484 ACUGCUAA A UCCUCAUG 1007 CATGAGGA GGCTAGCTACAACGA AGTAGTGT 2709 4490 AAAUCCUC A UGUUACUC 1008 GAGTTAGAG GGCTAGCTACAACGA AGTAGTGT 2710 4492 AUCCUCAU G UUACUCAG 1009 CTGAGTAA GGCTAGCTACAACGA ATGAGGAT 2711 4495 CUCAUGUU A CUCAGUGU 1010 ACACTGAG GGCTAGCTACAACGA ATGAGGAT 2711 4495 CUCAUGUU A CUCAGUGU 1010 ACACTGAG GGCTAGCTACAACGA ACAGTGAG 2712 4500 GUUACUCA G UGUUAGAG 1011 CTCTAACA GGCTAGCTACAACGA ACAGTGAG 2712 4501 UACUCAGU G UUAGAGA 1011 CTCTAACA GGCTAGCTACAACGA TGAGTAAC 2713 4502 UACUCAGU G UUAGAGA 1012 TTCTCTAA GGCTAGCTACAACGA TCGTGATA 2714 4511 UUAGAGAA A UCCUUCCU 1013 AGGAAGGA GGCTAGCTACAACGA TTCTCTAA 2715 4522 CUUCCUAA A CCCAAUGA 1014 TCATTGG GGCTAGCTACAACGA TTCTCTAA 2715 4523 AACCCAAUG A UGACUUCC 1015 GGAAGTCA GGCTAGCTACAACGA TTCGTGAA 2716 4524 UAAACCCA A UGACUUCC 1015 GGAAGTCA GGCTAGCTACAACGA TTAGGAGA 2716 4538 ACUUCCCU G CUCCAACC 1017 GGTTGGAG GGCTAGCTACAACGA CATTGGGT 2718 4538 ACUUCCCU G CUCCAACC 1017 GGTTGGAG GGCTAGCTACAACGA CATTGGGT 2718 4544 CUGCUCCA A CCCCCGCC 1018 GGCAGGTGA GGCTAGCTACAACGA TGGGGTG 2721 4550 CAACCCCC G CCACCCA 1019 TGAGGTGG GGCTAGCTACAACGA GGGGGGG 2722 4561 ACCUCAGG C CACCCACA 1019 TGAGGTGG GGCTAGCTACAACGA GGGGGGG 2722 4561 ACCUCAGG C CACCCACA 1019 TGAGGTGG GGCTAGCTACAACGA GGCGGGGG 2722 4563 CUCAGGG A CCGCAGGA 1022 GTCCTGAG GGCTAGCTACAACGA GGCGGGGG 2722 4565 CAGGGCAC C CAGGACA 1022 GTCCTGAG GGCTAGCTACAACGA GCCCTGAG 2725 4561 ACCUCAGG C CAGGAGA 1022 GTCCTGAG GGCTAGCTACAACGA GCCCTGAG 2725 4563 CUCAGGG A CCGCAGGA 1022 GTCCTGAG GGCTAGCTACAACGA GCCCTGAG 2725 4564 CAGGACGA C CAGGACA 1023 TGGTCCTG GGCTAGCTACAACGA GCCCTGAG 2726 4565 CAGGGCAC C CAGGACA 1023 GTGTCTG GGCTAGCTACAACGA GCCCTGAG 2726 4566 CACCCAGGA C CAGGACA 1023 GTGTCTG GGCTAGCTACAACGA GCTGCTGC 2726 4579 CAGGAGGC A CUGAUCAC 1028 GATTGAG GGCTAGCTACAACGA GAGC	4460	AAAUAGUG A CAAGUGAA	1001	TTCACTTG GGCTAGCTACAACGA CACTATTT	2703
4473         UGAAGAAC A CUACUGCU         1004         AGCAGTAG GGCTAGCTACAACGA GTTCTTCA         2706           4476         AGAACACU A CUGCUAAA         1005         TTTAGCAG GGCTAGCTACAACGA AGTGTTCT         2707           4479         ACACUACU G CUAAAUCC         1006         GGATTTAG GGCTAGCTACAACGA AGTGTGTC         2709           4484         ACUGCUAA A UCCUCAUG         1007         CATGAGGA GGCTAGCAACGA TTAGCAGT         2709           4490         AAAUCCUC A UGUUACUC         1008         GAGTAACA GGCTAGCTACAACGA ATGAGGAT         2710           4492         AUCCUCAU G UGAGGA         1010         ACACTGAG GGCTAGCTACAACGA ACTAGG         2712           4500         GUACUCAG G UGUAGGA         1011         CTCTAACA GGCTAGCTACAACGA ACTAGAG         2712           4500         GUACUCAGU G UGUAGGA         1011         CTCTAACA GGCTAGCTACAACGA ACTAGAGT         2714           4501         UUAGAGAA A UCCUUCCU         1013         AGGAAGGA GGCTAGCTACAACGA TCTCTCTAA         2714           4511         UUAGAGAA A UCCUUCCU         1013         AGGAAGGA GGCTAGCTACAACGA TTAGGAAG         2716           4522         CUUCCUAA A CCCAAUGA         1014         TCATTGGG GGCTAGCTACAACGA TGGGTTTA         2717           4530         ACCAAUGA         A UUACCCU         1015         GGAAGTAC GGCTAACAACAA GGCTAGAGA	4464	AGUGACAA G UGAAGAAC	1002	GTTCTTCA GGCTAGCTACAACGA TTGTCACT	2704
4476 AGAACACU A CUGCUAAA  4479 ACACUACU G CUAAAUCC  4479 ACACUACU G CUAAAUCC  4479 ACACUACU G CUAAAUCC  4484 ACUGCUAA A UCCUCAUG  4484 ACUGCUAA A UCCUCAUG  4484 ACUGCUAA A UCCUCAUG  4490 AAAUCCU C A UGUUACUC  4490 AAAUCCUC A UGUUACUC  4490 ACACUACUG UUACUCCA  4491 AUCCUCAU G UUACUCCA  4492 AUCCUCAU G UUACUCCA  4492 AUCCUCAU G UUACUCCA  4492 AUCCUCAU G UUACUCCA  4495 CUCAUGUU A CUCAGUGU  4495 CUCAUGUU A CUCAGUGU  4500 GUUACUCA G UGUUAGAG  4500 GUUACUCA G UGUUAGAG  4501 UACUCAGU G UUAGAGA  4501 UACUCAGA A CCCAAUGA  4501 UAAACCCA A UGACUUCC  4501 UAAACCCA A UGACUUCC  4503 ACCCAAUG A UCCCUCCU  4503 ACCCAAUG A UCCCCUCC  4016 CAGGGAAG GGCTAGCTACAACGA TAGGAAG  4538 ACUUCCCU G CUCCAACC  4017 GGTTGGAG  4538 ACUUCCCU G CUCCAACC  4010 GGTTGGAG  4553 CCCCGCC A CCCCAGCC  4010 GGTTGGAG  4554 CUCCUCAA A CCCCCGCC  4010 GGTTGGAG  4555 CAACCCCC G CCACCUCA  4010 TAGGGTAG  4556 CACCCCGC A CCUCAGGG  4550 CACCCCCG C CCACCUCA  4010 TAGGGTAG  4551 ACCUCAGG G CACGCAGG  4021 TAGGGTAG  4552 CUCAAGGG  4553 CCCCGCC A CCUCAGGG  4554 ACCUCAGGG  4555 CAGGGCAC G CAGGAGCA  4021 TAGGGTAG  4556 CAGGGCAC G CAGGAGCA  4021 TAGGGTAG  4556 CAGGAGCA G CAGCAGG  4570 CACGCAGG TAGCTACAACGA GGCCGGGG  4571 CACGAGACA G CUCAACC  4570 CAGGACCA G UUGAUCC  4570 CAGGACCA G CAGCAGG  4571 CAGGACCA G UUGAUCC  4571 CAGGACCA G UUGAUCC  4571 CAGGACCA G UUGAUCC  4571 CAGGACCA G UUGAUCC  4572 CAGGACCA G UUGAUCC  4572 CAGGACCA G UUGAUCC  4572 CAGGACCA G CAGCAGA  4579 CACGCAGG A CCCCAACC  4579 CACGCAGG A CCCCAACCA  4579 CACGCAGG A CCCCAACCA  4579 CACGCACUG A UCACCAA  4579 CACGCACCA A UGACCCA  4570 CAGGACCA G CAGCAGCA  4570 CAGGACCA G CAGCAGCA  4571 CAGGACCA G CACCACAC  4571 CAGGAC	4471	AGUGAAGA A CACUACUG	1003	CAGTAGTG GGCTAGCTACAACGA TCTTCACT	2705
4479 ACACUACU G CUAAAUCC 1006 GGATTTAG GGCTAGCTACAACGA AGTAGTGT 2708 4484 ACUGCUAA A UCCUCAUG 1007 CATGAGGA GGCTAGCTACAACGA TTAGCAGT 2709 4490 AAAUCCUCA UGUUACUC 1008 GAGTAACA GGCTAGCTACAACGA TTAGCAGT 2710 4492 AUCCUCAU G UUACUCAG 1009 CTGAGTAA GGCTAGCTACAACGA AGGATTT 2710 4492 AUCCUCAU G UUACUCAG 1009 CTGAGTAA GGCTAGCTACAACGA AGAGATT 2711 4492 AUCCUCAU A CUCAGUSU 1010 ACACTGAG GGCTAGCTACAACGA AACATGAG 2712 4500 GUUACUCA G UGUUAGAG 1011 CTCTAACA GGCTAGCTACAACGA AACATGAG 2712 4500 UACUCAGU G UUAGAGAA 1011 CTCTAACA GGCTAGCTACAACGA ACTGAGTAA 2714 4511 UUAGAGAA A UCCUUCCU 1013 AGGAAGGA GGCTAGCTACAACGA TTCTCTAA 2715 4522 CUUCCUAA A CCCAAUGA 1014 TCATTGGG GGCTAGCTACAACGA TTCTCTAA 2716 4527 UAAACCCA A UGACUUCC 1015 GGAAGTCA GGCTAGCTACAACGA TTGGGAG 7716 4528 ACCUACUG G CUCCAACC 1015 GGAAGTCA GGCTAGCTACAACGA TAGGAGA 7716 4538 ACUUCCCU G CUCCAACC 1017 GGTTGGAG GGCTAGCTACAACGA CATTGGGT 2718 4538 ACUUCCCU G CUCCAACC 1017 GGTTGGAG GGCTAGCTACAACGA CATTGGGT 2719 4544 CUGCUCCA A CCCCCGCC 1018 GGCGGGGG GGCTAGCTACAACGA AGGGAAGT 2719 4553 CCCCCCGC C CCACCUCA 1019 TGAGGTGG GGCTAGCTACAACGA GGGGAGG 2720 4550 CAACCCCC G CCACCUCA 1019 TGAGGTGG GGCTAGCTACAACGA GGGGAGG 2720 4551 CCCCCGCC C CCUCAGGG 1020 CCCTGAGG GGCTAGCTACAACGA GGGGGTG 2721 4553 CCCCCGCC C CCUCAGGG 1020 CCCTGAGG GGCTAGCTACAACGA CCTGAGGT 2721 4563 CUCAGGGC C CGCACCUCA 1019 TGAGGTGG GGCTAGCTACAACGA GGCGGGG 2722 4565 CAGGGCAC G CAGGACG 1021 CCTGCGTG GGCTAGCTACAACGA CCTGAGGT 2724 4565 CAGGGCAC G CAGGACG 1021 CCTGCGTG GGCTAGCTACAACGA CCTGAGGT 2724 4566 CACCAGG A CCCAGGAG 1022 CCCTGAGG GGCTAGCTACAACGA CCTGAGGT 2724 4570 CACGAGGA C CAGGAACG 1022 GTCCTGC GGCTAGCTACAACGA CCTGAGGT 2726 4571 CAGGACCA G UUGAUUG 1024 CAAACTGG GGCTAGCTACAACGA CCTGCGTG 2726 4572 CAGGACCA G UUGAUUG 1024 CAAACTGG GGCTAGCTACAACGA CCTGCGTG 2726 4574 CAGGACCA G UUGAUUG 1025 CAATCAAA GGCTAGCTACAACGA CCTGCCTG 2727 4590 CACGAGGA C CAGGACCA 1023 TGGTCCTG GGCTAGCTACAACGA CCTGCCTG 2731 4591 CACGCACGA A UCACCCA 1029 GTGATCAG GGCTAGCTACAACGA CCATGCTC 2731 4592 GGAGCUG A CCCAUGC 1029 GTGATCAG GGCTAGCTACAACGA CAGTGC	4473	UGAAGAAC A CUACUGCU	1004	AGCAGTAG GGCTAGCTACAACGA GTTCTTCA	2706
4484         ACUGCUAA A UCCUCAUG         1007         CATGAGGA GGCTAGCACAGCA TTAGCAGT         2709           4490         AAAUCCUC A UGUUACUC         1008         GAGTAACA GGCTAGCACAGA GAGGATTT         2710           4492         AUCCUCAU G UUACUCAG         1009         CTGAGTAA GGCTAGCACAGA ATGAGGAT         2711           4495         CUCAUGUU A CUCAGUGU         1010         ACACTGAG GGCTAGCACACAACGA ACATGAG         2712           4500         GUUACUCA G UGUAGAG         1011         CTCTAACA GGCTAGCTACAACGA TGAGTAC         2713           4502         UACUCAGU G UUAGAGAA         1012         TTCTCTAA GGCTAGCACAACGA TGAGTACA         2713           4511         UUAGAGAA A UCCUUCCU         1013         AGGAAGGA GGCTAGCTACAACGA TTCTCTAA         2715           4522         CUUCCUAA A CCCAAUGA         1014         TCATTGGG GGCTAGCACACGA TGGGTTAC         2716           4530         ACCCAAUG A CUCCCUG         1015         GGAAGTCA GGCTACAACGA AGGAACT         2717           4538         ACUUCCU G CUCCAACC         1017         GGTTGGA         GGTTAGCTACAACGA AGGAACT         2721           4550         CAACCCCC G CACCUCA         1018         GGCGGGGG GGCTAGCTACAACGA AGGACAGA         2722           4551         ACCCAGCG A CCUCAGGG         1020         CCCTGAGG         GGCTAGCTACAACGA GGG	4476	AGAACACU A CUGCUAAA	1005	TTTAGCAG GGCTAGCTACAACGA AGTGTTCT	2707
4490         AAAUCCUC A UGUUACUC         1008         GAGTAACA GGCTAGCTACAACGA GAGGATTT 2710           4492         AUCCUCAU G UUACUCAG         1009         CTGAGTAA GGCTAGCAACGA ATGAGGAT 2711           4495         CUCAUGUU A CUCAGUGU         1010         ACACTGAG GGCTAGCAACGA AACATGAG 2712           4500         GUUACUCA G UGUUAGAG         1011         CTCTAACA GGCTAGCTACAACGA TGAGTAAC 2713           4502         UACUCAGU G UUAGAGAA 1011         TTCTCTAA GGCTAGCTACAACGA TGAGTAAC 2714           4511         UUAGAGAA A UCCUUCCU         1013         AGGAAGGA GGCTAGCTACAACGA TCTAGATA 2715           4522         CUUCCUAA A CCCAAUGA 1014         TCATTGGG GGCTAGCACACGA TTAGGAAG 2716           4527         UAAACCCA A UGACUUCC 1015         GGAAGTCA GGCTACAACGA TGGGTTTA 2717           4530         ACCCAAUG A CUUCCUGG 1016         CAGGGAAG GGCTAGCTACAACGA CATGGGT 2718           4538         ACUUCCU G CUCCAACC 1017         GGTTGGAG GGCTAGCTACAACGA AGGAAGT 2720           4544         CUGCUCCA A CCCCGCC 1018         GGCGGGGG GGCTAGCTACAACGA AGGACA GGGGGTTG 2721           4550         CAACCCCC G CACCUCA 1019         TGAGGTGG GGCTAGCTACAACGA GGGGGTTG 2721           4551         ACCUCAGG CACGAGG 1022         CCCTGAGG GGCTAGCTACAACGA GGCGGGG 2722           4563         CUCAGGGC A CGCAGGAC 1023         TGGTCTGG GGCTAGCTACAACGA GCCTGAGT 2724           4565 </td <td>4479</td> <td>ACACUACU G CUAAAUCC</td> <td>1006</td> <td>GGATTTAG GGCTAGCTACAACGA AGTAGTGT</td> <td>2708</td>	4479	ACACUACU G CUAAAUCC	1006	GGATTTAG GGCTAGCTACAACGA AGTAGTGT	2708
4492         AUCCUCAU G UIACUCAG         1009         CTGAGTAA GGCTAGCTACAACGA ATGAGGAT         2711           4495         CUCAUGUU A CUCAGUGU         1010         ACACTGAG GGCTAGCTACAACGA AACATGAG         2712           4500         GUUACUCA G UGUUAGAG         1011         CTCTAACA GGCTAGCTACAACGA TGAGTAAC         2713           4502         UACUCAGU G UUAGAGAA         1012         TTCTCTAA GGCTAGCTACAACGA ACTGAGTA         2714           4511         UUAGAGAA A UCCUUCCU         1013         AGGAAGGA GGCTAGCTACAACGA TTCCTAAA         2715           4522         CUUCCUAA A CCCAAUGA         1014         TCATTGGG GGCTAGCTACAACGA TTAGGAAC         2716           4527         UAAACCCA A UGACUUCC         1015         GGAAGTCA GGCTAGCTACAACGA TTAGGAC         2717           4538         ACUUCCCU G CUCCAACC         1017         GGTTGGAG         GGCTAGCTACAACGA CTTGGGT         2719           4544         CUGCUCCA A CCCCCGCC         1018         GGCGGGGG GGCTAGCTACAACGA TGGAGCA         2720           4553         CCCCCGCC A CCUCAGGG         1020         CCCTGAGG GGCTAGCTACAACGA GGCGGGGG         2722           4554         ACCUCAGG G CAGGAGG         1021         CCTGCGGTG GGCTAGCTACAACGA GCCTGAGG         2722           4555         CCCCGGCC A CGGAGCA         1022         GTCCTGCGTG GGCTAGCTACAACGA	4484	· ACUGCUAA A UCCUCAUG	1007	CATGAGGA GGCTAGCTACAACGA TTAGCAGT	2709
4495 CUCAUGUU A CUCAGUGU 1010 ACACTGAG GGCTAGCTACAACGA AACATGAG 2712 4500 GUUACUCA G UGUUAGAG 1011 CTCTAACA GGCTAGCTACAACGA TGAGTAAC 2713 4502 UACUCAGU G UUAGAGAA 1012 TTCTCTAA GGCTAGCTACAACGA ACTGAGTA 2714 4511 UUAGAGAA A UCCUUCCU 1013 AGGAAGGA GGCTAGCTACAACGA TTCTCTAA 2715 4522 CUUCCUAA A CCCAAUGA 1014 TCATTGGG GGCTAGCTACAACGA TTAGGAAG 2716 4527 UAAACCCA A UGACUUCC 1015 GGAAGTCA GGCTAGCTACAACGA TGGGTTTA 2717 4530 ACCCAAUG A CUUCCCUG 1016 CAGGGAAG GGCTAGCTACAACGA TGGGTTTA 2717 4531 ACUUCCCU G CUCCAACC 1017 GGTTGGAG GGCTAGCTACAACGA CATTGGGT 2718 4538 ACUUCCCU G CUCCAACC 1017 GGTTGGAG GGCTAGCTACAACGA CATTGGGT 2719 4544 CUGCUCCA A CCCCCGCC 1018 GGCGGGGG GGCTAGCTACAACGA TGGGTTG 2720 4550 CAACCCCC G CCACCUCA 1019 TGAGGTGG GGCTAGCTACAACGA GGGGAACT 2721 4553 CCCCCGCC A CCUCAGGG 1020 CCCTGAGG GGCTAGCTACAACGA GGGGGGTG 2722 4561 ACCUCAGG CACGCAGG 1021 CCTCGGGG GGCTAGCTACAACGA GGCGAGGG 2722 4561 ACCUCAGG CACGCAGG 1021 CCTCGGGG GGCTAGCTACAACGA CCTGAGGT 2724 4565 CAGGGCAC G CAGGACCA 1022 GTCCTGCG GGCTAGCTACAACGA GCCCTGAG 2724 4565 CAGGGCAC G CAGGACCA 1022 GTCCTGCG GGCTAGCTACAACGA GCCCTGAG 2724 4565 CAGGGCAC G CAGGACCA 1023 TGGTCCTG GGCTAGCTACAACGA GTGCCCTG 2725 4570 CACGCAGG A CCAGUUUG 1024 CAAACTGG GGCTAGCTACAACGA CCTGAGGT 2726 4574 CAGGACCA G UUUGAUUG 1025 CAATCAAA GGCTAGCTACAACGA CCTGCGTG 2726 4579 CACGAUG A UUGAUGA 1026 CTCCTCAA GGCTAGCTACAACGA CCTGCGTG 2727 4599 CACGAUUG A UUGAGGAG 1026 CTCCTCAA GGCTAGCTACAACGA CCTGCCTG 2728 4587 AUUGAGGA G CUGCACUG 1027 CAGTGCAG GGCTAGCTACAACGA CAACTGG 2728 4590 GAGGAGCU G CACUGAUC 1028 GATCAGT GGCTAGCTACAACGA CAACTGG 2732 4590 GAGGAGCU A CCCAGACC 1031 GATCAGA GGCTAGCTACAACGA CAACTGG 2732 4590 CACGAUGA A UCACCCAA 1030 TTGGGTGA GGCTAGCTACAACGA CAGTGCTC 2730 4592 GGAGCUG A CCCAAUGC 1032 GTGATCAG GGCTAGCTACAACGA CAGTGCTC 2731 4590 CACGAUG A UCACCCAA 1030 TTGGGTGA GGCTAGCTACAACGA CAGTGCAG 2732 4599 CACUGAUC A CCCAAUGC 1031 GCATTGGG GGCTAGCTACAACGA GAGCTCCC 2732 4604 AUCACCCA A UGCAUCC 1033 GCTGGTGA GGCTAGCTACAACGA GATCGTC 2733 4604 AUCACCCA A UGCACCC 1033 GCTGGTGA GGCTAGCTACAACGA GATCGTG	4490	AAAUCCUC A UGUUACUC	1008	GAGTAACA GGCTAGCTACAACGA GAGGATTT	2710
4500 GUIACUCA G UGUIAGAG 1011 CTCTAACA GGCTAGCTACAACGA TGAGTAAC 2713 4502 UACUCAGU G UUAGAGAA 1012 TTCTCTAA GGCTAGCTACAACGA ACTGAGTA 2714 4511 UUAGAGAA A UCCUUCCU 1013 AGGAAGGA GGCTAGCTACAACGA ACTGAGTA 2715 4522 CUUCCUAA A CCCAAUGA 1014 TCATTGGG GGCTAGCTACAACGA TTCTCTAA 2715 4527 UAAACCCA A UGACUUCC 1015 GGAAGTCA GGGCTAGCAACGA TTGGGATA 2717 4530 ACCCAAUGA CUUCCCUG 1016 CAGGGAAG GGCTAGCTACAACGA CATTGGGT 2718 4538 ACUUCCCU G CUCCAACC 1017 GGTTGGAG GGCTAGCTACAACGA AGGGAAGT 2719 4544 CUGCUCCA A CCCCCGCC 1018 GGCGGGGG GGCTAGCTACAACGA AGGGAAGT 2720 4550 CAACCCC G CCACCUCA 1019 TGAGGTGG GGCTAGCTACAACGA GGGGGTTG 2721 4553 CCCCCGCC A CCUCAGGG 1020 CCCTGAGG GGCTAGCTACAACGA GGGGGTTG 2721 4561 ACCUCAGG G CACGUCA 1019 TGAGGTGG GGCTAGCTACAACGA GGGGGTG 2722 4561 ACCUCAGG G CACGCAGG 1021 CCTGAGG GGCTAGCTACAACGA GCGGGGGG 2722 4563 CUCAGGGC C CGCAGGAC 1022 GTCCTGAG GGCTAGCTACAACGA GCCGGGGG 2722 4565 CAGGGCAC G CAGGACCA 1023 TGGTCCTG GGCTAGCTACAACGA CCTGAGGT 2723 4565 CAGGGCAC G CAGGACCA 1023 TGGTCCTG GGCTAGCTACAACGA GCCCTGAG 2724 4565 CAGGGCAC G CAGGACCA 1023 TGGTCCTG GGCTAGCTACAACGA CCTGAGGT 2725 4570 CACGCAGG A CCAGUUUG 1024 CAAACTGG GGCTAGCTACAACGA CCTGAGGT 2726 4574 CAGGACCA G UUUGAUUG 1025 CAATCAAA GGCTAGCTACAACGA TGGTCCTG 2727 4579 CCAGUUGA UUGAGGAA 1026 CACGTAGCTACAACGA CAAACTGG CTGCTG 2727 4579 CCAGUUGA UUGAGGAA 1026 CTCCTCAA GGCTAGCTACAACGA CAAACTGG 2728 4587 AUUGAGGA G CUGCACUG 1027 CAGTGAG GGCTAGCTACAACGA CAAACTGG 2728 4587 AUUGAGGA G CUGCACUG 1027 CAGTGAG GGCTAGCTACAACGA CAAACTGG 2728 4589 CAGGACCA A CUGAUCAC 1028 GATCAGT GGCTAGCTACAACGA AGCTCCT 2730 4599 CAGUGAUC A CCCAAUGC 1031 GCATTGGG GGCTAGCTACAACGA GCAGTCCC 2731 4596 CUGCACUG A UCACCCAA 1030 TTGGGTGA GGCTAGCTACAACGA GCAGTCCC 2731 4599 CACUGAUC A CCCAAUGC 1031 GCATTGGG GGCTAGCTACAACGA GCAGTCCC 2731 4599 CACUGAUC A CCCAAUGC 1031 GCATTGGG GGCTAGCTACAACGA GCAGTCCC 2731 4604 AUCACCCA A UGCAUCAC 1032 GTGATGCA GGCTAGCTACAACGA GATCAGTG 2732 4606 CACCCAAUGC A UCACCGU 1033 ACGTGATG GGCTAGCTACAACGA GATCAGTG 2735 4608 CCCAAUGC A UCACCGU 1033 ACGTGATG GGCTAGCTACAACGA GATCAG	4492	AUCCUCAU G UUACUCAG	1009	CTGAGTAA GGCTAGCTACAACGA ATGAGGAT	2711
4502 UACUCAGU G UUAGAGAA  1012 TTCTCTAA GGCTAGCTACAACGA ACTGAGTA  4511 UUAGAGAA A UCCUUCCU  1013 AGGAAGGA GGCTAGCTACAACGA TTCTCTAA  4522 CUUCCUAA A CCCAAUGA  1014 TCATTGGG GGCTAGCTACAACGA TTAGGAAG  4527 UAAACCCA A UGACUUCC  1015 GGAAGTCA GGCTAGCTACAACGA TTAGGAAG  4528 ACUUCCCUG  1016 CAGGGAAG GGCTAGCTACAACGA TGGGTTTA  4530 ACCCAAUG A CUUCCCUG  1016 CAGGGAAG GGCTAGCTACAACGA CATTGGGT  4538 ACUUCCCU G CUCCAACC  1017 GGTTGGAG GGCTAGCACACGA AGGGAAGT  4544 CUGCUCCA A CCCCCGCC  1018 GGCGGGGG GGCTAGCACACGA AGGGAAGT  4550 CAACCCCC G CCACCUCA  4550 CAACCCCC G CCACCUCA  4551 CCCCCGCC A CCUCAGGG  1020 CCCTGAGG GGCTAGCTACAACGA GGGGGGGG  4553 CCCCCGCC A CCUCAGGG  1020 CCCTGAGG GGCTAGCTACAACGA GGGGGGGG  4551 ACCUCAGG G CACGCAGG  1021 CCTGCGTG GGCTAGCACACGA GGCGGGGG  4561 ACCUCAGG G CACGCAGG  1022 GTCCTGCG GGCTAGCTACAACGA GGCGGGGG  4565 CAGGGCAC G CAGGACCA  1023 TGGTCCTG GGCTAGCTACAACGA GCCCTGAGGT  4570 CACGCAGG A CCAGUUUG  1024 CAAACTGG GGCTAGCTACAACGA GCCCTGAG  4570 CACGCAGG A CCAGUUUG  1024 CAAACTGG GGCTAGCTACAACGA CTGCCTGC  4571 CAGGACCA G UUUGAUUG  1025 CAATCAAA GGCTAGCTACAACGA CTGCCTG  4572 CCAGUUUG A UUGAGGAG  1026 CTCCTCAA GGCTAGCTACAACGA TGGTCCTG  4579 CCAGUUUG A UUGAGGAG  1027 CAGTGCAG GGCTAGCTACAACGA TGGTCCTG  4570 CAGGACCA G UUUGAUUG  1026 CTCCTCAA GGCTAGCTACAACGA CAAACTGG  4570 CAGGACCA G UUGACCU  1028 GATCAGTG GGCTAGCTACAACGA CAAACTGG  4570 CAGGACCA G UUGACCU  1029 GTGATCAA GGCTAGCTACAACGA CAAACTGG  4572 CAGGUUG A UCACCCAA  1030 TTGGGTGA GGCTAGCTACAACGA CAGTGCAG  4592 GGAGCUG A CUGAUCAC  1029 GTGATCAG GGCTAGCTACAACGA CAGTGCAG  4592 GGAGCUG A CUGAUCAC  1029 GTGATCAG GGCTAGCTACAACGA GATCAGTG  4592 GGAGCUG A CUGAUCAC  1029 GTGATCAG GGCTAGCTACAACGA GATCAGTG  4599 CACUGAUC A CCCAAUGC  1031 GCATTGGG GGCTACCAACGA AGCTCCT  2731  4596 CUGCACUG A UGACCCC  1031 GCATTGGG GGCTACCAACGA AGCTCCT  2732  4599 CACUGAUC A CCCAAUGC  1031 GCATTGGG GGCTACCAACGA AGCTCCT  2733  4604 AUCACCCA A UGCAUCAC  1032 GTGATCAG GGCTACCAACGA AGTGCAG  4606 CACCCAAUGC  AUCACCGA  1034 GTACGTGA GGCTACCAACGA ATTGGGTG  2735  4608 CCCAAUGC A UCACCCC  1035	4495	CUCAUGUU A CUCAGUGU	1010	ACACTGAG GGCTAGCTACAACGA AACATGAG	2712
4511 UUAGAGAA A UCCUUCCU 1013 AGGAAGGA GGCTAGCTACAACGA TTCTCTAA 2715 4522 CUUCCUAA A CCCAAUGA 1014 TCATTGGG GGCTAGCTACAACGA TTAGGAAG 2716 4527 UAAACCCA A UGACUUCC 1015 GGAAGTCA GGCTAGCTACAACGA TTAGGAAG 2717 4530 ACCCAAUG A CUUCCCUG 1016 CAGGGAAG GGCTAGCTACAACGA CATTGGGT 2718 4538 ACUUCCCU G CUCCAACC 1017 GGTTGGAG GGCTAGCAACGA AGGGAAGT 2719 4544 CUGCUCCA A CCCCCGCC 1018 GGCGGGGG GGCTAGCACACGA AGGGAAGT 2720 4550 CAACCCCC G CCACCUCA 1019 TGAGGTGG GGCTAGCACACGA GGGGGGG 2721 4553 CCCCCGCC A CCUCAGGG 1020 CCCTGAGG GGCTAGCACACGA GGGGGGG 2722 4561 ACCUCAGG G CACGCAGG 1021 CCTGCGTG GGCTACAACGA GGCGGGGG 2722 4563 CUCAGGGC A CGCAGAGG 1021 CCTGCGTG GGCTAGCACACGA GCCGTGAGT 2723 4563 CUCAGGGC A CGCAGAGA 1022 GTCCTGCG GGCTAGCTACAACGA GCCCTGAGG 2724 4565 CAGGGCAC G CAGGACCA 1023 TGGTCCTG GGCTAGCTACAACGA GCCCTGAG 2724 4565 CAGGGCAC G CAGGACCA 1023 TGGTCCTG GGCTAGCTACAACGA GCCCTGAG 2725 4570 CACGCAGG A CCAGUUUG 1024 CAAACTGG GGCTAGCTACAACGA CCTGCGTG 2726 4574 CAGGACCA G UUUGAUUG 1025 CAATCAAA GGCTAGCTACAACGA TGGTCCTG 2726 4575 CCAGUUUG A UUGAGGAG 1026 CTCCTCAA GGCTAGCTACAACGA TGGTCCTG 2727 4579 CCAGUUUG A UUGAGGAG 1026 CTCCTCAA GGCTAGCTACAACGA CAAACTGG 2728 4587 AUUGAGGA G CUGCACUG 1028 GATCAGTG GGCTAGCTACAACGA AGCTCCTC 2730 4590 GAGGAGCU G CACUGAUC 1028 GATCAGT GGCTAGCTACAACGA CAAACTGG 2728 4590 GAGGAGCU G CACUGAUC 1028 GATCAGT GGCTAGCTACAACGA AGCTCCTC 2730 4592 GGAGCUGC A CUGAUCAC 1029 GTGATCAG GGCTAGCTACAACGA AGCTCCTC 2731 4596 CUGCACUG A UCACCCAA 1030 TTGGGTGA GGCTAGCTACAACGA GAGCTCC 2731 4596 CUGCACUG A UCACCCAA 1030 TTGGGTGA GGCTAGCTACAACGA GATCAGTG 2732 4599 CACUGAUC A CCCAAUGC 1031 GCATTGGG GGCTAGCTACAACGA GATCAGTG 2733 4604 AUCACCCA A UGCAUCAC 1032 GTGATCAC GGCTAGCTACAACGA AGTGCAG 2732 4606 CACCCAAUG C AUCACGU 1033 ACGTGATG GGCTAGCTACAACGA ATTGGGTG 2735 4608 CCCAAUGC A UCACCUAC 1034 GTACGTGA GGCTAGCAACCAA ATTGGGTG 2735 4601 AUCACCCA A UGCAUCAC 1034 GTACGTGA GGCTACCAACGA GATCAGTG 2735 4601 AUCACCCA A UGCAUCAC 1034 GTACGTGA GGCTACCAACGA GATCAGTA 2734 4601 AUCACCAA AGCAUCAC 1035 GGGGTACGAACGA GATGCAT 2735	4500	GUUACUCA G UGUUAGAG	1011	CTCTAACA GGCTAGCTACAACGA TGAGTAAC	2713
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4538 ACUUCCCU G CUCCAACC 1017 GGTTGGAG GGCTAGCTACAACGA AGGGAAGT 2719 4544 CUGCUCCA A CCCCGGC 1018 GGCGGGGG GGCTAGCTACAACGA TGGAGCAG 2720 4550 CAACCCCC G CCACCUCA 1019 TGAGGTGG GGCTAGCTACAACGA GGGGGTTG 2721 4553 CCCCCGGC A CCUCAGGG 1020 CCCTGAGG GGCTAGCTACAACGA GGCGGGGG 2722 4561 ACCUCAGG G CACGCAGG 1021 CCTGCGTG GGCTAGCTACAACGA GCCGGGGG 2722 4563 CUCAGGGC A CGCAGGAC 1022 GTCCTGCG GGCTAGCTACAACGA GCCCTGAGG 2724 4565 CAGGGCAC G CAGGACCA 1023 TGGTCCTG GGCTAGCTACAACGA GCCCTGAG 2724 4565 CAGGGCAC G CAGGACCA 1023 TGGTCCTG GGCTAGCTACAACGA GTGCCCTG 2725 4570 CACGCAGG A CCAGUUUG 1024 CAAACTGG GGCTAGCTACAACGA CCTGCGTG 2726 4574 CAGGACCA G UUUGAUUG 1025 CAATCAAA GGCTAGCTACAACGA TGGTCCTG 2727 4579 CCAGUUUG A UUGAGGAG 1026 CTCCTCAA GGCTAGCTACAACGA TGGTCCTG 2728 4587 AUUGAGGA G CUGCACUG 1027 CAGTGCAG GGCTAGCTACAACGA CAAACTGG 2728 4590 GAGGAGCU G CACUGAUC 1028 GATCAGTG GGCTAGCTACAACGA AGCTCCTC 2730 4592 GGAGCUGC A CUGAUCAC 1029 GTGATCAG GGCTAGCTACAACGA AGCTCCTC 2731 4596 CUGCACUG A UCACCCAA 1030 TTGGGTGA GGCTAGCTACAACGA CAGTGCAG 2732 4599 CACUGAUC A CCCAAUGC 1031 GCATTGGG GGCTAGCTACAACGA CAGTGCAG 2732 4599 CACUGAUC A CCCAAUGC 1031 GCATTGGG GGCTAGCTACAACGA GATCAGTG 2733 4604 AUCACCCA A UGCAUCAC 1032 GTGATGCA GGCTAGCTACAACGA GATCAGTG 2734 4606 CACCCAAU G CAUCACCU 1033 ACGTGATG GGCTAGCTACAACGA ATTGGGTO 2735 4608 CCCAAUGC A UCACCCCC 1035 GGGTTACG GGCTAGCTACAACGA GATCAGTG 2735 4608 CCCCAAUGC A UCACCCCC 1035 GGGTTACG GGCTAGCTACAACGA GATCGGT 2736 4611 AAUGCAUC A CGUACCCC 1035 GGGTTACG GGCTAGCTACAACGA GATCGGT 2736	4527	UAAACCCA A UGACUUCC	1015	GGAAGTCA GGCTAGCTACAACGA TGGGTTTA	2717
4544 CUGCUCCA A CCCCCGCC 1018 GGCGGGGG GGCTAGCTACAACGA TGGAGCAG 2720 4550 CAACCCCC G CCACCUCA 1019 TGAGGTGG GGCTAGCTACAACGA GGGGGTTG 2721 4553 CCCCGGCC A CCUCAGGG 1020 CCCTGAGG GGCTAGCTACAACGA GGCGGGG 2722 4561 ACCUCAGG G CACGCAGG 1021 CCTGCGTG GGCTAGCTACAACGA CCTGAGGT 2723 4563 CUCAGGGC A CGCAGGAC 1022 GTCCTGCG GGCTAGCTACAACGA CCTGAGGT 2724 4565 CAGGGCAC G CAGGACCA 1023 TGGTCCTG GGCTAGCTACAACGA GTCCCTG 2725 4570 CACGCAGG A CCAGUUUG 1024 CAAACTGG GGCTAGCTACAACGA CCTGCGTG 2726 4574 CAGGACCA G UUUGAUUG 1025 CAATCAAA GGCTAGCTACAACGA TGGTCCTG 2727 4579 CCAGUUUG A UUGAGGAG 1026 CTCCTCAA GGCTAGCTACAACGA CAAACTGG 2728 4587 AUUGAGGA G CUGCACUG 1027 CAGTGCAG GGCTAGCTACAACGA TCCTCAAT 2729 4590 GAGGAGCU G CACUGAUC 1028 GATCAGTG GGCTAGCTACAACGA AGCTCCC 2730 4592 GGAGCUGC A CUGAUCAC 1029 GTGATCAG GGCTAGCTACAACGA AGCTCCC 2731 4596 CUGCACUG A UCACCCAA 1030 TTGGGTGA GGCTAGCTACAACGA CAGTGCAG 2732 4599 CACUGAUC A CCCAAUGC 1031 GCATTGGG GGCTAGCTACAACGA CAGTGCAG 2732 4599 CACUGAUC A CCCAAUGC 1031 GCATTGGG GGCTAGCTACAACGA CAGTGCAG 2732 4604 AUCACCCA A UGCAUCAC 1032 GTGATGCA GGCTAGCTACAACGA GATCAGTG 2733 4604 AUCACCCA A UGCAUCAC 1033 ACGTGATG GGCTAGCTACAACGA ATTGGGTG 2733 4606 CACCCAAU G CAUCACGU 1033 ACGTGATG GGCTAGCTACAACGA ATTGGGTG 2735 4608 CCCAAUGC A UCACCCU 1033 ACGTGATG GGCTAGCTACAACGA GATCAGTG 2736 4611 AAUGCAUC A CGUACCCC 1035 GGGGTAGCTACAACGA GATCAGTG 2736	4530	ACCCAAUG A CUUCCCUG	1016	CAGGGAAG GGCTAGCTACAACGA CATTGGGT	2718
4550 CAACCCC G CCACCUCA 1019 TGAGGTGG GGCTAGCTACAACGA GGGGGTTG 2721 4553 CCCCCGCC A CCUCAGGG 1020 CCCTGAGG GGCTAGCTACAACGA GGCGGGGG 2722 4561 ACCUCAGG G CACGCAGG 1021 CCTGCGTG GGCTAGCTACAACGA CCTGAGGT 2723 4563 CUCAGGGC A CGCAGGAC 1022 GTCCTGCG GGCTAGCTACAACGA GCCCTGAG 2724 4565 CAGGGCAC G CAGGACCA 1023 TGGTCCTG GGCTAGCTACAACGA GTGCCCTG 2725 4570 CACGCAGG A CCAGUUUG 1024 CAAACTGG GGCTAGCTACAACGA CCTGCGTG 2726 4574 CAGGACCA G UUUGAUUG 1025 CAATCAAA GGCTAGCTACAACGA TGGTCCTG 2727 4579 CCAGUUUG A UUGAGGAG 1026 CTCCTCAA GGCTAGCTACAACGA CAAACTGG 2728 4587 AUUGAGGA G CUGCACUG 1027 CAGTGCAG GGCTAGCTACAACGA TCCTCAAT 2729 4590 GAGGAGCU G CACUGAUC 1028 GATCAGTG GGCTAGCTACAACGA AGCTCCTC 2730 4592 GGAGCUGC A CUGAUCAC 1029 GTGATCAG GGCTAGCTACAACGA GAGCTCCC 2731 4596 CUGCACUG A UCACCCAA 1030 TTGGGTGA GGCTAGCTACAACGA CAGTGCAG 2732 4599 CACUGAUC A CCCAAUGC 1031 GCATTGGG GGCTAGCTACAACGA GATCAGTG 2733 4604 AUCACCCA A UGCAUCAC 1032 GTGATGCA GGCTAGCTACAACGA GATCAGTG 2734 4606 CACCCAAUG CAUCACGU 1033 ACGTGATG GGCTAGCTACAACGA ATTGGGTG 2735 4608 CCCCAAUGC A UCACGUAC 1034 GTACGTG GGCTAGCTACAACGA GATCAGTG 2736 4611 AAUGCAUC A CGUACCCC 1035 GGGGTACG GGCTAGCTACAACGA GATTGGGT 2736	4538	ACUUCCCU G CUCCAACC	1017	GGTTGGAG GGCTAGCTACAACGA AGGGAAGT	2719
4553 CCCCGGC A CCUCAGGG 1020 CCCTGAGG GGCTAGCTACAACGA GGCGGGGG 2722 4561 ACCUCAGG G CACGCAGG 1021 CCTGCGTG GGCTAGCTACAACGA CCTGAGGT 2723 4563 CUCAGGGC A CGCAGGAC 1022 GTCCTGCG GGCTAGCTACAACGA CCTGAGG 2724 4565 CAGGGCAC G CAGGACCA 1023 TGGTCCTG GGCTAGCTACAACGA GTCCCTG 2725 4570 CACGCAGG A CCAGUUUG 1024 CAAACTGG GGCTAGCTACAACGA CCTGCGTG 2726 4574 CAGGACCA G UUUGAUUG 1025 CAATCAAA GGCTAGCTACAACGA TGGTCCTG 2727 4579 CCAGUUUG A UUGAGGAG 1026 CTCCTCAA GGCTAGCTACAACGA TGGTCCTG 2727 4587 AUUGAGGA G CUGCACUG 1027 CAGTGCAG GGCTAGCTACAACGA TCCTCAAT 2729 4590 GAGGAGCU G CACUGAUC 1028 GATCAGTG GGCTAGCTACAACGA AGCTCCTC 2730 4592 GGAGCUGC A CUGAUCAC 1029 GTGATCAG GGCTAGCTACAACGA AGCTCCTC 2731 4596 CUGCACUG A UCACCCAA 1030 TTGGGTGA GGCTAGCTACAACGA CAGTGCAG 2732 4599 CACUGAUC A CCCAAUGC 1031 GCATTGGG GGCTAGCTACAACGA GATCAGTG 2733 4604 AUCACCCA A UGCAUCAC 1032 GTGATGCA GGCTAGCTACAACGA GATCAGTG 2734 4606 CACCCAAU G CAUCACCU 1033 ACGTGATG GGCTAGCTACAACGA ATTGGGTG 2735 4608 CCCAAUGC A UCACGUAC 1034 GTACGTGA GGCTAGCTACAACGA ATTGGGTG 2736 4611 AAUGCAUC A CGUACCCC 1035 GGGGTACC GGCTAGCTACAACGA GATCAGTG 2736	4544	CUGCUCCA A CCCCCGCC	1018	GGCGGGGG GGCTAGCTACAACGA TGGAGCAG	2720
4561 ACCUCAGG G CACGCAGG 1021 CCTGCGTG GGCTAGCTACAACGA CCTGAGGT 2723 4563 CUCAGGGC A CGCAGGAC 1022 GTCCTGCG GGCTAGCTACAACGA GCCCTGAG 2724 4565 CAGGGCAC G CAGGACCA 1023 TGGTCCTG GGCTAGCTACAACGA GTCCCTG 2725 4570 CACGCAGG A CCAGUUUG 1024 CAAACTGG GGCTAGCTACAACGA CCTGCGTG 2726 4574 CAGGACCA G UUUGAUUG 1025 CAATCAAA GGCTAGCTACAACGA TGGTCCTG 2727 4579 CCAGUUUG A UUGAGGAG 1026 CTCCTCAA GGCTAGCTACAACGA CAAACTGG 2728 4587 AUUGAGGA G CUGCACUG 1027 CAGTGCAG GGCTAGCTACAACGA CAAACTGG 2728 4590 GAGGAGCU G CACUGAUC 1028 GATCAGTG GGCTAGCTACAACGA AGCTCCTC 2730 4592 GGAGCUGC A CUGAUCAC 1029 GTGATCAG GGCTAGCTACAACGA GCAGCTCC 2731 4596 CUGCACUG A UCACCCAA 1030 TTGGGTGA GGCTAGCTACAACGA CAGTGCAG 2732 4599 CACUGAUC A CCCAAUGC 1031 GCATTGGG GGCTAGCTACAACGA GATCAGTG 2733 4604 AUCACCCA A UGCAUCAC 1032 GTGATGCA GGCTAGCTACAACGA GATCAGTG 2734 4606 CACCCAAU G CAUCACC 1033 ACGTGATG GGCTAGCTACAACGA ATTGGGTG 2735 4608 CCCAAUGC A UCACGUAC 1034 GTACGTGA GGCTAGCTACAACGA ATTGGGTG 2736 4611 AAUGCAUC A CGUACCCC 1035 GGGGTACC GGCTAGCTACAACGA GATTGGGT 2737	4550	CAACCCCC G CCACCUCA	1019	TGAGGTGG GGCTAGCTACAACGA GGGGGTTG	2721
4563 CUCAGGGC A CGCAGGAC 1022 GTCCTGCG GGCTAGCTACAACGA GCCCTGAG 2724 4565 CAGGGCAC G CAGGACCA 1023 TGGTCCTG GGCTAGCTACAACGA GTGCCTG 2725 4570 CACGCAGG A CCAGUUUG 1024 CAAACTGG GGCTAGCTACAACGA CCTGCGTG 2726 4574 CAGGACCA G UUUGAUUG 1025 CAATCAAA GGCTAGCTACAACGA TGGTCCTG 2727 4579 CCAGUUUG A UUGAGGAG 1026 CTCCTCAA GGCTAGCTACAACGA CAAACTGG 2728 4587 AUUGAGGA G CUGCACUG 1027 CAGTGCAG GGCTAGCTACAACGA TCCTCAAT 2729 4590 GAGGAGCU G CACUGAUC 1028 GATCAGTG GGCTAGCTACAACGA AGCTCCTC 2730 4592 GGAGCUGC A CUGAUCAC 1029 GTGATCAG GGCTAGCTACAACGA GCAGCTCC 2731 4596 CUGCACUG A UCACCCAA 1030 TTGGGTGA GGCTAGCTACAACGA CAGTGCAG 2732 4599 CACUGAUC A CCCAAUGC 1031 GCATTGGG GGCTAGCTACAACGA GATCAGTG 2733 4604 AUCACCCA A UGCAUCAC 1032 GTGATGCA GGCTAGCTACAACGA GATCAGTG 2734 4606 CACCCAAU G CAUCACGU 1033 ACGTGATG GGCTAGCTACAACGA ATTGGGTG 2735 4608 CCCAAUGC A UCACGUAC 1034 GTACGTGA GGCTAGCTACAACGA GCATTGGG 2736 4611 AAUGCAUC A CGUACCCC 1035 GGGGTACG GGCTAGCTACAACGA GATGCATT 2737	4553	CCCCCGCC A CCUCAGGG	1020	CCCTGAGG GGCTAGCTACAACGA GGCGGGGG	2722
4565 CAGGGCAC G CAGGACCA 1023 TGGTCCTG GGCTAGCTACAACGA GTGCCCTG 2725 4570 CACGCAGG A CCAGUUUG 1024 CAAACTGG GGCTAGCTACAACGA CCTGCGTG 2726 4574 CAGGACCA G UUUGAUUG 1025 CAATCAAA GGCTAGCTACAACGA TGGTCCTG 2727 4579 CCAGUUUG A UUGAGGAG 1026 CTCCTCAA GGCTAGCTACAACGA CAAACTGG 2728 4587 AUUGAGGA G CUGCACUG 1027 CAGTGCAG GGCTAGCTACAACGA TCCTCAAT 2729 4590 GAGGAGCU G CACUGAUC 1028 GATCAGTG GGCTAGCTACAACGA AGCTCCTC 2730 4592 GGAGCUGC A CUGAUCAC 1029 GTGATCAG GGCTAGCTACAACGA GCAGCTCC 2731 4596 CUGCACUG A UCACCCAA 1030 TTGGGTGA GGCTAGCTACAACGA CAGTGCAG 2732 4599 CACUGAUC A CCCAAUGC 1031 GCATTGGG GGCTAGCTACAACGA GATCAGTG 2733 4604 AUCACCCA A UGCAUCAC 1032 GTGATGCA GGCTAGCTACAACGA TGGGTGAT 2734 4606 CACCCAAU G CAUCACGU 1033 ACGTGATG GGCTAGCTACAACGA ATTGGGTG 2735 4608 CCCAAUGC A UCACGUAC 1034 GTACGTGA GGCTAGCTACAACGA GCATTGGG 2736 4611 AAUGCAUC A CGUACCCC 1035 GGGGTACG GGCTAGCTACAACGA GATGCATT 2737	4561	ACCUCAGG G CACGCAGG	1021	CCTGCGTG GGCTAGCTACAACGA CCTGAGGT	2723
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4574 CAGGACCA G UUUGAUUG 1025 CAATCAAA GGCTAGCTACAACGA TGGTCCTG 2727 4579 CCAGUUUG A UUGAGGAG 1026 CTCCTCAA GGCTAGCTACAACGA CAAACTGG 2728 4587 AUUGAGGA G CUGCACUG 1027 CAGTGCAG GGCTAGCTACAACGA TCCTCAAT 2729 4590 GAGGAGCU G CACUGAUC 1028 GATCAGTG GGCTAGCTACAACGA AGCTCCTC 2730 4592 GGAGCUGC A CUGAUCAC 1029 GTGATCAG GGCTAGCTACAACGA GCAGCTCC 2731 4596 CUGCACUG A UCACCCAA 1030 TTGGGTGA GGCTAGCTACAACGA CAGTGCAG 2732 4599 CACUGAUC A CCCAAUGC 1031 GCATTGGG GGCTAGCTACAACGA GATCAGTG 2733 4604 AUCACCCA A UGCAUCAC 1032 GTGATGCA GGCTAGCTACAACGA TGGGTGAT 2734 4606 CACCCAAU G CAUCACGU 1033 ACGTGATG GGCTAGCTACAACGA ATTGGGTG 2735 4608 CCCAAUGC A UCACGUAC 1034 GTACGTGA GGCTAGCTACAACGA GCATTGGG 2736 4611 AAUGCAUC A CGUACCCC 1035 GGGGTACG GGCTAGCTACAACGA GATGCATT 2737	4565	CAGGGCAC G CAGGACCA	1023	TGGTCCTG GGCTAGCTACAACGA GTGCCCTG	2725
4579 CCAGUUUG A UUGAGGAG 1026 CTCCTCAA GGCTAGCTACAACGA CAAACTGG 2728 4587 AUUGAGGA G CUGCACUG 1027 CAGTGCAG GGCTAGCTACAACGA TCCTCAAT 2729 4590 GAGGAGCU G CACUGAUC 1028 GATCAGTG GGCTAGCTACAACGA AGCTCCTC 2730 4592 GGAGCUGC A CUGAUCAC 1029 GTGATCAG GGCTAGCTACAACGA GCAGCTCC 2731 4596 CUGCACUG A UCACCCAA 1030 TTGGGTGA GGCTAGCTACAACGA CAGTGCAG 2732 4599 CACUGAUC A CCCAAUGC 1031 GCATTGGG GGCTAGCTACAACGA GATCAGTG 2733 4604 AUCACCCA A UGCAUCAC 1032 GTGATGCA GGCTAGCTACAACGA GATCAGTG 2734 4606 CACCCAAU G CAUCACGU 1033 ACGTGATG GGCTAGCTACAACGA ATTGGGTG 2735 4608 CCCCAAUGC A UCACGUAC 1034 GTACGTGA GGCTAGCTACAACGA GCATTGGG 2736 4611 AAUGCAUC A CGUACCCC 1035 GGGGTACG GGCTAGCTACAACGA GATGCATT 2737	4570	CACGCAGG A CCAGUUUG	1024	CAAACTGG GGCTAGCTACAACGA CCTGCGTG	2726
4587 AUUGAGGA G CUGCACUG 1027 CAGTGCAG GGCTAGCTACAACGA TCCTCAAT 2729 4590 GAGGAGCU G CACUGAUC 1028 GATCAGTG GGCTAGCTACAACGA AGCTCCTC 2730 4592 GGAGCUGC A CUGAUCAC 1029 GTGATCAG GGCTAGCTACAACGA GCAGCTCC 2731 4596 CUGCACUG A UCACCCAA 1030 TTGGGTGA GGCTAGCTACAACGA CAGTGCAG 2732 4599 CACUGAUC A CCCAAUGC 1031 GCATTGGG GGCTAGCTACAACGA GATCAGTG 2733 4604 AUCACCCA A UGCAUCAC 1032 GTGATGCA GGCTAGCTACAACGA TGGGTGAT 2734 4606 CACCCAAU G CAUCACGU 1033 ACGTGATG GGCTAGCTACAACGA ATTGGGTG 2735 4608 CCCAAUGC A UCACGUAC 1034 GTACGTGA GGCTAGCTACAACGA GCATTGGG 2736 4611 AAUGCAUC A CGUACCCC 1035 GGGGTACG GGCTAGCTACAACGA GATGCATT 2737	4574	CAGGACCA G UUUGAUUG	1025	CAATCAAA GGCTAGCTACAACGA TGGTCCTG	2727
4590 GAGGAGCU G CACUGAUC 1028 GATCAGTG GGCTAGCTACAACGA AGCTCCTC 2730 4592 GGAGCUGC A CUGAUCAC 1029 GTGATCAG GGCTAGCTACAACGA GCAGCTCC 2731 4596 CUGCACUG A UCACCCAA 1030 TTGGGTGA GGCTAGCTACAACGA CAGTGCAG 2732 4599 CACUGAUC A CCCAAUGC 1031 GCATTGGG GGCTAGCTACAACGA GATCAGTG 2733 4604 AUCACCCA A UGCAUCAC 1032 GTGATGCA GGCTAGCTACAACGA TGGGTGAT 2734 4606 CACCCAAU G CAUCACGU 1033 ACGTGATG GGCTAGCTACAACGA ATTGGGTG 2735 4608 CCCAAUGC A UCACGUAC 1034 GTACGTGA GGCTAGCTACAACGA GCATTGGG 2736 4611 AAUGCAUC A CGUACCCC 1035 GGGGTACG GGCTAGCTACAACGA GATGCATT 2737	4579	CCAGUUUG A UUGAGGAG	1026	CTCCTCAA GGCTAGCTACAACGA CAAACTGG	2728
4592 GGAGCUGC A CUGAUCAC 1029 GTGATCAG GGCTAGCTACAACGA GCAGCTCC 2731 4596 CUGCACUG A UCACCCAA 1030 TTGGGTGA GGCTAGCTACAACGA CAGTGCAG 2732 4599 CACUGAUC A CCCAAUGC 1031 GCATTGGG GGCTAGCTACAACGA GATCAGTG 2733 4604 AUCACCCA A UGCAUCAC 1032 GTGATGCA GGCTAGCTACAACGA TGGGTGAT 2734 4606 CACCCAAU G CAUCACGU 1033 ACGTGATG GGCTAGCTACAACGA ATTGGGTG 2735 4608 CCCAAUGC A UCACGUAC 1034 GTACGTGA GGCTAGCTACAACGA GCATTGGG 2736 4611 AAUGCAUC A CGUACCCC 1035 GGGGTACG GGCTAGCTACAACGA GATGCATT 2737	4587	AUUGAGGA G CUGCACUG	1027	CAGTGCAG GGCTAGCTACAACGA TCCTCAAT	2729
4596 CUGCACUG A UCACCCAA 1030 TTGGGTGA GGCTAGCTACAACGA CAGTGCAG 2732 4599 CACUGAUC A CCCAAUGC 1031 GCATTGGG GGCTAGCTACAACGA GATCAGTG 2733 4604 AUCACCCA A UGCAUCAC 1032 GTGATGCA GGCTAGCTACAACGA TGGGTGAT 2734 4606 CACCCAAU G CAUCACGU 1033 ACGTGATG GGCTAGCTACAACGA ATTGGGTG 2735 4608 CCCAAUGC A UCACGUAC 1034 GTACGTGA GGCTAGCTACAACGA GCATTGGG 2736 4611 AAUGCAUC A CGUACCCC 1035 GGGGTACG GGCTAGCTACAACGA GATGCATT 2737	4590	GAGGAGCU G CACUGAUC	1028	GATCAGTG GGCTAGCTACAACGA AGCTCCTC	2730
4599 CACUGAUC A CCCAAUGC 1031 GCATTGGG GGCTAGCTACAACGA GATCAGTG 2733 4604 AUCACCCA A UGCAUCAC 1032 GTGATGCA GGCTAGCTACAACGA TGGGTGAT 2734 4606 CACCCAAU G CAUCACGU 1033 ACGTGATG GGCTAGCTACAACGA ATTGGGTG 2735 4608 CCCAAUGC A UCACGUAC 1034 GTACGTGA GGCTAGCTACAACGA GCATTGGG 2736 4611 AAUGCAUC A CGUACCCC 1035 GGGGTACG GGCTAGCTACAACGA GATGCATT 2737	4592	GGAGCUGC A CUGAUCAC	1029	GTGATCAG GGCTAGCTACAACGA GCAGCTCC	2731
4604 AUCACCCA A UGCAUCAC 1032 GTGATGCA GGCTAGCTACAACGA TGGGTGAT 2734 4606 CACCCAAU G CAUCACGU 1033 ACGTGATG GGCTAGCTACAACGA ATTGGGTG 2735 4608 CCCAAUGC A UCACGUAC 1034 GTACGTGA GGCTAGCTACAACGA GCATTGGG 2736 4611 AAUGCAUC A CGUACCCC 1035 GGGGTACG GGCTAGCTACAACGA GATGCATT 2737	4596	CUGCACUG A UCACCCAA	1030	TTGGGTGA GGCTAGCTACAACGA CAGTGCAG	2732
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4606 CACCCAAU G CAUCACGU 1033 ACGTGATG GGCTAGCTACAACGA ATTGGGTG 2735 4608 CCCAAUGC A UCACGUAC 1034 GTACGTGA GGCTAGCTACAACGA GCATTGGG 2736 4611 AAUGCAUC A CGUACCCC 1035 GGGGTACG GGCTAGCTACAACGA GATGCATT 2737	4604	AUCACCCA A UGCAUCAC	1032	GTGATGCA GGCTAGCTACAACGA TGGGTGAT	2734
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ACTO TOTAL CONTROL OF THE CONTROL OF	4611	AAUGCAUC A CGUACCCC	1035		
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4615 CAUCACUU A CCCCACUU 1037 TGGCCCAG GCTTAGCTACACAGA ACGTEART 2739 4629 CUGACCCA CUGGGCA 1040 TGGCCAG GCTTAGCTACACAGA GGGGTAGG 2744 4629 CUGGCCCU G CAGCCCU 1039 AGGGCTGG GGCTAGCTACACAGA GGGGGTGG 2744 4629 CUGGCCCU G CAGCCCAA 1041 TGGGGGG GGCTAGCTACACGA TGGCCCAG 2742 4634 CCAGCCCU G CAGCCCAA 1041 TGGGGGG GGCTAGCTACACGA TGGCCAGG 2744 4647 AGCCCAAA A CCCAGGGC 1043 GCCTGGG GGCTAGCTACACGA TGGCAGGG 2744 4648 AGCCCAAA A CCCAGGGC 1043 GCCTGGG GGCTAGCTACAACGA TGCCAGGC 2744 4644 AGCCCAAA A CCCAGGGC 1044 GCTTGTG GGCTAGCTACAACGA TTGGGGC 2745 4651 AACCCAGG G CAACAACC 1042 GCTTGTG GGCTAGCTACAACGA TTGGGGC 2746 4652 ACAGGCCA A CAAGCCCG 1045 GCGGGTG GGCTAGCTACAACGA TTGGGCT 2746 4654 CCAGGGCA A CAAGCCCG 1045 GCGGGTTG GGCTAGCTACAACGA TGCCAGGC 2747 4666 CCCGUUA G CCCCAGGG 1045 CGGGCTG GGCTAGCTACAACGA TGCCACGG 2747 4666 CCCGUUA G CCCCAGGG 1048 CCTGGGG GGCTAGCTACAACGA TGCCCTGG 2754 4666 CCCCGUUA G CCCCAGGG 1049 GCCAGTGA GGCTAGCTACAACGA TGACCGCG 2754 4667 ACGAGGG A CAAGCCCG 1049 GCCAGTGA GGCTAGCTACAACGA TGACCGCG 2750 4679 AGGGGAUC A CUGGCCUG 1051 CCAGCCAG GGCTAGCTACAACGA CACCCCT 2752 4681 AGUCACUG G CUGGCCUG 1051 CAGCCAG GGCTAGCTACAACGA CACCCCT 2752 4683 GAUCACUG G CUGGCCUG 1051 CAGCCAG GGCTAGCTACAACGA CACCCACT 2754 4687 ACUGGCUG G CAACAUCU 1053 AGATGTTG GGCTAGCTACAACGA TCAGGCAC 2754 4698 UGAGCAAC A CUUCGGG 1051 CAGGCCAG GGCTAGCTACAACGA CACCACT 2754 4699 UGAGCAAC A CUUCGGG 1051 CAGGCCAG GGCTAGCTACAACGA CACCACT 2754 4719 UCUCAGGA G UCUCUGG 1051 CAGGCCAG GGCTAGCTACAACGA TCAGGCA 2756 4719 CUCACCAG G CAACAUCU 1053 AGATGTTC GGCTAGCTACAACGA TCAGGCA 2756 4719 CUCACCAG G CAACAUCU 1053 AGATGTTC GGCTAGCTACAACGA TCAGGCA 2756 4719 CUCACCAG G CAACAUCU 1053 AGATGTTC GGCTAGCTACAACGA TCAGCAC 2756 4719 UCUCAGGA G UCCCUAA 1055 TCCCCAG GGCTAGCTACAACGA TCGCTACT 2756 4719 UCUCAGGA G UCCCUAA 1055 TCCCCAG GGCTAGCTACAACGA TCGCTACT 2756 4719 UCUCACGA G UCCCUAA 1057 TAGGCCT GGCTAGCTACAACGA TCGCTACT 2756 4719 UCUACCAG G CUCAGAGC 1058 GCTAGCTACAACGA TCGCTACA 2757 4719 UUAAGACA A CAUCUGG 1056 CTAGCTACAGCA GCTAGCTACAACGA TCTCTTAG 2766 4719 CAACAGC A CAUCUGA 105					
4625 CCCACUGG G CCAGCCCU 1039 AGGGCTGG GGCTAGCTACAACGA CCAGTGGG 2741 4629 UGGGCCA G CCCUGCAG 1040 CTGCAGGG GGCTAGCTACAACGA TGGCCCAG 2742 4634 CAGCCCU G CACCAAAC 1041 TGGGGCTG GGCTAGCTACAACGA TGGCCCAG 2742 4637 GCCCUGCA G CCCAAAC 1042 GTTTTGGG GGCTAGCTACAACGA TGGCGGG 2744 4644 AGCCCAAA A CCCAGGGG 1043 GCCTGGGG GGCTAGCTACAACGA TGCAGGGC 2744 4651 AACCCAGG G CAACAAC 1042 GTTTTGGG GGCTAGCTACAACGA TGCAGGGC 2745 4652 ACACCAGG C AACAACC 1044 GCTTGTTG GGCTAGCTACAACGA TGCCTGG 2747 4653 GGCAACAA C ACACGAGC 1045 CGGGGTTG GGCTAGCTACAACGA TGCCTGG 2747 4658 GGCAACAA C ACACGCC 1047 GGGGCTAG GGCTAGCTACAACGA TGCCTGG 2747 4659 GGCAACAA C CCCGUUAG 1046 CTAACGGG GGCTAGCTACAACGA TGCCTGG 2746 4662 ACAAGCCC G UUAGCCCC 1047 GGGGCTAG GGCTAGCTACAACGA TGCCTGG 2749 4662 ACAAGCCC G UUAGCCCC 1047 GGGGCTAG GGCTAGCTACAACGA TAACGGGC 2750 4663 GCCCGUUA G CCCCAGGG 1048 CCCTGGG GGCTAGCTACAACGA TAACGGGC 2750 4676 CCCAGGGG A UCACUGGC 1049 GCCAGTGA GGCTAGCTACAACGA TAACGGGC 2751 4663 GAUCACUG G CUGAGCCA 1051 CAGCCAG GGCTAGCTACAACGA CCCCTGGG 2751 4663 GAUCACUG G CUGAGCCA 1052 TGCTCAGG GGCTAGCTACAACGA CACCCAT 2752 4663 GAUCACUG G CUGAGCCA 1052 TGCTCAGG GGCTAGCTACAACGA CACCCAT 2754 4663 UGGCCUG G CUGAGCCA 1052 TGCTCAGG GGCTAGCTACAACGA CACCCAT 2754 4669 UGGCCUG G CUCAGACC 1053 AGATGTTG GGCTAGCTACAACGA CACCCAT 2754 4669 UGGCCUG G CUCAGACC 1053 AGATGTTG GGCTAGCTACAACGA TGCGCCAG 2755 4669 UGGCCUAG G CACCAGCC 1055 AGATGTTC GGCTAGCTACAACGA TGCGCCAG 2755 4669 UGGCCUAG G CUCAGAC 1055 CTAGAGGA GGCTAGCTACAACGA TCGCCAGC 2756 4670 UCUCAGGA G CUCUCAG 1055 CTAGAGGA GGCTAGCTACAACGA TCGCCAGC 2756 4770 UCUCAGGA G CUCUCAG 1055 CTAGAGGA GGCTAGCTACAACGA TCGCCAGC 2757 4770 UCUCAGGA G CUCAGAC 1055 CTAGAGGA GGCTAGCTACAACGA TCGCCAGC 2757 4771 UCUCAGGA G CCUAAGAC 1057 TAGGCC GGCTAGCTACAACGA TCGCCAGC 2757 4771 UCUCAGCAG G CUCAAGAC 1058 CTAGAGGA GGCTAGCTACAACGA TCGCCAG 2757 4771 UCUCAGGA G CUCAAGAC 1058 CTAGAGGA GGCTAGCTACAACGA TCGCCAG 2757 4772 UCUCAGGA A CAUGUGGA 1059 CTACATG GGCTAGCTACAACGA TCGCCAG 2757 4773 UAAGACAA C UAUGAGGA 1059 CTACATG GGCTAGCTACAACGA TCGCTAC 2757 4773 UAA	4615	CAUCACGU A CCCCACUG	1037	CAGTGGGG GGCTAGCTACAACGA ACGTGATG	2739
4629 CUGGGCCA G CCCUGCAG 1040 CTGCAGGG GGCTAGCTACAACGA TGGCCCAG 2742 4634 CCAGCCCU G CAGCCCAA 1041 TTGGGCTG GCCTAGCTACAACAG AGGGCTGG 2743 46374 CCCCUGCA G CCCAAAAC 1042 GTTTGGG GGCTAGCTACAACAG AGGGCTGG 2743 4644 AGCCCAAA A CCCAGGGC 1043 GCCTGGG GGCTAGCTACAACAG TTTGGGCT 2745 4654 CAGAGGCG CAACAACC 1044 GCTTGTTG GGCTAGCTACAACAG TTTGGGCT 2746 4651 AACCCAGG G CAACAACC 1045 GGGGTTG GGCTAGCTACAACAG TTGGCCTG 2746 4652 ACAAGCCC G UUAGCCCC 1045 GGGGTTG GGCTAGCTACAACAG TTGTGCC 2748 4653 GGCACAA G CCCGUUAG 1046 CTAACGGG GGCTAGCTACAACAG TTGTGCC 2748 4656 GCCCGUUA G CCCCGUGG 1047 GGGGCTAA GGCTACAACAG TTGTGCC 2749 4656 GCCCGUUA G CCCCAGGG 1048 CCCTGGG GGCTTAGCTACAACAG TACAGGC 2749 4657 AGGGGALA G CCCCGGGG 1049 GCCAGTGA GGCTAGCACACAG TACAGGCC 2752 4679 AGGGGALA C CUGGCUGG 1049 GCCAGTGA GGCTAGCACACAG TACAGGCC 2752 4683 AGUCACUG G CUGGCCUG 1050 CAGGCCAG GGCTTAGCTACAACGA CAGCCAGT 2752 4684 ACUGCCUG G CUGGCCUG 1051 CAGGCCAG GGCTTAGCTACAACGA CAGCCAGT 2754 4685 ACUGCCUG G CUGGCCUG 1051 CAGGCCAG GGCTTAGCTACAACGA CAGCCAGT 2754 4687 ACUGGCUG G CUGGCCUG 1051 CAGGCCAG GGCTTAGCTACAACGA CAGCCAGT 2754 4689 UGACCUG G CUGGCCUG 1051 CAGGCCAG GGCTTAGCTACAACGA CAGCCAGT 2754 4699 UGAGCAAC A UCUCGGG 1051 CAGGCCAG GGCTTAGCTACAACGA CAGCCAGT 2754 4699 UGAGCAAC A UCUCGGGA 1055 TCCCGAGA GGCTTAGCTACAACGA TCCGCCAG 2755 4719 UCUCGGGA G CACAUCUG J 1054 CCGAGGAG GGCTTAGCTACAACGA TCCGCAG 2756 4719 UCUCGGGA G CACAUCUG J 1055 CCGAGGAG GGCTTAGCTACAACGA TCCGCAG 2756 4719 UCUCAGGA G CCUCAGGA 1055 CCGAGGC GGCTTAGCAACAG TCCCTAG 2756 4719 UCUCAGGA G UCUCCUGA 1055 CCGAGGC GGCTTAGCAACAGA TCCGCAG 2756 4719 UCUAGCAG G CUDAAGAC 1058 GCTAGGCTACAACGA TCCGCAG 2756 4719 UCUAGCAG A CAUCUGG 1057 CCCCTAG GGCTAGCTACAACGA TCCTAGGC 2756 4719 UCUAGCAG G CUDAAGAC 1058 GCTTAGCAG GGCTTACAACGA TCCTAGGC 2759 4719 UCUAGCAG A CAUCUGG 1057 CTCCCTAG GGCTAGCTACAACGA TCTCTAG 2756 4719 UCUAGCAG A CAUCUGG 1057 CTCCCTAG GGCTAGCTACAACGA TCTCTAG 2756 4719 UCUAGCAG A CAUCUGA 1059 CCCCCCC GGCCTAGCTACAACGA TCTCTTAG 2766 4719 CAGCACA UGAGAAG 1051 CCCCCCC GGCTAGCTACAACACA TCTCTTC 2766 4719 UAACACA C U	4620	CGUACCCC A CUGGGCCA	1038	TGGCCCAG GGCTAGCTACAACGA GGGGTACG	2740
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4651 AACCCAGG G CAACAAGC 1044 GCTTGTTG GGCTAGCTACAACGA CCTGGGTT 2746 4654 CCAGGGCA A CAAGCCCG 1045 CGGGCTTG GGCTAGCTACAACGA TGCCCTGG 2747 4656 GCAACAA G CCGUUMA 1046 CTAACGGG GGCTAGCTACAACGA TGCCCTGG 2748 4662 ACAAGCCC G UUAGCCCC 1047 GGGGCTAG GGCTAGCTACAACGA GTGCTCCC 2748 4666 GCCGGUUA G CCCCAGGG 1048 CCCTGGGG GGCTAGCTACAACGA GTGCTGCC 2748 4666 GCCGGUUA G CCCCAGGG 1049 CCCTGGGG GGCTAGCTACAACGA TAACGGGC 2750 4679 AGGGGAUC A CUGGCUG 1049 CCAGGCAG GGCTAGCTACAACGA CACTGGGC 2751 4679 AGGGGAUC A CUGGCUG 1051 CAGGCCAG GGCTAGCTACAACGA CACTGATC 2752 4683 GAUCACUG G CUGGCCUG 1051 CAGGCCAG GGCTAGCTACAACGA CACTGATC 2754 4683 AGUCACUG G CUGAGCCA 1052 TGCTCAGG GGCTAGCTACAACGA CACTGATC 2754 4683 UGGCCUG G CCUGAGCA 1052 TGCTCAGG GGCTAGCTACAACGA CACTGATC 2754 4693 UGGCCUG G CACACACCU 1053 AGATGTTG GGCTAGCTACAACGA CACGCACT 2754 4696 CCUGAGCA A CAUCUCGG 1054 CGGAGATG GGCTAGCTACAACGA TGCCCAT 2754 4697 UGUCGGGA A CAUCUCGG 1055 TCCCGAGA GGCTAGCTACAACGA TCCCGAGG 2756 4698 UGAGCAAC A UCUCGGG 1054 CGGAGAT GGCTAGCTACAACGA TCCCGAGG 2756 4698 UGAGCAAC A UCUCGGG 1055 TCCCGAGA GGCTAGCTACAACGA TCCCGAGA 2757 4707 UCUCGGGA G UCUCUCAG 1056 CTAGAGGA GGCTAGCTACAACGA TCCCGAGA 2757 4719 UCUCGGGA G UCUCUCAG 1057 TAGGCCTG GGCTAGCTACAACGA TCCCGAGA 2758 4719 UCUCGGGA CACACACU 1057 TAGGCCTG GGCTAGCTACAACGA TCCCGAGA 2759 4719 UCUCGGGA CUAAGAC 1058 GTCTTAGG GGCTAGCTACAACGA TCCCGAGA 2759 4726 GGCCUAAG A CAUGUGAG 1059 CTCACATG GGCTAGCTACAACGA TCCCAGAG 2756 4726 GGCCUAAG A CAUGUGAG 1059 CTCACATG GGCTAGCTACAACGA CTGCTAGA 2761 4726 CCUAAGAC A UGUGAGGA 1061 TCCCCTCA GGCTAGCTACAACGA TTTTTTC 2764 4727 AAAAAAA G CAAAAAGC 1062 GCTTTTTG GGCTAGCTACAACGA TTTTTTTC 2764 4752 GAAAAAAA G CAAAGAGA 1065 TCCCCTCG GGCTAGCTACAACGA TTTTTTTC 2764 4753 AAAAAAA G CAAAGAGA 1065 TCCCCTCG GGCTAGCTACAACGA TTTTTTTC 2764 4754 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	4637	GCCCUGCA G CCCAAAAC	1042	GTTTTGGG GGCTAGCTACAACGA TGCAGGGC	2744
4654 CCAGGGCA A CAAGCCCG 1045 CGGGCTTG GGCTAGCTACAACGA TGCCCTGG 2747 4658 GGCAACAA G CCCGUUAG 1046 CTAACGGG GGCTAGCTACAACGA TTGTTGCC 2748 4666 GCCCGUUA G CCCCCAGGG 1048 CCCTGGGG GGCTAGCTACAACGA GGGCTTGT 2749 4666 GCCCGUUA G CCCCAGGG 1048 CCCTGGGG GGCTAGCTACAACGA AGGGCTTGT 2749 4667 ACCCGGUUA G CCCCAGGG 1048 CCCTGGGG GGCTAGCTACAACGA CCCCTGGG 2751 4677 AGGGGAUC A CUGGCUGG 1050 CCAGCCAG GGCTAGCTACAACGA CCCCTGGG 2751 4683 GAUCACUG G CUGGCUGG 1051 CAGGCCAG GGCTAGCTACAACGA CCCCTGGG 2751 4684 GAUCACUG G CUGGCUGG 1051 CAGGCCAG GGCTAGCTACAACGA CAGTGATC 2752 4687 ACUGGCUG G CUGACCU 1051 CAGGCCAG GGCTAGCTACAACGA CAGTGATC 2754 4693 UGGCCUGA G CAACAUCU 1053 AGATGTTG GGCTAGCTACAACGA CAGTGATC 2754 4694 UGAGCAAC A CUCUCGGGA 1054 CCGAGAGT GGCTAGCTACAACGA TCAGGCCA 2756 4698 UGAGCAAC A CUCUCGGA 1055 CCCGAGAG GGCTAGCTACAACGA TCAGGCCA 2757 4707 UCUCGGGA G CAACAUCU 1055 AGATGTTG GGCTAGCTACAACGA TCAGGCCA 2757 4707 UCUCGGGA G CAACAUCU 1055 AGATGTTG GGCTAGCTACAACGA TCCCGAGA 2756 4715 GUCCUCUA G CAGGCCUA 1055 TCCCGAGA GGCTAGCTACAACGA TCCCGAGA 2756 4716 UCUCAGGAG A CUCUCUAG 1056 CTAGAGGA GGCTAGCTACAACGA TCCCGAGA 2757 4719 UCUAGCAG G CCUAAGAC 1058 GTCTTAGG GGCTAGCTACAACGA TCAGGAC 2759 4719 UCUAGCAG G CCUAAGAC 1058 GTCTTAGG GGCTAGCTACAACGA TCAGGAC 2759 4726 CGCUAAGAC A UGUGAGGA 1059 CTCACATG GGCTAGCTACAACGA TTGAGCC 2761 4728 CCUAAGAC A UGUGAGGA 1060 TCCTCACA GGCTAGCTACAACGA TTGAGCC 2761 4728 CCUAAGAC A UGUGAGGA 1060 TCCTCACA GGCTAGCTACAACGA TTGTTTT 2763 4752 GAAAAAAA G CAAGAGGAG 1061 TCCCTCTC GGCTAGCTACAACGA TTTTTTC 2764 4759 AGCAAAAA G CAAGAGGAG 1061 TCCCTCT GGCTAGCTACAACGA TTTTTTC 2764 4759 AGCAAAAA G CAAGAGGAG 1063 CTCCCTCA GGCTAGCTACAACGA TTTTTTC 2765 4777 AAAGAGAA C CAAGAGAG 1063 CTCCCTG GGCTAGCTACAACGA TTTTTTC 2766 4780 GAGAAAGA A CUGUAGAA 1065 TCTCCTC GGCTAGCTACAACGA TTTTTTC 2766 4780 GAGAAAGA G CAAGAGAA 1065 TCTCCTC GGCTAGCTACAACGA TTTTTTC 2767 4790 GAGAAGGC A UGUAGAA 1066 CTTCCAA GGCTAGCTACAACGA TTTTTCC 2767 4810 AUUUGAGAC A CCAUGUGA 1068 ATGCCCC GGCTAGCTACAACGA CTTTTCC 2767 4810 AUUUGAGAC A CCAUGUGA 1068 ATGCCCC GGCTAGCTACAACGA C	4644	AGCCCAAA A CCCAGGGC	1043	GCCCTGGG GGCTAGCTACAACGA TTTGGGCT	2745
4658 GGCAACAA G CCCGUUAG 1046 CTAACGGG GGCTAGCTACAACGA TTGTTGCC 2748 4662 ACAAGCCC G UUAGCCCC 1047 GGGGCTAA GGCTAGCTACAACGA GGGCTTGT 2749 4666 GCCCGGUUA G CCCCAGGGG 1048 CCCTGGGG GGCTAGCTACAACGA ACACGCCCTCGG 2750 4676 CCCAGGGG A UCACUGGC 1049 GCCAGTAA GGCTAGCTACAACGA ACACGCCCTGGG 2751 4679 AGGGAUC A CUGGCUGG 1050 CCAGCCAG GGCTAGCTACAACGA CCCCTCGG 2751 4683 GAUCACUG G CUGGCUG 1051 CAGGCCAG GGCTAGCTACAACGA CACTGCAC 2752 4683 GAUCACUG G CUGGCCUG 1051 CAGGCAG GGCTAGCTACAACGA CACTGCAC 2752 4683 UGGCCUGA G CACAUCU 1053 AGATGTT GGCTAGCTACAACGA CAGTGAC 2754 4693 UGGCCUGA G CACAUCU 1053 AGATGTT GGCTAGCTACAACGA CAGCCAGT 2754 4698 UGAGCAAC A CUCUCGGG 1054 CCGAGAGA GGCTAGCTACAACGA CAGCCAGT 2754 4699 UGAGCAAC A UCUCGGG 1054 CCGAGAGA GGCTAGCTACAACGA TCCCGAG 2756 4698 UGAGCAAC A UCUCGGG 1055 CCCGAGAG GGCTAGCTACAACGA TCCCGAGA 2756 4707 UCUCGGGA G UCUCUGG 1055 CCCGAGAG GGCTAGCTACAACGA TCCCGAGA 2757 4707 UCUCGGGA G UCUCUGA 1055 CCGAGAG GGCTAGCTACAACGA TCCCGAGA 2756 4719 UCUAGCAG G CCUAAGAC 1058 GTCTTAGG GGCTAGCTACAACGA TCCCGAGA 2756 4719 UCUAGCAG G CCUAAGAC 1058 GTCTTAGG GGCTAGCTACAACGA CTCCCTAGA 2760 4726 GGCCUAAG A CAUGUGAG 1059 CTCACATG GGCTAGCTACAACGA CTGCTAGA 2760 4728 CCUAAGAC A UGUGAGGA 1060 TCCCCCAC GGCTAGCTACAACGA CTGCTAGA 2760 4752 GACAAAAA G CAAAAACC 1062 GCTTTTG GGCTAGCTACAACGA CTTAGGC 2761 4752 GAAAAAA G CAAAAACC 1062 GCTTTTTG GGCTAGCTACAACGA TTTTTTC 2764 4752 GAAAAAA G CAAAAACC 1062 CCTTTTTG GGCTAGCTACAACGA TTTTTTC 2764 4759 AGCAAAAA G CAAAAACC 1062 CCTTTTTG GGCTAGCTACAACGA TTTTTTC 2764 4769 GAGAAAAA G CAAAAACC 1062 CCTTTTTG GGCTAGCTACAACGA TTTTTTC 2764 47790 GAGAAAAA G CAAAAACC 1062 CCTTTTTG GGCTAGCTACAACGA TTTTTTC 2764 4788 GGGAGAA A UUUGAGAC 1067 GTCCCTCC GGCTAGCTACAACGA TTTTTTC 2764 4807 AAUUUGAG A CCCACCAU 1066 ATGCTACAA GGCTAGCTACAACGA CTTCTCCC 2767 4814 GACCCAC A UGAGAAA 1066 CTTCCATG GGCTAGCTACAACGA CTTCTCCC 2767 4814 GACCCAC A UGAGAAA 1066 CTTCCATG GGCTAGCTACAACGA GCCTCCCC 2777 4815 GAGACGA C CACAGGG C CCCACCAU 1067 GCTAGCTACAACGA GCCTCCCC 2777 4816 GGGCCCA C GGAGGGGC C CCCACCAU 1067 GCTAGCTACAACGA GCCTCCC	4651	AACCCAGG G CAACAAGC	1044	GCTTGTTG GGCTAGCTACAACGA CCTGGGTT	2746
4662 ACABGCCC G UUAGCCCC 1047 GGGGCTAA GGCTAGCTACAACGA GGCTTGT 2749 4666 GCCCGUUA G CCCCAGGG 1048 CCCTGGG GGTTAGCTACAACGA TAACGGC 2750 4676 CCCAGGGG A UCACUGCC 1049 GCCAGTGA GGCTAGCTACAACGA CCCCTGGG 2751 4677 AGGGGAUC A CUGGCUGG 1050 CCAGCCAG GGCTAGCTACAACGA CCCCTGGG 2751 4683 GAUCACUG G CUGAGCA 1051 CAGGCCAG GGCTAGCTACAACGA CACCCCT 2752 4683 ACUGGCUG G CCUGAGCA 1052 TGCTCAGG GGCTAGCTACAACGA CACCAGCCAC 2753 4687 ACUGGCUG G CCUGAGCA 1052 TGCTCAGG GGCTAGCTACAACGA CAGCCACT 2753 4689 UGGCCUGA G CAACAUCU 1053 AGATGTTG GGCTAGCTACAACGA CAGCCACT 2756 4699 UGAGCAAC A UCUCGGG 1054 CCGAGATG GGCTAGCTACAACGA TCCAGGC 2756 4699 UGAGCAAC A UCUCGGGA 1055 TCCCGAGA GGCTAGCTACAACGA TGCTCAGG 2756 4699 UGAGCAAC A UCUCGGGA 1055 TCCCGAGA GGCTAGCTACAACGA TGCTCAG 2757 4707 UCUCGGGA G UCCUCUAG 1056 TCCGAGAG GGCTAGCTACAACGA TGCTCAG 2757 4715 GUCCUCUA G CAGGCCUA 1057 TAGGCCTG GGCTAGCTACAACGA TCCTAGG 2759 4719 UCUACGGG G CUAAGAC 1058 GTCTTAGG GGCTAGCTACAACGA TCCTAGA 2759 4719 UCUACGGG G CUAGGGC 1058 GTCTTAGG GGCTAGCTACAACGA TCCTAGA 2750 4726 GGCCUAAG A CAUGUGAG 1059 CTCACATG GGCTAGCTACAACGA TTCTAGC 2761 4727 CUAAGACA UGUGAGG 1059 CTCACATG GGCTAGCTACAACGA CTCTAGA 2761 4759 CCUAAGAC A UGUGAGGA 1060 TCCTCACA GGCTAGCTACAACGA CTTCTAGC 2761 4759 AGCAAAAA G CAAGAGGA 1061 CCTCCTCA GGCTAGCTACAACGA TTTTTTC 2766 4759 AGCAAAAA G CAAGAGGA 1061 CCTCCTCA GGCTAGCTACAACGA TTTTTTC 2766 4768 GGGAGAAG C CAUGAGAA 1065 TCTCCTTG GGCTAGCTACAACGA TTTTTTC 2766 47790 GAGAAGAC A UGUGAGA 1065 TCTCCTTG GGCTAGCTACAACGA TTTTTCT 2766 4800 GAGAAAGA A UUUGAGAC 1067 GTCTCATA GGCTAGCTACAACGA TTTTTCC 2769 4800 GAGAAAGA A UUUGAGAC 1067 GTCTCATA GGCTAGCTACAACGA TTTTTCC 2769 4800 GAGAAAGA A UUUGAGAC 1067 GTCTCAAA GGCTAGCTACAACGA TTTTTCC 2769 4810 AUUUGAGAC C ACGAUGU 1069 ACTGCTCA GGCTAGCTACAACGA CTCTCACT 2772 4814 GAGCACCA UUUGAGA 1065 TCTCCTGTG GGCTAGCTACAACGA GTCTCACC 2773 4816 CCCACGU G UGAGCAA 1067 GTCTCAAA GGCTAGCTACAACGA GCCCTCC 2773 4816 CCCACGU G UGAGCAA 1067 GTCTCCC GGCTAGCTACAACGA GCCCTCC 2773 4816 CCCACGU G CACAGGGG 1071 GCCCCC GGCTAGCTACAACGA GCCCTCC 2774 4817 GGGACGG	4654	CCAGGGCA A CAAGCCCG	1045	CGGGCTTG GGCTAGCTACAACGA TGCCCTGG	2747
4666 GCCCGUUA G CCCCAGGG 1048 CCCTGGGG GGCTAGCTACAACGA TAACGGC 2750 4676 CCCAGGGG A UCACUGGC 1049 GCCAGTGA GGCTAGCTACAACGA CCCCTGGG 2751 4679 AGGGGAUC A CUGGCUGG 1050 CCAGCCAG GGCTAGCTACAACGA GATCCCCT 2752 4683 GAUCACUG G CUGGCUG 1051 CAGGCCAG GGCTAGCTACAACGA CATCCCCT 2752 4683 GAUCACUG G CUGGCUG 1051 CAGGCCAG GGCTAGCTACAACGA CAGTGATC 2753 4687 ACUGGCUG G CUGAGCA 1052 TGCTCAGG GGCTAGCTACAACGA CAGCAGT 2754 4693 UGGCCUGA G CAACAUCU 1053 AGATGTTG GGCTAGCTACAACGA CAGCAGT 2754 4693 UGGCCUGA G CAUCUCGG 1054 CGCAGATT GGCTAGCTACAACGA TGCTCAG 2756 4698 UGAGCACA A UCUCGGGA 1055 TCCCGAGA GGCTAGCTACAACGA TGCTCAG 2756 4698 UGAGCACA UCUCGGGA 1055 TCCCGAGA GGCTAGCTACAACGA TGCTCAG 2757 4707 UCUCGGGA G UCCUCUGA 1056 CTAGAGGA GGCTAGCTACAACGA TCCCGAGA 2758 4715 GUCCUCUA G CAGGCCUA 1057 TAGGCCT GGCTAGCTACAACGA TCCCGAGA 2758 4715 UCUACGCAG G CCUAAGAC 1057 TAGGCCT GGCTAGCTACAACGA TCCCGAGA 2758 4719 UCUACGCAG G CCUAAGAC 1058 GTCTTAGG GGCTAGCTACAACGA TCCCGAGA 2760 4728 CCUAAGAC A UGUGAGGA 1069 CTCACATG GGCTAGCTACAACGA CTCCTAGA 2760 4726 GGCCUAAGA A CAUGUGAG 1059 CTCACATG GGCTAGCTACAACGA CTCTTAGG 2761 4726 CGCAAAAAC UGAGGAGA 1060 TCCCTCAC AGCTACAACGA CTCTTAGG 2761 4730 UAAGACAU G UGAGGAGG 1061 CTCCTCAC AGCTACAACGA TTCTTTCC 2764 4759 AGCAAAAA G CAAAAAGC 1062 GCTTTTTG GGCTAGCTACAACGA TTCTTTC 2764 4759 AGCAAAAA G CAAGAGAA 1063 CTCCCTTG GGCTAGCTACAACGA TTCTTTTC 2764 4759 AGCAAAAA G CAAGAGAA 1064 TCCCCGG GGCTAGCTACAACGA TTCTTTTC 2764 4788 GGGAGAA A CCGGGAGA 1064 TCCCCTCA GGCTAGCTACAACGA TTCTTTTC 2766 4789 GGAGAAAA G CAUGAGAA 1065 TCCCTTA GGCTAGCTACAACGA TTCTTTC 2766 4789 GGAGAAAA G CAUGAGAA 1065 TCCCTTA GGCTAGCTACAACGA TTCTTTC 2766 4780 GGAGAAAA A UUUGAGAC 1067 TCCCTACA GGCTAGCTACAACGA TTCTTCT 2766 4780 GAGAAAAG A UUUGAGAC 1067 TCCCTCC GGCTAGCTACAACGA CTCTTCC 2767 4780 GAGAAAAG A UUUGAGAC 1067 TCCCTCC GGCTAGCTACAACGA CTCTTCC 2767 4880 GGAGAGA A UGAGGAAA 1065 TCCCTTG GGCTAGCTACAACGA CTCTTCC 2767 4880 GGAGAGA A UGAGGAAG 1064 TCCCCGC GGCTAGCTACAACGA CTCTTCC 2767 4880 GGAGCCC A UGAGGAG 1071 TGCCCGC GGCTAGCTACAACGA CTCTTCC 2779 4881 GGAGCGCC A C	4658	GGCAACAA G CCCGUUAG	1046	CTAACGGG GGCTAGCTACAACGA TTGTTGCC	2748
4676 CCCAGGGG A UCACUGGC 1049 GCCAGCAG GGCTAGCTACAACGA CCCCTGGG 2751 4679 AGGGGAUC A CUGGCUGG 1050 CCAGCCAG GGCTAGCTACAACGA GATCCCCT 2752 4683 GAUCACUG G CUGGCCUG 1051 CAGGCCAG GGCTAGCTACAACGA CAGTGATC 2753 ACGGCAG GCCAGCCACACACGA CAGTGATC 2753 ACGGCCAG GCCAGCCACACACGA CAGTGATC 2753 ACGGCCAG CCCCCCCC 2754 AC697 ACUGCCUG G CCUGAGCA 1052 TGCTCAGG GGCTAGCTACAACGA CAGCCAGT 2754 AC697 UGGCCUG G CACAAUCU 1053 AGATGTTG GGCTAGCTACAACGA TCAGGCCAG 2755 CCGAGAGT GGCTAGCTACAACGA TCAGGCCAG 2755 TCCCGAGA GGCTAGCTACAACGA TCAGGCCAG 2755 TCCCGAGA GCTAGCTACAACGA TCAGGCCA 2755 TCCCGAGA GCTAGCTACAACGA TCAGGCCA 2757 TACCCCUCUA G CACACCCAC 1055 TCCCGAGA GCTAGCTACAACGA TCAGGCCA 2757 TACCCCUCUA G CACACCCAC 1055 TCCCGAGA GCTAGCTACAACGA TCAGAGCA 2759 TCCCCAGA GCTAGCTACAACGA TCAGAGCA 2759 TCCCCACA GCCTACAACGA TCCCCAGA 2758 TCCCCACAC GCCTACAACGA CCCCAGA 2759 UCCUCUA G CAGGCCUA 1057 TAGGCCTG GGCTAGCTACAACGA TCAGAGCA 2759 TCCCCACA GCCTACAACGA CTCCTAGA 2760 TCCCCACA GCCTACAACGA CTCCTAGA 2760 TCCCCACA GCCTACAACGA CTCCTAGA 2760 TCCCCACA GCCTACAACCA ACCCACACA ACCCACACACA ACCCACACACA ACCCACACACACA ACCCACACACACACACACACACACACACACACACACACAC	4662	ACAAGCCC G UUAGCCCC	1047	GGGGCTAA GGCTAGCTACAACGA GGGCTTGT	2749
4679 AGGGAUC A CUGGCUGG 1050 CCAGCCAG GGCTAGCTACAACGA GATCCCCT 2752 4683 GAUCACUG G CUGGACCAG 1051 CAGGCCAG GGCTAGCTACAACGA CAGTGATC 2753 4687 ACUGGCUG G CUGAGCA 1052 TGCTCAGG GGCTAGCTACAACGA CAGTGATC 2754 4693 UGGCCUGA G CAACAUCU 1053 AGATGTTG GGCTAGCTACAACGA CAGCACGT 2755 4696 CCUGAGCA A CAUCUCGG 1054 CCGAGATG GGCTAGCTACAACGA TGCTCAGG 2756 4698 UGAGCAAC A UCUCGGGA 1055 TCCCGAGA GGCTAGCTACAACGA TGCTCAGG 2756 4698 UGAGCAAC A UCUCGGGA 1055 TCCCGAGA GGCTAGCTACAACGA TCCCGAGA 2757 4707 UCUCGGGA G UCCUCUAG 1057 TAGGCCTG GGCTAGCTACAACGA TCCCGAGA 2757 4715 GUCCUCUA G CAGGCCUA 1057 TAGGCCTG GGCTAGCTACAACGA TCCCGAGA 2758 4716 GUCCUCUA G CAGGCCUA 1057 TAGGCCTG GGCTAGCTACAACGA TCCCGAGA 2759 4719 UCUAGGGA G CCUAAGAC 1058 GTCTTAGG GGCTAGCTACAACGA TAGAGGAC 2759 4719 UCUAGGAG A CAUGUGAG 1059 CTCACATG GGCTAGCTACAACGA CTAGGCC 2761 4728 CCUAAGAC A UGUGAGGA 1065 TCCTCACAG GGCTAGCTACAACGA CTAGGCC 2761 4728 CCUAAGAC A UGUGAGGA 1061 TCCTCACA GGCTAGCTACAACGA TGTCTTAGGC 2761 4752 GAAAAAAA G CAAAGACG 1062 GCTTTTTTTTTC 2764 4753 UAAGACAA A CCAGGAGAG 1063 CTCCCTTG GGCTAGCTACAACGA TTTTTTC 2764 4755 AAGAGAAA C CAAGGGAG 1063 CTCCCTTG GGCTAGCTACAACGA TTTTTTC 2764 4757 AAAGAGAA A CCGGGAGA 1064 TCTCCCCG GGCTAGCTACAACGA TTTTTCT 2766 4768 GGGAGAAGA A CGGGAGAA 1064 TCTCCCG GGCTAGCTACAACGA TTTTTCT 2766 4768 GGGAGAAGA A UGAGAAA 1065 TTCTCAT GGCTAGCTACAACGA TTTTTCT 2766 4768 GGGAGAAGA A UGAGAAA 1066 CTTTCTCA GGCTAGCTACAACGA TTCTCTCT 2766 4800 GAGAAAGA A UUUGAGAC 1067 GTCTCAA GGCTAGCTACAACGA TTCTCTCT 2766 4800 GAGAAAGA A UUUGAGAC 1067 GTCTCAA GGCTAGCTACAACGA CTTCTCTC 2767 4810 GAGAAAGA A UUUGAGAC 1067 GTCTCAA GGCTAGCTACAACGA CTTCTCTC 2767 4811 GACGACCA UGAGAA 1066 CTTTCCA GGCTAGCTACAACGA CTTCTCTC 2768 4801 AAUUUGAG A CACAUGU 1069 ACATGGTG GGCTAGCTACAACGA CTTCTCTC 2768 4802 CCQGCGCG CACAGGGG 1072 CCCCTC GGCTAGCTACAACGA CTCAAATT 2770 4816 CGCACCAU GUGGCA 1071 TGCCCAC GGCTAGCTACAACGA CCCACATG 2771 4811 GACGCACC A UGUGGCA 1071 TGCCCACA GGCTAGCTACAACGA CCCACATG 2772 4822 AUGUGGC A CACAUGU 1069 ACATGGT GGCTAGCTACAACGA CCCACATG 2773 4824 GGGCCCC A CAGGAGGG	4666	GCCCGUUA G CCCCAGGG	1048	CCCTGGGG GGCTAGCTACAACGA TAACGGGC	2750
4683 GAUCACUG G CUGGCCUG 1051 CAGGCCAG GGCTAGCTACAACGA CAGTGATC 2753 4687 ACUGGCUG G CCUGAGCA 1052 TGCTCAGG GGCTAGCTACAACGA CAGCCAGT 2754 4693 UGGCCUGA G CAACAUCU 1053 AGATGTTG GGCTAGCTACAACGA CAGCCAGT 2754 4696 CCUGAGCA A CAUCUCGG 1054 CCGAGATG GGCTAGCTACAACGA TCGTGCAC 2755 4698 UGAGCAAC A UCUCGGGA 1055 TCCCGAGA GGCTAGCTACAACGA TGCTGCAC 2757 4707 UCUCGGGA G UCCUCUAG 1056 CTAGAGGA GGCTAGCTACAACGA TGCTGCAC 2757 4707 UCUCGGGA G UCCUCUAG 1056 CTAGAGGA GGCTAGCTACAACGA TCCCGAGA 2758 4715 GUCCUCUA G CAGGCCUA 1057 TAGGCCTG GGCTAGCTACAACGA TAGAGGA C759 4719 UCUGAGCAG G CCUAAGAC 1058 GTCTTAGG GGCTAGCTACAACGA CTGCTAGA 2759 4719 UCUGAGCAG G CCUAAGAC 1058 GTCTTAGG GGCTAGCTACAACGA CTGCTAGA 2759 4726 GGCCUAAG A CAUGUGAG 1059 CTCACATG GGCTAGCTACAACGA CTGCTAGA 2760 4728 CCUAAGAC A UGUGAGGA 1060 TCCTCACA GGCTAGCTACAACGA CTTAGGCC 2761 4730 UAAGACAU G UGAGGAGA 1060 TCCTCACA GGCTAGCTACAACGA ATGTCTTAG 2762 4752 GAAAAAAA G CAAAGACG 1062 GCTTTTTG GGCTAGCTACAACGA ATGTCTTA 2764 4752 AGCAAAAA G CAAAGACG 1062 GCTTTTTG GGCTAGCTACAACGA TTTTTTCT 2764 4759 AGCAAAAA G CAAGGGAG 1064 TCCCCCGG GGCTAGCTACAACGA TTTTTTCT 2764 4788 GGGAGAAG C CUUGAGAA 1065 TCTCCCTG GGCTAGCTACAACGA TTTTTCT 2766 4788 GGGAGAAG C AUGAGAAA 1065 TTTCCCTG GGCTAGCTACAACGA TCTCTCT 2768 4800 GAGAAAGA A UUUGAGAC 1067 GTCTCAAA GGCTAGCTACAACGA TCTCTCT 2768 4800 GAGAAAGA A UUUGAGAC 1067 GTCTCAAA GGCTAGCTACAACGA TCTCTCT 2768 4801 AAUUUGAG A CCAUGUU 1069 ACATGGTG GGCTAGCTACAACGA TCTTCTC 2769 4801 AUUUGAGA C CCAUGUU 1069 ACATGGTG GGCTAGCTACAACGA TCTTCTC 2770 4814 GACGCACC A UGUGGGCA 1071 TGCCCACA GGCTAGCTACAACGA GTCTCAAAT 2771 4816 CGCACCAU GUGGCA 1071 TGCCCACA GGCTAGCTACAACGA GTCTCAAAT 2771 4811 UGAGACGC A CGAUGUG 1069 ACATGGTG GGCTAGCTACAACGA GTCTCAAAT 2771 4814 GACGCACA UGUGGCA 1071 TGCCCACA GGCTAGCTACAACGA GCCCACTT 2776 4820 CAUGUGG G CACGGAGG 1073 CCCCCTCC GGCTAGCTACAACGA GCCCCTCC 2779 4837 GGGACGGG A CGGGAGG 1073 CCCCCTCC GGCTAGCTACAACGA GCCCACTT 2776 4821 GGGGCUC A CGAGGAGG 1073 CCCCCTCC GGCTAGCTACAACGA CCCCTCC 2779 4832 GGGGGGG A CGGGAGG 1074 CCCCCCC GGCTAGCTACAACGA CCCCTCC	4676	CCCAGGGG A UCACUGGC	1049	GCCAGTGA GGCTAGCTACAACGA CCCCTGGG	2751
4687 ACUGGCUG G CCUGAGCA 1052 TGCTCAGG GGCTAGCTACAACGA CAGCCAGT 2754 4693 UGGCCUGA G CAACAUCU 1053 AGATSTTG GGCTAGCTACAACGA TCAGGCCA 2755 4696 CCUGAGCA A CAUCUCGG 1054 CCGAGATG GGCTAGCTACAACGA TCAGGCCA 2755 4698 UGAGCACA A UCUCGGGA 1055 TCCCGAGA GGCTAGCTACAACGA TGCTCAGG 2756 4707 UCUCGGGA G UCUCUAG 1055 TCCCGAGA GGCTAGCTACAACGA TGCTCAG 2757 4707 UCUCGGGA G UCUCUAG 1055 TCCCGAGA GGCTAGCTACAACGA TGCTCAGA 2758 4715 GUCCUCUA G CAGGCCUA 1057 TAGGCCTG GGCTAGCTACAACGA TCCCGAGA 2758 4719 UCUAGCAG G CCUAAGAC 1058 GTCTTAGG GGCTAGCTACAACGA CTGCTAGA 2759 4726 GGCCUAAG A CAUGUGAG 1058 GTCTAGAG GGCTAGCTACAACGA CTGCTAGA 2750 4726 GGCCUAAG A CAUGUGAG 1058 GTCTAGAG GGCTAGCTACAACGA CTGCTAGA 2760 4728 CCUAAGAC A UGUGAGGA 1060 TCCCCACA GGCTAGCTACAACGA CTGCTAGG 2761 4730 UAAGACAU G UGAGGGA 1061 CCTCCCTCA GGCTAGCTACAACGA CTTTAGGC 2761 4730 UAAGACAU G UGAGGAG 1061 CCTCCCTCA GGCTAGCTACAACGA ATOTCTTA 2763 4752 GAAAAAAA G CAAAAAGC 1062 GCTTTTG GGCTAGCTACAACGA ATOTCTTA 2763 4753 AGCAAAAA G CAAGAGGA 1061 CCTCCCTCA GGCTAGCTACAACGA TTTTTTCT 2766 4759 AGCAAAAA G CAAGAGGA 1064 TCTCCCGG GGCTAGCTACAACGA TTTTTTCT 2766 4768 GGGAGAGG C CAUGAGAA 1065 TCTCCAT GGCTAGCTACAACGA TTCTCTCT 2767 4788 GGGAAGGC A UGAGGAAA 1065 TCTCCAT GGCTAGCTACAACGA TTCTCCC 2767 4790 GAGAAGGC A UGAGGAAA 1065 TCTCCAT GGCTAGCTACAACGA TCTTCTCC 2767 4800 AAUUUGAG A CGCACAU 1068 ATGGTGCG GGCTAGCTACAACGA TCTTCTCC 2769 4801 AAUUUGAG A CGCACAU 1068 ATGGTGCG GGCTAGCTACAACGA TCTTCTCC 2769 4801 AAUUUGAG A CCACCAU 1069 ACATGGTG GGCTAGCTACAACGA TCTTCTCC 2769 4814 GACGCAC A UGUGGGCA 1071 TGCCCACA GGCTAGCTACAACGA TCTTCACA 2771 4816 CGCACCAU GUGGGCA 1071 TGCCCACA GGCTAGCTACAACGA GCTTCCAAA 2772 4814 GACGCAC A UGUGGGCA 1071 TGCCCCACA GGCTAGCTACAACGA TCTCAAA 2772 4816 CGCACCAU GUGGGCA 1071 TGCCCCCC GGCTAGCTACAACGA TCTCAAA 2771 4820 CCAUGUGG C CACGGAGG 1072 CGCCCC GGCTAGCTACAACGA TCGCACT 2777 4821 CGCCCCCC A UGUCGCC 1077 TGCCATGG GGCTAGCTACAACGA TCGCACT 2777 4821 CGCCCCA A UGCCAUUU 1078 AAATGGC GGCTAGCTACAACGA TGGCTACACCA 2778 4822 AUGUGGGG A CGAGGAG 1072 CGCCCC GGCCTAGCTACAACGA TGGCTACCACGA T	4679	AGGGGAUC A CUGGCUGG	1050	CCAGCCAG GGCTAGCTACAACGA GATCCCCT	2752
4693 UGGCCUGA G CAACAUCU 1053 AGATGTTG GGCTAGCTACAACGA TCAGGCCA 2755 4696 CCUGAGCA A CAUCUCGG 1054 CCGAGATG GGCTAGCTACAACGA TGCTCAGG 2756 4698 UGAGCAAC A UCUCGGGA 1055 TCCCGAGA GGCTAGCTACAACGA GTCGTCA 2757 4707 UCUCGGGA G UCCUCUAG 1056 CTAGAGGA GGCTAGCTACAACGA TCCCGAGA 2758 4715 GUCCUCUA G CAGGCCUA 1057 TAGGCCTG GGCTAGCTACAACGA TCCCGAGA 2758 4719 UCUAGCAG G CCUAAGAC 1058 GTCTTAGG GGCTAGCTACAACGA TCCCGAGA 2759 4719 UCUAGCAG G CCUAAGAC 1058 GTCTTAGG GGCTAGCTACAACGA CTGCTAGA 2760 4726 GGCCUAAG A CAUGUGAG 1059 CTCACATG GGCTAGCTACAACGA CTGCTAGG 2761 4728 CCUAAGAC A UGUGAGGA 1060 TCCTCACA GGCTAGCTACAACGA GTCTTAGG 2762 4730 UAAGACAU G UGAGGAGG 1061 CCCTCCTCA GGCTAGCTACAACGA GTCTTAGG 2762 4752 GAAAAAA G CAAGGAG 1061 CCCCCTCA GGCTAGCTACAACGA TTTTTTC 2764 4753 AGCAAAAA G CAAGGAG 1063 CTCCCTTA GGCTAGCTACAACGA TTTTTTC 2764 4757 AAAGAGAA A CCGGGAGA 1064 TCTCCCGG GGCTAGCTACAACGA TTTTTCT 2766 4788 GGGAGAAG G CAUGAGAA 1065 TTCTCTTG GGCTAGCTACAACGA TTTTTCT 2766 4788 GGGAGAAG G CAUGAGAA 1065 TTCTCTTG GGCTAGCTACAACGA TTTTCTCT 2766 4790 GAGAAGGA A UUUGAGAC 1067 STCTCATG GGCTAGCTACAACGA TTTTCTC 2767 4800 GAGAAAGA A UUUGAGAC 1067 STCTCAAA GGCTAGCTACAACGA TCTTCCC 2767 4801 AAUUUGAG A CGCACCAU 1068 ATGGTGCG GGCTAGCTACAACGA CTCTTCC 2768 4801 AAUUUGAGA C CCAUGUG 1069 ACATGGTG GGCTAGCTACAACGA CTCTAAAT 2770 4811 UGAGACGC A CCAUGUG 1069 ACATGGTG GGCTAGCTACAACGA GCTTCCA 2772 4814 GACGCACC A UGUGGGCA 1071 TGCCCACA GGCTAGCTACAACGA GCTCCAA 2771 4816 CGCACCAU GUGGGCACG 1072 CGTGCCCA GGCTAGCTACAACGA GTCTCAA 2771 4820 CCAUGUGG G CACGAGGG 1073 CCTCCGTG GGCTAGCTACAACGA GCCTCCA 2776 4821 AUGUGGGC A CGGAGGG 1073 CCTCCGTG GGCTAGCTACAACGA GCCCATC 2776 4822 AUGUGGGC A CGGAGGG 1073 CCTCCGTG GGCTAGCTACAACGA GCCCCCC 2778 4824 GGGGCCCA G GCAGCACU 1069 GACAGGAG GCCACAT 2776 4825 GGGACGGG G CUCAGCAA 1071 TGCCCAC GGCTAGCTACAACGA GCCCACTC 2777 4837 GGGACGGG CUCAGCAA 1076 TTGCTGG GGCTAGCTACAACGA CCCCCTCC 2778 4842 GGGGCUCA G CAAUGCCA 1077 TGCCATG GGCTAGCTACAACGA CCCCCTCC 2778 4845 GCUCAGCA A UGCCAUUU 1078 AAATGGC GGCTAGCTACAACGA CCCCATCG 2778 4846 GCCACCAU G CAA	4683	GAUCACUG G CUGGCCUG	1051	CAGGCCAG GGCTAGCTACAACGA CAGTGATC	2753
4696         CCUGAGCA A CAUCUCGG         1054         CCGAGATG GCTAGCTACAACGA TGCTCAGG         2756           4698         UGAGCAAC A UCUCGAGA         1055         TCCCGAGA GGCTAGCTACAACGA GTTGCTCA         2757           4707         UCUGAGA G UCCUCUAG         1056         CTAGAGGA GGCTAGCTACAACGA TCCCGAGA         2758           4715         GUCCUCUA G CAGGCCUA         1057         TAGGCCTG GGCTAGCTACAACGA TCGCTAGA         2759           4719         UCUAGCAG G CCUAAGAC         1058         GTCTTAGG GGCTAGCTACAACGA TGGTACAA         2760           4726         GGCCUAAG A CAUGUGAG         1059         CTCACATG GGCTAGCTACAACGA CTTAGGC         2761           4728         CCUAAGAC A UGUGAGA         1060         TCCTCACA GGCTAGCTACAACGA ATGTCTTA         2762           4730         UAAGACAU G UGAGGAGG         1061         CCTCTCTAG GGCTAGCTACAACGA ATGTCTTA         2762           4752         GAAAAAAA G CAAGGGAG         1062         GCTTTTG GGCTAGCTACAACGA TTTTTCT         2765           4777         AAAGAGAA A CCGGGAGA         1064         TCTCCCGG GGCTAGCTACAACGA TTCTCTT         2766           4780         GAGAAGGC A UGAGAAAA         1065         TCTCCAAG GGCTAGCTACAACGA TTCTCTC         2766           4790         GAGAAGGC A UGAGGAAA         1066         CTTTCCAA         GGCTAGCTACAACGA CTCT	4687	ACUGGCUG G CCUGAGCA	1052	TGCTCAGG GGCTAGCTACAACGA CAGCCAGT	2754
4698         UGAGCAAC A UCUCGGGA         1055         TCCCGAGA GCTAGCTACAACGA GTTGCTCA         2757           4707         UCUCGGGA G UCCUCUAG         1056         CTAGAGGA GGCTAGCTACAACGA TCCCGAGA         2758           4715         GUCCUCUA G CAGGCCUA         1057         TAGGCCTG GGCTAGCTACAACGA CTCCGAGA         2759           4719         UCUAGCAG G CCUAAGAC         1058         GTCTACATG GGCTAGCTACAACGA CTCAGAGA         2760           4726         GGCCUAAGA C AUGUGAGGA         1059         CTCACATG GGCTAGCTACAACGA CTTAGGC 2761           4728         CCUAAGAC A UGUGAGGA         1060         TCCTCACA GGCTAGCTACAACGA GTCTAGGC 2762           4730         UAAGACAU G UGAGGAG         1061         CCTCCTCA GGCTAGCTACAACGA TTTTTTTC         2762           4752         GAAAAAAG C CAAGGAGA         1063         CTCCCTTG GGCTAGCTACAACGA TTTTTTCT         2764           4759         AGCAAAAA G CAAGGAGA         1063         CTCCCTTG GGCTAGCTACAACGA TTTCTTT         2766           4777         AAAGAGAA A CCGAGAAA         1065         TTCTCATG GGCTAGCTACAACGA TTTCTCC         2267           4790         GAGAAAGA A UUUGAGAC         1067         TCTCAAA GGCTAGCTACAACGA CTTCTCCC         2767           4800         GAGAAAGA A UUUGAGAC         1069         ACTGGTG GGCTAGCTACAACGA CTTCTAAA         2771 <t< td=""><td>4693</td><td>UGGCCUGA G CAACAUCU</td><td>1053</td><td>AGATGTTG GGCTAGCTACAACGA TCAGGCCA</td><td>2755</td></t<>	4693	UGGCCUGA G CAACAUCU	1053	AGATGTTG GGCTAGCTACAACGA TCAGGCCA	2755
4707 UCUCGGGA G UCCUCUAG 4715 GUCCUCUA G CAGGCCUA 4715 GUCCUCUA G CAGGCCUA 4719 UCUAGCAG G CCUARGAC 4726 GGCCUARGA C 1058 GTCTTAGG GGCTAGCTACAACGA TAGAGGAC 4726 GGCCUARGA C AUGUGAG 4726 GGCCUARGA C AUGUGAG 4728 CCUARGAC A UGUGAGG 4728 CCUARGAC A UGUGAGG 4730 UAAGACAU G UGAGGAGG 4752 GAAAAAAA G CAAAAAGC 4752 GAAAAAAA G CAAAAAGC 4752 GAAAAAAA G CAAAAAGC 4759 ACCAAAAA G CAAGGAGA 4757 AAAGAGAA A UGUGAGA 4759 ACCAAAAA G CAAGGAA 4759 AGCAAAAA G CAAGGAA 4759 AGCAAAAA G CAAGGAA 4750 UAUGAGAA A UGUGAGAA 4750 GAGAAAAAA G CAAAAAGC 4759 AGCAAAAA G CAAGGAA 4764 TCTCCCTG GGCTAGCTACAACGA ATGTCTTA 4777 AAAGAGAA A CCGGGAGA 4065 TCTCCCTG GGCTAGCTACAACGA TTTTTTCC 4764 4777 AAAGAGAA A CCGGGAGA 4065 TCTCCCTG GGCTAGCTACAACGA TTTTTCC 4766 47790 GAGAAAAA G CAUGAGAA 4065 TCTCCCTG GGCTAGCTACAACGA TTTTTCC 4760 GAGAAAAG G CAUGAGAA 4065 TCTCCATG GGCTAGCTACAACGA TCTCTCC 4760 GAGAAAGA A UUUGAGAC 4760 GAGAAAGA A UUUGAGAC 4760 GAGAAAGA A UUUGAGAC 4800 GAGAAAGA A UUUGAGAC 4800 UUUGAGAC G CACCACUU 4800 UUUGAGAC G CACCACUU 4800 UUUGAGACG CACCAUGU 4800 UUUGAGACG CACCAUGU 4801 ACATGGTG GGCTAGCTACAACGA CTTCTCC 4811 UGAGACGC A CCAUGUG 4810 ACATGGTG GGCTAGCTACAACGA GCTCTCAA 4811 UGAGACGC A CUGUGGCA 4811 UGAGACGC A CUGUGGCA 4811 UGAGACGC A CCAUGUG 4810 CCCACCAUG GCCTACCAACGA GCTCTCAA 4811 UGAGACGC A UGUGGGCA 4811 UGAGACGC A CCACAGGA 4811 UGAGACGC A CCACAGGA 4811 UGAGACGC A CCACAGGA 4811 UGAGACGC A CCACAGGA 4811 UGAGACGC A CCACACGA GCCCCCC 4821 AUGUGAGG G CACCACGA 4822 AUGUGAGG G CACCACGA 4822 AUGUGAGG G CACCACGA 4822 AUGUGAGC A CGGAGGG 1071 TGCCCCCG GGCTAGCTACAACGA GCCCCACC 4822 AUGUGAGC A CGGAGGG 1072 CCTCCTG GGCTAGCTACAACGA CCACATGG 4824 AUGUGAGA CCCCCCCC 4832 GGAGGGGG CCCACACGA TCTCCCCCCCCCCCCCCCCC	4696	CCUGAGCA A CAUCUCGG	1054	CCGAGATG GGCTAGCTACAACGA TGCTCAGG	2756
4715 GUCCUCUA G CAGGCCUA 1057 TAGGCCTG GGCTAGCTACAACGA TAGAGGAC 2759 4719 UCUAGCAG G CCUARGAC 1058 GTCTTAGG GGCTAGCTACAACGA CTGCTAGA 2760 4726 GGCCUAGA A CAUGUGAG 1059 CTCACATG GGCTAGCTACAACGA CTCGTAGA 2760 4728 CCUARGAC A UGUGAGGA 1060 TCCTCACA GGCTAGCTACAACGA CTTAGGC 2761 4730 UAAGACCU G UGAGGAG 1061 CCTCCTCA GGCTAGCTACAACGA GTCTTAGG 2762 4752 GAAAAAA G CAAAAAGC 1062 GCTTTTG GGCTAGCTACAACGA TTTTTTC 2764 4759 AGCAAAAA G CAAGGGAG 1063 CTCCCTTG GGCTAGCTACAACGA TTTTTTCT 2765 4777 AAAGAGAA A CCGGGAGA 1064 TCTCCCGG GGCTAGCTACAACGA TTTTTTCT 2766 4778 GGGAGAAG C CAUGAGAA 1065 TCTCCTG GGCTAGCTACAACGA TTTTTCT 2766 4788 GGGAGAAG C CAUGAGAA 1065 TCTCCTG GGCTAGCTACAACGA TTTTTCC 2767 4790 GAGAAAGA A UUUGAGAC 1066 CTTTCTCA GGCTAGCTACAACGA CTTCTCCC 2767 4800 GAGAAAGA A UUUGAGAC 1067 GTCTCAAA GGCTAGCTACAACGA CTTCTCC 2769 4807 AAUUUGAG A CSCACCAU 1068 ATGGTGCG GGCTAGCTACAACGA CTTCTCC 2769 4807 AAUUUGAGA C GCACAUGU 1069 ACATGGTG GGCTAGCTACAACGA CTCTAAAT 2770 4809 UUUGAGAC G CACAUGU 1069 ACATGGTG GGCTAGCTACAACGA CTCTAAAT 2770 4810 GAGAAGGA C CCAUGUGG 1070 CCACATGG GGCTAGCTACAACGA GCGTCTCA 2772 4814 GACGCCAC A UGUGGGCA 1071 TGCCCACA GGCTAGCTACAACGA GGCTCCCA 2772 4816 CGCACCAU G UGGGCACG 1072 CGTGCCCA GGCTAGCTACAACGA GCGTCCCA 2772 4820 CCAUGUGG G CACGAGGG 1073 CCTCCCTG GGCTAGCTACAACGA GCGTCCC 2773 4820 CCAUGUGG A CGGAGGG 1073 CCTCCCTG GGCTAGCTACAACGA CCACATGG 2775 4821 GGAGGGGG A CGGAGGG 1074 CCCCTCC GGCTAGCTACAACGA CCACCATG 2776 4822 AUGUGGG A CGGAGGG 1074 CCCCTCC GGCTAGCTACAACGA CCCCCTC 2777 4837 GGGACGGG G CUCAGCAA 1075 GAGCCCC GGCTAGCTACAACGA CCCCCTC 2777 4842 GGGGCUCA G CAUGCCA 1075 GAGCCCC GGCTAGCTACAACGA CCCCCTC 2777 4842 GGGACGGG G CUCAGCAA 1076 TGCCGAG GGCTAGCTACAACGA CCCCCTC 2779 4845 GCCAACGAA UCCCAGC 1075 GAGCCCC GGCTAGCTACAACGA CCCCTCC 2779 4846 GCCACCAC A UGCCAUUU 1078 AAATGCA GGCTAGCTACAACGA CCCCTCC 2779 4847 UCAGCAAU G CCAUUUCA 1079 TGGCATG GGCTAGCTACAACGA TGGCACC 2780 4859 UUUCAGGG C CAUUUCA 1081 GGAAGCCA GGCTAGCTACAACGA CCCCTCC 2782 4850 CCUUCAC G CUCUCAC 1081 GGAAGCCA GGCTAGCTACAACGA CCCTCCA 2781 4851 CCUUCAC A	4698	UGAGCAAC A UCUCGGGA	1055	TCCCGAGA GGCTAGCTACAACGA GTTGCTCA	2757
4719 UCUAGCAG G CCUAAGAC 1058 GTCTTAGG GGCTAGCTACAACGA CTGCTAGA 2760 4726 GGCCUAAGA CAUGUGAG 1059 CTCACATG GGCTAGCTACAACGA CTTAGGCC 2761 4728 CCUAAGAC A UGUGAGGA 1060 TCCTCACA GGCTAGCTACAACGA GTCTTAGG 2762 4730 UAAGACAU G UGAGGAGG 1061 CCTCCTCA GGCTAGCTACAACGA GTCTTAGG 2763 4752 GAAAAAAA G CAAAAAGC 1062 GCTTTTG GGCTAGCTACAACGA TTTTTTCC 7763 4759 AGCAAAAA G CAAGGGAG 1061 CCTCCTCG GGCTAGCTACAACGA TTTTTTCC 7764 4759 AGCAAAAA G CAAGGGAG 1063 CTCCCTTG GGCTAGCTACAACGA TTTTTCCT 2764 4768 GGAGAAGA A CCGGGAGA 1064 TCTCCCGG GGCTAGCTACAACGA TTTCTCT 2766 4770 AAAGAGAA A CCGGGAGA 1065 TTCTCATG GGCTAGCTACAACGA TTCTCTC 2767 4790 GAGAAAGA A UUUGAGAA 1065 TTCTCATG GGCTAGCTACAACGA TTCTCCC 2767 4800 GAGAAGA A UUUGAGAC 1066 CTTTCTCA GGCTAGCTACAACGA CTCTCCC 2767 4800 GAGAAGA A UUUGAGAC 1066 ATGGTGC GGCTAGCTACAACGA CTCTACATT 2770 4801 UUUGAGAC G CACCAUGU 1069 ACATGGT GGCTAGCTACAACGA CTCTAAATT 2770 4811 UGAGACGC A CCAUGUG 1069 ACATGGT GGCTAGCTACAACGA CTCCAAATT 2771 4811 UGAGACGC A CCAUGUG 1070 CCACATGG GGCTAGCTACAACGA GCGTCCAA 2772 4814 GACGCACCA UGUGGGCA 1071 TGCCCACA GGCTAGCTACAACGA GCGTCCCA 2772 4816 CGCACCAU U UGGGCACG 1071 TGCCCACA GGCTAGCTACAACGA GTCTCAA 2773 4822 AUGUGGG G CACGGAGG 1073 CCTCCGTG GGCTAGCTACAACGA CCACATGG 2775 4822 AUGUGGG G CACGGAGG 1073 CCTCCGTG GGCTAGCTACAACGA CCACATGG 2776 4832 GGAGGGG A CGGAGGGG 1074 CCCCTCCG GGCTAGCTACAACGA CCACATGG 2776 4832 GGAGGGG A CGGAGGGG 1073 CCTCCGTG GGCTAGCTACAACGA CCACATGG 2776 4832 GGAGGGG A CGGAGGGG 1073 CCTCCGTG GGCTAGCTACAACGA CCACATGG 2776 4842 GCGCCCA G CAAUGCC 1075 GAGCCCC GGCTAGCTACAACGA CCACATGG 2776 4854 GCUCAGCA UUUCAGUG 1075 GAGCCCC GGCTAGCTACAACGA CCACATGG 2776 4856 CCAUUUCA G UGCCAUUU 1078 GAGCCCC GGCTAGCTACAACGA TGGCCC 2777 4857 GGACAGCA UUUCAGUG 1080 GAGCCC GGCTAGCTACAACGA CCACTGGA 2780 4856 CCAUUCA G UUCCAGG 1080 GGAGGCA GGCTAGCTACAACGA CCCACTGG 2780 4857 GCUCCAG G CUCCCAG 1081 GGAGGCA GGCTAGCTACAACGA CACGATGG 2780 4857 GCUCCAG G CUCCCAG 1082 CTGGAAG GGCTAGCTACAACGA CACGATGG 2785 4859 UUCCAGUG G CUCCCAG 1082 CTGGAAG GGCTAGCTACAACGA CAGAGGGT 2785 4851 ACCCUUCA A C	4707	UCUCGGGA G UCCUCUAG	1056	CTAGAGGA GGCTAGCTACAACGA TCCCGAGA	2758
4726 GGCCUAAG A CAUGUGAG 1059 CTCACATG GGCTAGCTACAACGA CTTAGGCC 2761 4728 CCUAAGAC A UGUGAGGA 1060 TCCTCACA GGCTAGCTACAACGA GTCTTAGG 2762 4730 UAAGACAU G UGAGGAGG 1061 CCTCCTCA GGCTAGCTACAACGA ATGTCTTA 2763 4752 GAAAAAAA G CAAAGAGC 1062 GCTTTTTG GGCTAGCTACAACGA TTTTTTC 2764 4753 AGCAAAAA G CAAGGAG 1063 CTCCCTTG GGCTAGCTACAACGA TTTTTTC 2764 4754 AAAGAGAA A CCGGGAGA 1064 TCTCCCCG GGCTAGCTACAACGA TTTTTCT 2765 4777 AAAGAGAA A CCGGGAGA 1064 TCTCCCCG GGCTAGCTACAACGA TTTTTCT 2765 4788 GGGAGAAG C CAUGAGAA 1065 TTCTCATG GGCTAGCTACAACGA TTCTCCCC 2767 4790 GAGAAAGA A UUUGAGAC 1067 GTCTCAA GGCTAGCTACAACGA CTCTCCC 2769 4800 GAGAAAGA A UUUGAGAC 1067 GTCTCAA GGCTAGCTACAACGA CTCTTCC 2769 4807 AAUUUGAG A CGCACCAU 1068 ATGGTGCG GGCTAGCTACAACGA CTCTAAATT 2770 4809 UUUGAGAC G CACCAUGU 1069 ACATGGTG GGCTAGCTACAACGA CTCTAAATT 2770 4811 UGAGACGC A CCAUGUG 1070 CCACATGG GGCTAGCTACAACGA GCGTCCAAA 2771 4814 GACGCACC A UGUGGGCA 1071 TGCCCACA GGCTAGCTACAACGA GCGTCCAA 2772 4816 CGCACCAU G UGGGCACG 1072 CGTGCCCA GGCTAGCTACAACGA GTGCTCCA 2772 4820 CCAUGUGG G CACGGAGG 1073 CCTCCGTG GGCTAGCTACAACGA GTGCTCCA 2775 4822 AUGUGGGC A CGGGAGG 1074 CCCCTCCG GGCTAGCTACAACGA CCACATGG 2775 4832 GGAGGGG A CGGGAGG 1074 CCCCTCCG GGCTAGCTACAACGA CCCCCTCC 2777 4837 GGGACCGG G CUCAGCAA 1075 TGCCTAGA GGCTAGCTACAACGA CCCCCTCC 2777 4837 GGGACCGG CUCAGCAA 1076 TTGCTGAG GGCTAGCTACAACGA CCCCCTCC 2777 4847 UCAGCAAU G CCAUUUCA 1079 TGAAATGG GGCTAGCTACAACGA TGAGCCC 2779 4848 GGGGCUCA G CAUGUCCA 1077 TGGCATG GGCTAGCTACAACGA TGAGCCC 2779 4847 UCAGCAAU G CCAUUUCA 1079 TAGAATGG GGCTAGCTACAACGA TGAGCCC 2778 4847 UCAGCAAU G CCAUUUCA 1079 TGAAATGG GGCTAGCTACAACGA TGAGCCC 2779 4856 CCAUUCAG G UGCCCCA 1083 GGCAGG GGCTAGCTACAACGA TGAGCCC 2778 4857 UCAGCAAU G CCAUUUCA 1079 TGAAATGG GGCTAGCTACAACGA TGAGCCC 2778 4858 CCUUCCA G UUUCAGUG 1080 CACTGAA GGCTAGCTACAACGA TGAGCCC 2789 4856 CCAUUCAG G UCCCCAG 1082 CTCGAGA GGCTAGCTACAACGA TGAGCAC CCTCAAT 2784 4859 UUUCAGUG G CUUCCCAG 1082 CTCGAGA GGCTAGCTACAACGA TGAGAGG TGAGAGC 2785 4851 CACUUCA A UUUGAGG 1085 CTCAAATG GGCTAGCTACAACGA CAAGAG	4715	GUCCUCUA G CAGGCCUA	1057	TAGGCCTG GGCTAGCTACAACGA TAGAGGAC	2759
4728         CCUAAGAC A UGUGAGGA         1060         TCCTCACA GGCTAGCTACAACGA GTCTTAGG         2762           4730         UAAGACAU G UGAGGAGG         1061         CCTCCTCA GGCTAGCTACAACGA ATGTCTTA         2763           4752         GAAAAAA G CAAAAAGC         1062         GCTTTTG GGCTAGCTACAACGA TTTTTTC         2764           4759         AGCAAAAA G CAAGAGA         1064         TCTCCCTG GGCTAGCTACAACGA TTTTTGCT         2765           4777         AAAGAGAA A CCGGAGA         1064         TCTCCCGG GGCTAGCTACAACGA TTCTCTT         2766           4788         GGGAGAAG G CAUGAGAA         1065         TTCTCATG GGCTAGCTACAACGA TCTCTCC         2767           4790         GAGAAGG A UGAGAAA         1066         CTTTCTCA GGCTAGCTACAACGA GCTTCTC         2768           4800         GAGAAAGA A UUUGAGAC         1067         GTCTCAAA GGCTAGCTACAACGA GCTTCTA         2770           4807         AAUUUGAGA C GCACCAU         1068         ATGGTGG GGCTAGCTACAACGA GTCCAAACGA CTCAAACGA         2771           4811         UGAGACG A CCAUGUG         1079         CCACATGG GGCTAGCTACAACGA GTCCAAACGA GTCCACACCA         2772           4814         GACGCACU G UGGGCACG         1071         TGCCCCA GGCTAGCTACAACGA ATGGTGCC         2773           4820         CCAUGUGG G CACGAGG         1072         CGTGCCCA GGCTAGCTACAACGA CCACA	4719	UCUAGCAG G CCUAAGAC	1058	GTCTTAGG GGCTAGCTACAACGA CTGCTAGA	2760
4730 UAAGACAU G UGAGGAGG 1061 CCTCCTCA GGCTAGCTACAACGA ATGTCTTA 2763 4752 GAAAAAAA G CAAAAAGC 1062 GCTTTTTG GGCTAGCTACAACGA TTTTTTC 2764 4759 AGCAAAAA G CAAGGGAG 1063 CTCCCTTG GGCTAGCTACAACGA TTTTTTC 2765 4777 AAAGAGAA A CCGGGAGA 1064 TCTCCCGG GGCTAGCTACAACGA TTTTTGCT 2766 4788 GGGAGAAG G CAUGAGAA 1065 TTCTCATG GGCTAGCTACAACGA CTTCTCCC 2767 4790 GAGAAGGA A UUGAGAAA 1065 CTTCTCAA GGCTAGCTACAACGA CTTCTCC 2768 4800 GAGAAAGA A UUUGAGAC 1067 GTCTCAAA GGCTAGCTACAACGA CCTTCTCC 2769 4801 AAUUUGAG A CGCACCAU 1068 ATGGTGGG GGCTAGCTACAACGA CTTCTCC 2769 4802 UUUGAGAC G CACCAUGU 1069 ACATGGTG GGCTAGCTACAACGA CTCAAATT 2770 4811 UGAGACGC A CCAUGUG 1069 ACATGGTG GGCTAGCTACAACGA GTCTCAAA 2771 4811 UGAGACGC A CCAUGUG 1070 CCACATGG GGCTAGCTACAACGA GTCTCAAA 2771 4814 GACGCACC A UGUGGGCA 1071 TGCCCACA GGCTAGCTACAACGA GTCTCAA 2772 4816 CGCACCAU G UGGGCACG 1072 CGTGCCCA GGCTAGCTACAACGA GTGCGTCC 2773 4816 CGCACCAU G UGGGCACG 1072 CGTGCCCA GGCTAGCTACAACGA ATGGTGCC 2774 4820 CCAUGUGG C CACGAGGG 1073 CCTCCGTG GGCTAGCTACAACGA CCACATGG 2775 4822 AUGUGGGC A CGGAGGGG 1074 CCCCTCCG GGCTAGCTACAACGA CCACATGC 2776 4822 GGGAGGGG A CGGAGGGG 1074 CCCCTCCG GGCTAGCTACAACGA CCCACATC 2776 4837 GGGACGGG G CUCAGCAA 1076 TTGCTGAG GGCTAGCTACAACGA CCCCCCC 2777 4842 GGGGCUCA G CAAUGCCA 1077 TGGCATTG GGCTAGCTACAACGA CCCCTCC 2777 4845 GCUCAGCA A UGCCAUUU 1078 AAATGGCA GGCTAAGCTACAACGA CCCCTCC 2779 4846 GCGACGCA A UGCCAUUU 1078 AAATGGCA GGCTAAGCTACAACGA TGCTGAGC 2780 4847 UCAGCAAU G CCAUUUCA 1079 TGAAATGG GGCTAGCTACAACGA TGCTGAGC 2780 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA TGCTGAGC 2780 4851 GCUCAGCA A UGCCAUUU 1078 AAATGGCA GGCTAAGCTACAACGA TGCTGAGC 2780 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA TGCTGAGC 2780 4851 GCACCUCUCA G CCCUCUCA 1081 GGAGGCCA GGCTAGCTACAACGA TGCTGAGC 2780 4850 GCAAUGCC A UUUCAGUG 1082 CTGGGAGG GGCTAGCTACAACGA TGCAGAA 2784 4850 GCACAUUCA G UCGCCAG 1082 CTGGGAGG GGCTAGCTACAACGA CACTGAAA 2784 4851 ACCCUUCA A CCUUCAA 1084 TAGAAGGG GGCTAGCTACAACGA CACGAAA 2784 4853 CCUUCAC A CUUCAGAC 1082 CTGGGAGG GGCTAGCTACAACGA	4726	GGCCUAAG A CAUGUGAG	1059	CTCACATG GGCTAGCTACAACGA CTTAGGCC	2761
4752 GAAAAAA G CAAAAAGC 1062 GCTTTTTG GGCTAGCTACAACGA TTTTTTC 2764 4759 AGCAAAAA G CAAGGGAG 1063 CTCCCTTG GGCTAGCTACAACGA TTTTTTC 2765 4777 AAAGAGAA A CCGGGAGA 1064 TCTCCCGG GGCTAGCTACAACGA TTTTTGCT 2766 4788 GGGAGAG G CAUGAGAA 1065 TTCTCATG GGCTAGCTACAACGA CTTCTCCC 2767 4790 GAGAAGG A UGAGAAA 1065 TTCTCATG GGCTAGCTACAACGA GCTTCTCC 2768 4800 GAGAAAGA A UUUGAGAC 1067 GTCTCAAA GGCTAGCTACAACGA GCCTTCTC 2769 4807 AAUUUGAG A CGCACCAU 1068 ATGGTGCG GGCTAGCTACAACGA CTCTCTC 2769 4809 UUUGAGAC G CACCAUGU 1069 ACATGGTG GGCTAGCTACAACGA CTCAAATT 2770 4811 UGAGACGC A CCAUGUG 1070 CCACATGG GGCTAGCTACAACGA GTCTCAAA 2771 4811 UGAGACGC A CCAUGUG 1070 CCACATGG GGCTAGCTACAACGA GTCTCAAA 2771 4814 GACGCACC A UGUGGGCA 1071 TGCCCACA GGCTAGCTACAACGA GGTCCCAA 2772 4814 GACGCACC A UGUGGGCA 1071 TGCCCACA GGCTAGCTACAACGA GGTCCCA 2773 4816 CGCACCAU G UGGGCACG 1072 CGTGCCCA GGCTAGCTACAACGA GGTGCGC 2773 4820 CCAUGUGG G CACGAGGG 1073 CCTCCGTG GGCTAGCTACAACGA CCACATGG 2775 4822 AUGUGGGC A CGGAGGG 1073 CCTCCGTG GGCTAGCTACAACGA CCACATGG 2775 4822 GGAGGGG A CGGGGGG 1074 CCCCTCCG GGCTAGCTACAACGA CCCCCTCC 2777 4837 GGGACGGG G CUCAGCAA 1075 GAGCCCCG GGCTAGCTACAACGA CCCCCTCC 2777 4842 GGGGCUCA G CAAUGCCA 1077 TGCCATTG GGCTAGCTACAACGA CCCCTCC 2777 4845 GCUCAGCA A UGCCAUUU 1078 AAATGGCA GGCTAGCTACAACGA TGAGCCC 2779 4846 GCUCAGCA A UGCCAUUU 1078 AAATGGCA GGCTAGCTACAACGA TGAGCCC 2779 4847 UCAGCAAU G CCAUUCCA 1079 TGAAATGG GGCTAGCTACAACGA TGCTGAGC 2780 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA TGCTGAGC 2780 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA TGCTGAGC 2782 4850 GCACUCCCA G CUCCCCAG 1081 GGAAGCCA GGCTAGCTACAACGA TGCTGAAC 2781 4850 GCACUCUA G UGCCUCCC 1081 GGAAGCCA GGCTAGCTACAACGA TGCTGAAC 2782 4851 ACCCUUCUA C CUUCAGCC 1082 CTGGGAAG GGCTAGCTACAACGA CACTGAAA 2784 4850 GCACUCCCA G CUCCCAG 1082 CTGGGAAG GGCTAGCTACAACGA CACTGAAA 2784 4850 GCAUUCCA G CUCCCAG 1082 CTGGGAAG GGCTAGCTACAACGA CACTGAAA 2784 4851 ACCCUUCUA A CUUUGAGG 1085 CTCAAATG GGCTAGCTACAACGA CACTGAAACGA CAGAGGT 2785 4883 CCUUCUAC A UUUGAGGG 1086 CCCCCACAAA GGCTAGCT	4728	CCUAAGAC A UGUGAGGA	1060	TCCTCACA GGCTAGCTACAACGA GTCTTAGG	2762
4759 AGCAAAAA G CAAGGGAG 1063 CTCCCTTG GGCTAGCTACAACGA TTTTTGCT 2765 4777 AAAGAGAA A CCGGGAGA 1064 TCTCCCGG GGCTAGCTACAACGA TTCTCTTT 2766 4788 GGGAGAG G CAUGAGAA 1065 TTCTCATG GGCTAGCTACAACGA TTCTCTTT 2766 4788 GGGAGAG G CAUGAGAA 1065 TTCTCATG GGCTAGCTACAACGA CTTCTCC 2767 4790 GAGAAGGC A UGAGAAAG 1066 CTTTCTCA GGCTAGCTACAACGA GCCTTCTC 2768 4800 GAGAAAGA A UUUGAGAC 1067 GTCTCAAA GGCTAGCTACAACGA TCTTCTC 2769 4807 AAUUUGAGA C GCCACCAU 1068 ATGGTGCG GGCTAGCTACAACGA CTCAAATT 2770 4809 UUUGAGAC G CACCAUGU 1069 ACATGGTG GGCTAGCTACAACGA GTCTCAAA 2771 4811 UGAGACGC A CCAUGUG 1070 CCACATGG GGCTAGCTACAACGA GCTCTCA 2772 4814 GACGCACC A UGUGGGCA 1071 TGCCCACA GGCTAGCTACAACGA GGTGCTC 2773 4816 CGCACCAU G UGGGCAC 1072 CGTGCCCA GGCTAGCTACAACGA GTGCTGC 2773 4820 CCAUGUGG G CACGAGAG 1073 CCTCCGTG GGCTAGCTACAACGA ATGGTGCG 2774 4821 AUGUGGGC A CGGAGGG 1073 CCTCCGTG GGCTAGCTACAACGA ATGGTGCG 2775 4822 AUGUGGGC A CGGAGGG 1074 CCCCTCCG GGCTAGCTACAACGA CCACATGG 2775 4832 GGAGGGGG A CGGGGCUC 1075 GAGCCCC GGCTAGCTACAACGA CCCCTCC 2777 4837 GGGACGGG G CUCAGCAA 1076 TTGCTGAG GGCTAGCTACAACGA CCCCTCC 2777 4842 GGGGCUCA G CAAUGCCA 1077 TGGCATTG GGCTAGCTACAACGA CCCCTCC 2779 4842 GGGGCUCA G CAAUGCCA 1077 TGGCATTG GGCTAGCTACAACGA TGGCTCC 2778 4843 GGGACGGG G CUCAGCAA 1076 TTGCTGAG GGCTAGCTACAACGA TGAGCCCC 2779 4844 GGCACCA UUUCAGUG 1080 AAATGGCA GGCTAGCTACAACGA TGAGCCCC 2779 4845 GCUCAGCA A UGCCAUUU 1078 AAATGGCA GGCTAGCTACAACGA TGCTGACC 2780 4847 UCAGCAAU G CCAUUUCA 1079 TGAAATGG GGCTAGCTACAACGA ATTGCTGA 2781 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA TGAAATGG 2781 4851 GCUUCCAG G UCCCCAG 1082 CTGGGAAG GGCTAGCTACAACGA TGAAATGG 2781 4852 CCUUCCAG G CUUCCCAG 1082 CTGGGAAG GGCTAGCTACAACGA TGAAATGG 2781 4853 CAGUUCCA G CUUCCAG 1082 CTGGGAAG GGCTAGCTACAACGA TGAAATGG 2783 4859 UUUCAGUG G CUUCCCAG 1082 CTGGGAAG GGCTAGCTACAACGA TGAAATGG 2783 4851 ACCCUUCU A CAUUUGAGG 1086 CCCCTCAA GGCTAGCTACAACGA CACTGAAA 2784 4867 GCUUCCA G CUUCCAG 1082 CTGGGAAG GGCTAGCTACAACGA CACTGAAA 2784 4863 CCUUCCAC A UUUGAGGG 1086 CCCCTAAA GGCTAGCTACAACGA CACTGAAG 27	4730	UAAGACAU G UGAGGAGG	1061	CCTCCTCA GGCTAGCTACAACGA ATGTCTTA	2763
4777 AAAGAGAA A CCGGGAGA 1064 TCTCCCGG GGCTAGCTACAACGA TTCTCTTT 2766 4788 GGGAGAAG G CAUGAGAA 1065 TTCTCATG GGCTAGCTACAACGA CTTCTCC 2767 4790 GAGAAGGC A UGAGAAAG 1066 CTTTCTCA GGCTAGCTACAACGA CTTCTCC 2768 4800 GAGAAAGA A UUUGAGAC 1067 GTCTCAAA GGCTAGCTACAACGA CCTTCTC 2769 4807 AAUUUGAG A CGCACCAU 1068 ATGGTGCG GGCTAGCTACAACGA CTCAAATT 2770 4809 UUUGAGAC G CACCAUGU 1069 ACATGGTG GGCTAGCTACAACGA CTCAAATT 2770 4811 UGAGACGC A CCAUGUG 1070 CCACATGG GGCTAGCACACGA GCTCCAAA 2771 4814 GACGCACC A UGUGGGCA 1071 TGCCCACA GGCTAGCACACGA GGTCTCA 2772 4816 CGCACCAU G UGGGCACC 1072 CGTGCCCA GGCTAGCACACGA GGTGCGTC 2773 4816 CGCACCAU G UGGGCACC 1072 CGTGCCCA GGCTAGCACACGA ATGGTGCG 2774 4820 CCAUGUGG G CACGGAGG 1073 CCTCCGTG GGCTACAACGA CCACATGG 2775 4822 AUGUGGGC A CGGAGGGG 1073 CCTCCGTG GGCTAGCACACGA CCACATGG 2775 4832 GGAGGGG A CGGGGGGC 1075 GAGCCCCG GGCTAGCTACAACGA CCACATG 2776 4832 GGAGGGG A CGGGGGCU 1075 GAGCCCCG GGCTAGCTACAACGA CCCCCCCC 2777 4837 GGGACGG G CUCAGCAA 1076 TTGCTGAG GGCTAGCTACAACGA CCCCCCCC 2777 4842 GGGGCUCA G CAAUGCCA 1077 TGGCATTG GGCTAGCTACAACGA CCCCCCCC 2778 4845 GCUCAGCA A UGCCAAUUU 1078 AAATGGCA GGCTAGCTACAACGA TGGTGCC 2779 4845 GCUCAGCA A UGCCAUUU 1078 AAATGGCA GGCTAGCTACAACGA TGGTGCC 2779 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA TGCTGAGC 2780 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA TGCTGAGC 2780 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA TGCTGAGC 2782 4850 GCAUUCCA G CUUCCCAG 1081 GGAAGCCA GGCTAGCTACAACGA TGGGAGC 2780 4867 GCUUCCCA G CUCUCAC 1081 GGAAGCCA GGCTAGCTACAACGA TGGGAGC 2782 4868 CCCUUCUA A CCCUUCUA 1084 TAGAAGGG GGCTAGCTACAACGA CACTGAAA 2784 4867 GCUUCCCA G CUCUCAC 1083 GGTCAGAG GGCTAGCTACAACGA CACTGAAA 2784 4867 GCUUCCCA G CUCUCAC 1083 GGTCAGAG GGCTAGCTACAACGA CACTGAAA 2784 4868 ACCCUUCUA A CAUUUGAG 1086 CCCCCCAAA GGCTAGCTACAACGA CACTGAAA 2784 4869 GCUUCCCA G CUCUCAC 1083 GGTCAGAG GGCTAGCTACAACGA CACTGAAA 2786 4873 CAGCUUCUA A CAUUUGAG 1086 CCCCCCAAA GGCTAGCTACAACGA CAGAGCTG 2786 4881 ACCCUUCUA A CAUUUGAG 1086 CCCCCAAAC GGCTAGCTACAACGA CAGAGCTG 2786	4752	GAAAAAA G CAAAAAGC	1062	GCTTTTTG GGCTAGCTACAACGA TTTTTTTC	2764
4788 GGGAGAAG G CAUGAGAA 1065 TTCTCATG GGCTAGCTACAACGA CTTCTCCC 2767 4790 GAGAAGGC A UGAGAAAG 1066 CTTTCTCA GGCTAGCTACAACGA GCCTTCTC 2768 4800 GAGAAAGA A UUUGAGAC 1067 GTCTCAAA GGCTAGCTACAACGA TCTTCTC 2769 4807 AAUUUGAG A CGCACCAU 1068 ATGGTGCG GGCTAGCTACAACGA CTCAAATT 2770 4809 UUUGAGAC G CACCAUGU 1069 ACATGGTG GGCTAGCTACAACGA GTCTCAAA 2771 4811 UGAGACGC A CCAUGUG 1070 CCACATGG GGCTAGCTACAACGA GCGTCTCA 2772 4814 GACGCACC A UGUGGGCA 1071 TGCCCACA GGCTAGCTACAACGA GCGTCTCA 2772 4816 CGCACCAU G UGGGCACG 1072 CGTGCCCA GGCTAGCTACAACGA GGTGCGTC 2773 4816 CGCACCAU G UGGGCACG 1072 CGTGCCCA GGCTAGCTACAACGA ATGGTGCG 2774 4820 CCAUGUGG G CACGGAGG 1073 CCTCCGTG GGCTAGCACACGA CCACATGG 2775 4822 AUGUGGGC A CGGAGGGG 1074 CCCCTCCG GGCTAGCTACAACGA CCACATGG 2776 4832 GGAGGGGG A CGGGGGCU 1075 GAGCCCCG GGCTAGCTACAACGA CCCCCCTC 2777 4837 GGGACGGG G CUCAGCAA 1076 TTGCTGAG GGCTAGCTACAACGA CCCCCTCC 2777 4842 GGGGCUCA G CAAUGCCA 1077 TGGCATTG GGCTAGCTACAACGA CCCCCTCC 2778 4842 GGGGCUCA G CAAUGCCA 1077 TGGCATTG GGCTAGCTACAACGA CCGGTCCC 2778 4845 GCUCAGCA A UGCCAUUU 1078 AAATGGCA GGCTAGCTACAACGA TGGTGCC 2779 4846 GCUCAGCA A UGCCAUUU 1078 AAATGGCA GGCTAGCTACAACGA TGGTGCC 2779 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA ATTGCTGA 2781 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA TGGTGAGC 2780 4847 UCAGCAAU G CCAUUUCA 1079 TGAAATGG GGCTAGCTACAACGA TGGTGAGC 2781 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA TGAGACCC 2778 4851 UUCAGUG G CUUCCCAG 1081 GGAAGCCA GGCTAGCTACAACGA TGAGAGC 2782 4852 UUUCAGUG G CUUCCCAG 1082 CTGGGAAG GGCTAGCTACAACGA TGAGAGC 2785 4863 CCUUCUA A CAUUUGAG 1085 CTCAAATG GGCTAGCTACAACGA CACTGAAA 2784 4867 GCUUCCCA G CUUCUA 1084 TAGAAGGG GGCTAGCTACAACGA CACTGAAA 2784 4867 GCUUCCCA CUUCUA 1084 TAGAAGGG GGCTAGCTACAACGA CACTGAAA 2784 4868 ACCCUUCUA A CAUUUGAG 1085 CTCAAATG GGCTAGCTACAACGA CAGAGCTG 2785 4873 CAGCUUCA A CUUUGAGG 1086 CCCCCCAAA GGCTAGCTACAACGA CAGAGGGT 2787	4759	AGCAAAAA G CAAGGGAG	1063	CTCCCTTG GGCTAGCTACAACGA TTTTTGCT	2765
4790 GAGAAGGC A UGAGAAAG 1066 CTTTCTCA GGCTAGCTACAACGA GCCTTCTC 2768 4800 GAGAAAGA A UUUGAGAC 1067 GTCTCAAA GGCTAGCTACAACGA TCTTTCTC 2769 4807 AAUUUGAG A CGCACCAU 1068 ATGGTGCG GGCTAGCTACAACGA TCTTTCTC 2769 4809 UUUGAGAC G CACCAUGU 1069 ACATGGTG GGCTAGCTACAACGA GTCTCAAA 2771 4811 UGAGACGC A CCAUGUGG 1070 CCACATGG GGCTAGCTACAACGA GCTCCAAA 2772 4814 GACGCACC A UGUGGGCA 1071 TGCCCACA GGCTAGCTACAACGA GGTGCGTC 2773 4816 CGCACCAU G UGGGCACG 1072 CGTGCCCA GGCTAGCTACAACGA ATGGTGCG 2774 4820 CCAUGUGG G CACGGAGG 1072 CGTGCCCA GGCTAGCTACAACGA ATGGTGCG 2775 4822 AUGUGGGC A CGGAGGG 1074 CCCCTCCG GGCTAGCTACAACGA CCACATGG 2775 4832 GGAGGGGG A CGGAGGG 1074 CCCCTCCG GGCTAGCTACAACGA CCCCCTCC 2777 4837 GGGACGGG G CUCAGCAA 1076 TTGCTGAG GGCTAGCTACAACGA CCCCCTCC 2777 4842 GGGGCUCA G CAAUGCCA 1077 TGGCATTG GGCTAGCTACAACGA CCCCCTCC 2778 4842 GGGGCUCA G CAAUGCCA 1077 TGGCATTG GGCTAGCTACAACGA TGGCCCC 2779 4845 GCUCAGCA A UGCCAUUU 1078 AAATGGCA GGCTAGCTACAACGA TGCTGAGC 2780 4847 UCAGCAAU G CCAUUUCA 1079 TGAAATGG GGCTAGCTACAACGA ATTGCTGAG 2781 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA TGCTGAGC 2782 4856 CCAUUUCA G UGGCUUCC 1081 GGAAGCCA GGCTAGCTACAACGA TGAAATGG 2783 4859 UUUCAGUG G CUUCCCAG 1082 CTGGGAAG GGCTAGCTACAACGA TGAAATGG 2783 4867 GCUUCCCA G CUCUGACC 1083 GGTAGCTAGCAACGA TGAAATGG 2785 4873 CAGCUCUA C CUUUCAA 1084 TAGAAGGG GGCTAGCTACAACGA CACTGAAA 2784 4873 CAGCUUCU A CAUUUGAG 1085 CTCAAATG GGCTAGCTACAACGA CACTGAAA 2786 4881 ACCCUUCUA CAUUUGAGG 1086 CCCTCAAA GGCTAGCTACAACGA CAGGACTG 2786 4881 ACCCUUCUA C CUUUCAA 1084 TAGAAGGG GGCTAGCTACAACGA CAGGACTG 2786 4881 ACCCUUCUA C CUUUCAA 1086 CCCTCAAA GGCTAGCTACAACGA CACTGAAA 2788 4891 AUUUGAGGG CCCAGCCA 1087 TGGCTGAG GGCTAGCTACAACGA CACTGAAA 2788 4891 AUUUGAGG G CCCAGCCA 1087 TGGCTGAG GGCTAGCTACAACGA CACTGAAA 2788 4891 AUUUGAGG G CCCAGCCA 1087 TGGCTGAG GGCTAGCTACAACGA CACTGAAA 2788	4777	AAAGAGAA A CCGGGAGA	1064	TCTCCCGG GGCTAGCTACAACGA TTCTCTTT	2766
4800 GAGAAAGA A UUUGAGAC 1067 GTCTCAAA GGCTAGCTACAACGA TCTTTCTC 2769 4807 AAUUUGAG A CGCACCAU 1068 ATGGTGCG GGCTAGCTACAACGA CTCAAATT 2770 4809 UUUGAGAC G CACCAUGU 1069 ACATGGTG GGCTAGCTACAACGA GTCTCAAA 2771 4811 UGAGACGC A CCAUGUGG 1070 CCACATGG GGCTAGCTACAACGA GCGTCTCA 2772 4814 GACGCACC A UGUGGGCA 1071 TGCCCACA GGCTAGCTACAACGA GCGTCTCA 2772 4816 CGCACCAU G UGGGCACG 1072 CGTGCCCA GGCTAGCTACAACGA ATGGTGCG 2774 4820 CCAUGUGG G CACGGAGG 1073 CCTCCGTG GGCTAGCTACAACGA ATGGTGCG 2775 4822 AUGUGGGC A CGGAGGGG 1074 CCCCTCCG GGCTAGCTACAACGA CCACATGG 2775 4832 GGAGGGGG A CGGGGGCU 1075 GAGCCCCG GGCTAGCTACAACGA CCCCCTCC 2777 4837 GGGACGGG G CUCAGCAA 1076 TTGCTGAG GGCTAGCTACAACGA CCCCTCC 2777 4842 GGGGCUCA G CAAUGCCA 1077 TGGCATTG GGCTAGCTACAACGA CCCCTCC 2779 4845 GCUCAGCA A UGCCAUUU 1078 AAATGGCA GGCTAGCTACAACGA TGAGCCCC 2779 4846 GCUCAGCA UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA ATTGCTGA 2781 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA TGAGCCC 2782 4856 CCAUUUCA G UGGCUUCC 1081 GGAAGCCA GGCTAGCTACAACGA TGAAATGG 2783 4859 UUUCAGUG G CUUCCCAG 1082 CTGGGAAG GGCTAGCTACAACGA TGAAATGG 2783 4867 GCUUCCCA G CUCUGACC 1083 GGTCAGGA GGCTAGCTACAACGA TGAAATGG 2783 4873 CAGCUCU A CAUUUGA 1084 TAGAAGG GGCTAGCTACAACGA CACTGAAA 2784 4881 ACCCUUCU A CAUUUGAGG 1085 CTCAAATG GGCTAGCTACAACGA CAGGAGCT 2786 4881 ACCCUUCU A CAUUUGAGG 1086 CCCTCAAA GGCTAGCTACAACGA CAGGAGCT 2786 4881 ACCCUUCU A CAUUUGAGG 1086 CCCCCCAAA GGCTAGCTACAACGA CAGAACGG 2786 4881 ACCCUUCUA C UUUGAGGG 1086 CCCCCAAAA GGCTAGCTACAACGA CAGGAGCT 2786 4881 ACCCUUCUA C UUUGAGGG 1086 CCCCCAAAA GGCTAGCTACAACGA CAGAACGG 2787	4788	GGGAGAAG G CAUGAGAA	1065	TTCTCATG GGCTAGCTACAACGA CTTCTCCC	2767
4807 AAUUUGAG A CGCACCAU 1068 ATGGTGCG GGCTAGCTACAACGA CTCAAATT 2770 4809 UUUGAGAC G CACCAUGU 1069 ACATGGTG GGCTAGCTACAACGA GTCTCAAA 2771 4811 UGAGACGC A CCAUGUGG 1070 CCACATGG GGCTAGCTACAACGA GCGTCTCA 2772 4814 GACGCACC A UGUGGGCA 1071 TGCCCACA GGCTAGCTACAACGA GGTGCGTC 2773 4816 CGCACCAU G UGGGCACG 1072 CGTGCCCA GGCTAGCACACGA ATGGTGCG 2774 4820 CCAUGUGG G CACGGAGG 1073 CCTCCGTG GGCTAGCACACGA ATGGTGCG 2775 4822 AUGUGGGC A CGGAGGG 1074 CCCCTCCG GGCTAGCACACGA CCACATGG 2775 4832 GGAGGGGG A CGGGGCUC 1075 GAGCCCCG GGCTAGCACACGA CCCCCTCC 2777 4837 GGGACGGG G CUCAGCAA 1076 TTGCTGAG GGCTAGCACACGA CCCCCTCC 2778 4842 GGGGCUCA G CAAUGCCA 1077 TGGCATTG GGCTAGCACACGA CCCCTCC 2779 4845 GCUCAGCA A UGCCAUUU 1078 AAATGGCA GGCTAGCTACAACGA TGAGCCCC 2779 4847 UCAGCAAU G CCAUUUCA 1079 TGAAATGG GGCTAGCTACAACGA ATTGCTGAC 2781 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA TGAGCCC 2782 4856 CCAUUUCA G UGGCUUCC 1081 GGAAGCCA GGCTAGCTACAACGA TGAAATGG 2781 4859 UUUCAGUG G CUUCCCAG 1082 CTGGGAAG GGCTAGCTACAACGA CACTGAAA 2784 4867 GCUUCCCA G CUCUGACC 1083 GGTCAGGCTAGCAACGA CACTGAAA 2784 4867 GCUUCCCA G CUCUGACC 1083 GGTCAGAG GGCTAGCTACAACGA CACTGAAA 2784 4873 CAGCUCUG A CCCUUCUA 1084 TAGAAGGG GGCTAGCTACAACGA CAGAGGT 2786 4881 ACCCUUCU A CAUUUGAGG 1086 CCCCTCAAA GGCTAGCTACAACGA CAGAGGT 2787 4883 CCUUCUCA A UUUGAGGG 1086 CCCCTCAAA GGCTAGCTACAACGA CAGAGGT 2787 4883 CCUUCUAC A UUUGAGGG 1086 CCCCCCAAA GGCTAGCTACAACGA CACGAAGGGT 2787	4790	GAGAAGGC A UGAGAAAG	1066	CTTTCTCA GGCTAGCTACAACGA GCCTTCTC	2768
4809 UJUGAGAC G CACCAUGU 1069 ACATGGTG GGCTAGCTACAACGA GTCTCAAA 2771 4811 UGAGACGC A CCAUGUGG 1070 CCACATGG GGCTAGCTACAACGA GCGTCTCA 2772 4814 GACGCACC A UGUGGGCA 1071 TGCCCACA GGCTAGCTACAACGA GCGTCTCA 2773 4816 CGCACCAU G UGGGCACG 1072 CGTGCCCA GGCTAGCTACAACGA ATGGTGCG 2774 4820 CCAUGUGG G CACGGAGG 1073 CCTCCGTG GGCTAGCTACAACGA ATGGTGCG 2775 4822 AUGUGGGC A CGGAGGG 1074 CCCCTCCG GGCTAGCTACAACGA CCACATGG 2775 4832 GGAGGGGG A CGGGGGUC 1075 GAGCCCCG GGCTAGCTACAACGA CCCCCTCC 2777 4837 GGGACGGG G CUCAGCAA 1076 TTGCTGAG GGCTAGCTACAACGA CCCCCTCC 2777 4842 GGGGCUCA G CAAUGCCA 1077 TGGCATTG GGCTAGCTACAACGA CCCCCTCC 2779 4845 GCUCAGCA A UGCCAUUU 1078 AAATGGCA GGCTAGCTACAACGA TGGTGAGC 2780 4847 UCAGCAAU G CCAUUUCA 1079 TGAAATGG GGCTAGCTACAACGA ATTGCTGAC 2781 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA ATTGCTGA 2781 4856 CCAUUUCA G UGGCUUCC 1081 GGAAGCCA GGCTAGCTACAACGA TGAAATGG 2783 4859 UUUCAGUG G CUUCCCAG 1082 CTGGGAAG GGCTAGCTACAACGA TGAAATGG 2783 4867 GCUUCCCA G CUCUGACC 1083 GGTCAGGCTACCAACGA TGAAATGG 2785 4873 CAGCUCUG A CCCUUCUA 1084 TAGAAGGG GGCTAGCTACAACGA CAGGAAGCT 2786 4881 ACCCUUCU A CAUUUGAGG 1085 CTCAAATG GGCTAGCTACAACGA AGAAGGGT 2787 4883 CCUUCUAC A UUUGAGGG 1086 CCCTCAAA GGCTAGCTACAACGA GAAGGGT 2787 4881 ACCCUUCU A CAUUUGAGG 1086 CCCTCAAA GGCTAGCTACAACGA CACGAAGGGT 2787	4800	GAGAAAGA A UUUGAGAC	1067	GTCTCAAA GGCTAGCTACAACGA TCTTTCTC	2769
4811 UGAGACGC A CCAUGUGG 1070 CCACATGG GGCTAGCTACAACGA GCGTCTCA 2772 4814 GACGCACC A UGUGGGCA 1071 TGCCCACA GGCTAGCTACAACGA GGTGCTC 2773 4816 CGCACCAU G UGGGCACG 1072 CGTGCCCA GGCTAGCTACAACGA ATGGTGCG 2774 4820 CCAUGUGG G CACGGAGG 1073 CCTCCGTG GGCTAGCTACAACGA CCACATGG 2775 4822 AUGUGGGC A CGGAGGG 1074 CCCCTCCG GGCTAGCTACAACGA CCACATGG 2776 4832 GGAGGGG A CGGGGGCUC 1075 GAGCCCCG GGCTAGCTACAACGA CCCCCTCC 2777 4837 GGGACGGG G CUCAGCAA 1076 TTGCTGAG GGCTAGCTACAACGA CCCCTCC 2778 4842 GGGGCUCA G CAAUGCCA 1077 TGGCATTG GGCTAGCTACAACGA CCCGTCC 2779 4845 GCUCAGCA A UGCCAUUU 1078 AAATGGCA GGCTAGCTACAACGA TGCTGAGC 2780 4847 UCAGCAAU G CCAUUUCA 1079 TGAAATGG GGCTAGCTACAACGA ATTGCTGA 2781 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA ATTGCTGA 2781 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA TGAAATGG 2782 4856 CCAUUUCA G UGGCUUCC 1081 GGAAGCCA GGCTAGCTACAACGA TGAAATGG 2783 4859 UUUCAGUG G CUUCCCAG 1082 CTGGGAAG GGCTAGCTACAACGA CACTGAAA 2784 4867 GCUUCCCA G CUCUGACC 1083 GGTCAGGTAGCTACAACGA CACTGAAA 2784 4867 GCUUCCCA G CUCUGACC 1083 GGTCAGGTAGCTACAACGA CACTGAAA 2784 4868 CAGCUUCU A CAUUUGAG 1085 CTCAAATG GGCTAGCTACAACGA CAGAGCTG 2786 4873 CAGCUCU A CAUUUGAG 1085 CTCAAATG GGCTAGCTACAACGA AGAAGGGT 2787 4881 ACCCUUCU A CAUUUGAG 1085 CTCAAATG GGCTAGCTACAACGA AGAAGGGT 2787 4883 CCUUCUAC A UUUGAGGG 1086 CCCTCAAA GGCTAGCTACAACGA GAAGGGT 2787 4883 CCUUCUAC A UUUGAGGG 1086 CCCTCAAA GGCTAGCTACAACGA GAAGGGT 2788	4807	AAUUUGAG A CGCACCAU	1068	ATGGTGCG GGCTAGCTACAACGA CTCAAATT	2770
4814 GACGCACC A UGUGGGCA 1071 TGCCCACA GGCTAGCTACAACGA GGTGCGTC 2773 4816 CGCACCAU G UGGGCACG 1072 CGTGCCCA GGCTAGCTACAACGA ATGGTGCG 2774 4820 CCAUGUGG G CACGGAGG 1073 CCTCCGTG GGCTAGCTACAACGA CCACATGG 2775 4822 AUGUGGGC A CGGAGGGG 1074 CCCCTCCG GGCTAGCTACAACGA GCCCACAT 2776 4832 GGAGGGG A CGGGGCUC 1075 GAGCCCCG GGCTAGCTACAACGA CCCCCTCC 2777 4837 GGGACGGG G CUCAGCAA 1076 TTGCTGAG GGCTAGCTACAACGA CCCCTCC 2778 4842 GGGGCUCA G CAAUGCCA 1077 TGGCATTG GGCTAGCTACAACGA TGCTGAGC 2779 4845 GCUCAGCA A UGCCAUUU 1078 AAATGGCA GGCTAGCTACAACGA TGCTGAGC 2780 4847 UCAGCAAU G CCAUUUCA 1079 TGAAATGG GGCTAGCTACAACGA ATTGCTGA 2781 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA GGCATTGC 2782 4856 CCAUUUCA G UGGCUUCC 1081 GGAAGCCA GGCTAGCTACAACGA TGAAATGG 2783 4859 UUUCAGUG G CUUCCCAG 1082 CTGGGAAG GGCTAGCTACAACGA CACTGAAA 2784 4867 GCUUCCCA G CUCUGACC 1083 GGTCAGAG GGCTAGCTACAACGA TGGGAAGC 2785 4873 CAGCUCUA CCUUCUA 1084 TAGAAGGG GGCTAGCTACAACGA CAGAGCTG 2786 4881 ACCCUUCUA CAUUUGAGG 1085 CTCAAATG GGCTAGCTACAACGA AGAAGGGT 2787 4883 CCUUCUAC A UUUGAGGG 1086 CCCTCAAA GGCTAGCTACAACGA GTAGAAGG 2788 4891 AUUUGAGG G CCCAGCCA 1087 TGGCTGGG GGCTAGCTACAACGA GTAGAAGG 2788	4809	UUUGAGAC G CACCAUGU	1069	ACATGGTG GGCTAGCTACAACGA GTCTCAAA	2771
4816 CGCACCAU G UGGGCACG 1072 CGTGCCCA GGCTAGCTACAACGA ATGGTGCG 2774 4820 CCAUGUGG G CACGGAGG 1073 CCTCCGTG GGCTAGCTACAACGA CCACATGG 2775 4822 AUGUGGGC A CGGAGGGG 1074 CCCCTCCG GGCTAGCTACAACGA CCACATGG 2776 4832 GGAGGGGG A CGGGGCUC 1075 GAGCCCCG GGCTAGCTACAACGA CCCCCTCC 2777 4837 GGGACGGG G CUCAGCAA 1076 TTGCTGAG GGCTAGCTACAACGA CCCCTCC 2778 4842 GGGGCUCA G CAAUGCCA 1077 TGGCATTG GGCTAGCTACAACGA TGAGCCCC 2779 4845 GCUCAGCA A UGCCAUUU 1078 AAATGGCA GGCTAGCTACAACGA TGCTGAGC 2780 4847 UCAGCAAU G CCAUUUCA 1079 TGAAATGG GGCTAGCTACAACGA ATTGCTGA 2781 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA GGCATTGC 2782 4856 CCAUUUCA G UGGCUUCC 1081 GGAAGCCA GGCTAGCTACAACGA TGAAATGG 2783 4859 UUUCAGUG G CUUCCCAG 1082 CTGGGAAG GGCTAGCTACAACGA TGAAATGG 2784 4867 GCUUCCCA G CUCUGACC 1083 GGTCAGAG GGCTAGCTACAACGA TGGGAAGC 2785 4873 CAGCUCUG A CCCUUCUA 1084 TAGAAGGG GGCTAGCTACAACGA CACTGAAA 2784 4861 ACCCUUCU A CAUUUGAGG 1085 CTCAAATG GGCTAGCTACAACGA AGAAGGGT 2786 4881 ACCCUUCU A CAUUUGAGG 1086 CCCTCAAA GGCTAGCTACAACGA AGAAGGGT 2786 4881 ACCCUUCU A CAUUUGAGG 1086 CCCCCCAAA GGCTAGCTACAACGA AGAAGGGT 2787 4883 CCUUCUAC A UUUGAGGG 1086 CCCTCAAA GGCTAGCTACAACGA GTAGAAGG 2788 4891 AUUUGAGG G CCCAGCCA 1087 TGGCTGGG GGCTAGCTACAACGA CCTCAAAT 2789	4811	UGAGACGC A CCAUGUGG	1070	CCACATGG GGCTAGCTACAACGA GCGTCTCA	2772
4820 CCAUGUGG G CACGGAGG 1073 CCTCCGTG GGCTAGCTACAACGA CCACATGG 2775 4822 AUGUGGGC A CGGAGGGG 1074 CCCCTCCG GGCTAGCTACAACGA GCCCACAT 2776 4832 GGAGGGGG A CGGGGCUC 1075 GAGCCCCG GGCTAGCTACAACGA CCCCCTCC 2777 4837 GGGACGGG G CUCAGCAA 1076 TTGCTGAG GGCTAGCTACAACGA CCCCCTCC 2778 4842 GGGGCUCA G CAAUGCCA 1077 TGGCATTG GGCTAGCTACAACGA TGAGCCCC 2779 4845 GCUCAGCA A UGCCAUUU 1078 AAATGGCA GGCTAGCTACAACGA TGCTGAGC 2780 4847 UCAGCAAU G CCAUUUCA 1079 TGAAATGG GGCTAGCTACAACGA ATTGCTGA 2781 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA GGCATTGC 2782 4856 CCAUUUCA G UGGCUUCC 1081 GGAAGCCA GGCTAGCTACAACGA TGAAATGG 2783 4859 UUUCAGUG G CUUCCCAG 1082 CTGGGAAG GGCTAGCTACAACGA TGAAATGG 2784 4867 GCUUCCCA G CUCUGACC 1083 GGTCAGAG GGCTAGCTACAACGA TGGGAAGC 2785 4873 CAGCUCUG A CCCUUCUA 1084 TAGAAGGG GGCTAGCTACAACGA CAGAGCTG 2786 4881 ACCCUUCU A CAUUUGAGG 1085 CTCAAATG GGCTAGCTACAACGA AGAAGGGT 2787 4883 CCUUCUAC A UUUGAGGG 1086 CCCCTCAAA GGCTAGCTACAACGA GTAGAAGG 2788 4891 AUUUGAGG G CCCAGCCA 1087 TGGCTGGG GGCTAGCTACAACGA GTAGAAGG 2788	4814	GACGCACC A UGUGGGCA	1071	TGCCCACA GGCTAGCTACAACGA GGTGCGTC	2773
4822 AUGUGGGC A CGGAGGGG 1074 CCCCTCCG GGCTAGCTACAACGA GCCCACAT 2776 4832 GGAGGGGG A CGGGGCUC 1075 GAGCCCCG GGCTAGCTACAACGA CCCCCTCC 2777 4837 GGGACGGG G CUCAGCAA 1076 TTGCTGAG GGCTAGCTACAACGA CCCCCTCC 2778 4842 GGGGCUCA G CAAUGCCA 1077 TGGCATTG GGCTAGCTACAACGA TGAGCCCC 2779 4845 GCUCAGCA A UGCCAUUU 1078 AAATGGCA GGCTAGCTACAACGA TGCTGAGC 2780 4847 UCAGCAAU G CCAUUUCA 1079 TGAAATGG GGCTAGCTACAACGA ATTGCTGA 2781 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA GGCATTGC 2782 4856 CCAUUUCA G UGGCUUCC 1081 GGAAGCCA GGCTAGCTACAACGA TGAAATGG 2783 4859 UUUCAGUG G CUUCCCAG 1082 CTGGGAAG GGCTAGCTACAACGA CACTGAAA 2784 4867 GCUUCCCA G CUCUGACC 1083 GGTCAGAG GGCTAGCTACAACGA TGGGAAGC 2785 4873 CAGCUCUG A CCCUUCUA 1084 TAGAAGGG GGCTAGCTACAACGA CAGAGCTG 2786 4881 ACCCUUCU A CAUUUGAG 1085 CTCAAATG GGCTAGCTACAACGA AGAAGGGT 2787 4883 CCUUCUAC A UUUGAGGG 1086 CCCCTCAAA GGCTAGCTACAACGA GTAGAAGG 2788 4891 AUUUGAGG G CCCAGCCA 1087 TGGCTGGG GGCTAGCTACAACGA CTCAAAT 2789	4816	CGCACCAU G UGGGCACG	1072	CGTGCCCA GGCTAGCTACAACGA ATGGTGCG	2774
4832 GGAGGGG A CGGGGCUC 1075 GAGCCCCG GGCTAGCTACAACGA CCCCCTCC 2777 4837 GGGACGGG G CUCAGCAA 1076 TTGCTGAG GGCTAGCTACAACGA CCCGTCCC 2778 4842 GGGGCUCA G CAAUGCCA 1077 TGGCATTG GGCTAGCTACAACGA TGAGCCCC 2779 4845 GCUCAGCA A UGCCAUUU 1078 AAATGGCA GGCTAGCTACAACGA TGCTGAGC 2780 4847 UCAGCAAU G CCAUUUCA 1079 TGAAATGG GGCTAGCTACAACGA ATTGCTGA 2781 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA GGCATTGC 2782 4856 CCAUUUCA G UGGCUUCC 1081 GGAAGCCA GGCTAGCTACAACGA TGAAATGG 2783 4859 UUUCAGUG G CUUCCCAG 1082 CTGGGAAG GGCTAGCTACAACGA CACTGAAA 2784 4867 GCUUCCCA G CUCUGACC 1083 GGTCAGAG GGCTAGCTACAACGA TGGGAAGC 2785 4873 CAGCUCUG A CCCUUCUA 1084 TAGAAGGG GGCTAGCTACAACGA CAGAGCTG 2786 4881 ACCCUUCU A CAUUUGAG 1085 CTCAAATG GGCTAGCTACAACGA AGAAGGGT 2787 4883 CCUUCUAC A UUUGAGGG 1086 CCCTCAAA GGCTAGCTACAACGA GTAGAAGG 2788 4891 AUUUGAGG G CCCAGCCA 1087 TGGCTGGG GGCTAGCTACAACGA CCTCAAAT 2789	4820	CCAUGUGG G CACGGAGG	1073	CCTCCGTG GGCTAGCTACAACGA CCACATGG	2775
4837 GGGACGGG G CUCAGCAA 1076 TTGCTGAG GGCTAGCTACAACGA CCCGTCCC 2778 4842 GGGGCUCA G CAAUGCCA 1077 TGGCATTG GGCTAGCTACAACGA TGAGCCCC 2779 4845 GCUCAGCA A UGCCAUUU 1078 AAATGGCA GGCTAGCTACAACGA TGCTGAGC 2780 4847 UCAGCAAU G CCAUUUCA 1079 TGAAATGG GGCTAGCTACAACGA ATTGCTGA 2781 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA GGCATTGC 2782 4856 CCAUUUCA G UGGCUUCC 1081 GGAAGCCA GGCTAGCTACAACGA TGAAATGG 2783 4859 UUUCAGUG G CUUCCCAG 1082 CTGGGAAG GGCTAGCTACAACGA CACTGAAA 2784 4867 GCUUCCCA G CUCUGACC 1083 GGTCAGAG GGCTAGCTACAACGA TGGGAAGC 2785 4873 CAGCUCUG A CCCUUCUA 1084 TAGAAGGG GGCTAGCTACAACGA CAGAGCTG 2786 4881 ACCCUUCU A CAUUUGAG 1085 CTCAAATG GGCTAGCTACAACGA AGAAGGGT 2787 4883 CCUUCUAC A UUUGAGGG 1086 CCCTCAAA GGCTAGCTACAACGA GTAGAAGG 2788 4891 AUUUGAGG G CCCAGCCA 1087 TGGCTGGG GGCTAGCTACAACGA CCTCAAAT 2789	4822	AUGUGGGC A CGGAGGGG	1074	CCCCTCCG GGCTAGCTACAACGA GCCCACAT	2776
4842 GGGGCUCA G CAAUGCCA 1077 TGGCATTG GGCTAGCTACAACGA TGAGCCCC 2779 4845 GCUCAGCA A UGCCAUUU 1078 AAATGGCA GGCTAGCTACAACGA TGCTGAGC 2780 4847 UCAGCAAU G CCAUUUCA 1079 TGAAATGG GGCTAGCTACAACGA ATTGCTGA 2781 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA GGCATTGC 2782 4856 CCAUUUCA G UGGCUUCC 1081 GGAAGCCA GGCTAGCTACAACGA TGAAATGG 2783 4859 UUUCAGUG G CUUCCCAG 1082 CTGGGAAG GGCTAGCTACAACGA CACTGAAA 2784 4867 GCUUCCCA G CUCUGACC 1083 GGTCAGAG GGCTAGCTACAACGA TGGGAAGC 2785 4873 CAGCUCUG A CCCUUCUA 1084 TAGAAGGG GGCTAGCTACAACGA CAGAGCTG 2786 4881 ACCCUUCU A CAUUUGAG 1085 CTCAAATG GGCTAGCTACAACGA AGAAGGGT 2787 4883 CCUUCUAC A UUUGAGGG 1086 CCCTCAAA GGCTAGCTACAACGA GTAGAAGG 2788 4891 AUUUGAGG G CCCAGCCA 1087 TGGCTGGG GGCTAGCTACAACGA CCTCAAAT 2789	4832	GGAGGGGG A CGGGGCUC	1075	GAGCCCCG GGCTAGCTACAACGA CCCCCTCC	2777
4845 GCUCAGCA A UGCCAUUU 1078 AAATGGCA GGCTAGCTACAACGA TGCTGAGC 2780 4847 UCAGCAAU G CCAUUUCA 1079 TGAAATGG GGCTAGCTACAACGA ATTGCTGA 2781 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA GGCATTGC 2782 4856 CCAUUUCA G UGGCUUCC 1081 GGAAGCCA GGCTAGCTACAACGA TGAAATGG 2783 4859 UUUCAGUG G CUUCCCAG 1082 CTGGGAAG GGCTAGCTACAACGA CACTGAAA 2784 4867 GCUUCCCA G CUCUGACC 1083 GGTCAGAG GGCTAGCTACAACGA TGGGAAGC 2785 4873 CAGCUCUG A CCCUUCUA 1084 TAGAAGGG GGCTAGCTACAACGA CAGAGCTG 2786 4881 ACCCUUCU A CAUUUGAG 1085 CTCAAATG GGCTAGCTACAACGA AGAAGGGT 2787 4883 CCUUCUAC A UUUGAGGG 1086 CCCTCAAA GGCTAGCTACAACGA GTAGAAGG 2788 4891 AUUUGAGG G CCCAGCCA 1087 TGGCTGGG GGCTAGCTACAACGA CCTCAAAT 2789	4837	GGGACGGG G CUCAGCAA	1076	TTGCTGAG GGCTAGCTACAACGA CCCGTCCC	2778
4847 UCAGCAAU G CCAUUUCA 1079 TGAAATGG GGCTAGCTACAACGA ATTGCTGA 2781 4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA GGCATTGC 2782 4856 CCAUUUCA G UGGCUUCC 1081 GGAAGCCA GGCTAGCTACAACGA TGAAATGG 2783 4859 UUUCAGUG G CUUCCCAG 1082 CTGGGAAG GGCTAGCTACAACGA CACTGAAA 2784 4867 GCUUCCCA G CUCUGACC 1083 GGTCAGAG GGCTAGCTACAACGA TGGGAAGC 2785 4873 CAGCUCUG A CCCUUCUA 1084 TAGAAGGG GGCTAGCTACAACGA CAGAGCTG 2786 4881 ACCCUUCU A CAUUUGAG 1085 CTCAAATG GGCTAGCTACAACGA AGAAGGGT 2787 4883 CCUUCUAC A UUUGAGGG 1086 CCCTCAAA GGCTAGCTACAACGA GTAGAAGG 2788 4891 AUUUGAGG G CCCAGCCA 1087 TGGCTGGG GGCTAGCTACAACGA CCTCAAAT 2789	4842	GGGGCUCA G CAAUGCCA	1077	TGGCATTG GGCTAGCTACAACGA TGAGCCCC	2779
4850 GCAAUGCC A UUUCAGUG 1080 CACTGAAA GGCTAGCTACAACGA GGCATTGC 2782 4856 CCAUUUCA G UGGCUUCC 1081 GGAAGCCA GGCTAGCTACAACGA TGAAATGG 2783 4859 UUUCAGUG G CUUCCCAG 1082 CTGGGAAG GGCTAGCTACAACGA CACTGAAA 2784 4867 GCUUCCCA G CUCUGACC 1083 GGTCAGAG GGCTAGCTACAACGA TGGGAAGC 2785 4873 CAGCUCUG A CCCUUCUA 1084 TAGAAGGG GGCTAGCTACAACGA CAGAGCTG 2786 4881 ACCCUUCU A CAUUUGAG 1085 CTCAAATG GGCTAGCTACAACGA AGAAGGGT 2787 4883 CCUUCUAC A UUUGAGGG 1086 CCCTCAAA GGCTAGCTACAACGA GTAGAAGG 2788 4891 AUUUGAGG G CCCAGCCA 1087 TGGCTGGG GGCTAGCTACAACGA CCTCAAAT 2789	4845	GCUCAGCA A UGCCAUUU	1078	AAATGGCA GGCTAGCTACAACGA TGCTGAGC	2780
4856 CCAUUUCA G UGGCUUCC 1081 GGAAGCCA GGCTAGCTACAACGA TGAAATGG 2783 4859 UUUCAGUG G CUUCCCAG 1082 CTGGGAAG GGCTAGCTACAACGA CACTGAAA 2784 4867 GCUUCCCA G CUCUGACC 1083 GGTCAGAG GGCTAGCTACAACGA TGGGAAGC 2785 4873 CAGCUCUG A CCCUUCUA 1084 TAGAAGGG GGCTAGCTACAACGA CAGAGCTG 2786 4881 ACCCUUCU A CAUUUGAG 1085 CTCAAATG GGCTAGCTACAACGA AGAAGGGT 2787 4883 CCUUCUAC A UUUGAGGG 1086 CCCTCAAA GGCTAGCTACAACGA GTAGAAGG 2788 4891 AUUUGAGG G CCCAGCCA 1087 TGGCTGGG GGCTAGCTACAACGA CCTCAAAT 2789	4847	UCAGCAAU G CCAUUUCA	1079	TGAAATGG GGCTAGCTACAACGA ATTGCTGA	2781
4859 UUUCAGUG G CUUCCCAG 1082 CTGGGAAG GGCTAGCTACAACGA CACTGAAA 2784 4867 GCUUCCCA G CUCUGACC 1083 GGTCAGAG GGCTAGCTACAACGA TGGGAAGC 2785 4873 CAGCUCUG A CCCUUCUA 1084 TAGAAGGG GGCTAGCTACAACGA CAGAGCTG 2786 4881 ACCCUUCU A CAUUUGAG 1085 CTCAAATG GGCTAGCTACAACGA AGAAGGGT 2787 4883 CCUUCUAC A UUUGAGGG 1086 CCCTCAAA GGCTAGCTACAACGA GTAGAAGG 2788 4891 AUUUGAGG G CCCAGCCA 1087 TGGCTGGG GGCTAGCTACAACGA CCTCAAAT 2789	4850	GCAAUGCC A UUUCAGUG	1080	CACTGAAA GGCTAGCTACAACGA GGCATTGC	2782
4867 GCUUCCCA G CUCUGACC 1083 GGTCAGAG GGCTAGCTACAACGA TGGGAAGC 2785 4873 CAGCUCUG A CCCUUCUA 1084 TAGAAGGG GGCTAGCTACAACGA CAGAGCTG 2786 4881 ACCCUUCU A CAUUUGAG 1085 CTCAAATG GGCTAGCTACAACGA AGAAGGGT 2787 4883 CCUUCUAC A UUUGAGGG 1086 CCCTCAAA GGCTAGCTACAACGA GTAGAAGG 2788 4891 AUUUGAGG G CCCAGCCA 1087 TGGCTGGG GGCTAGCTACAACGA CCTCAAAT 2789	4856	CCAUUUCA G UGGCUUCC	1081	GGAAGCCA GGCTAGCTACAACGA TGAAATGG	2783
4873 CAGCUCUG A CCCUUCUA 1084 TAGAAGGG GGCTAGCTACAACGA CAGAGCTG 2786 4881 ACCCUUCU A CAUUUGAG 1085 CTCAAATG GGCTAGCTACAACGA AGAAGGGT 2787 4883 CCUUCUAC A UUUGAGGG 1086 CCCTCAAA GGCTAGCTACAACGA GTAGAAGG 2788 4891 AUUUGAGG G CCCAGCCA 1087 TGGCTGGG GGCTAGCTACAACGA CCTCAAAT 2789	4859	UUUCAGUG G CUUCCCAG	1082	CTGGGAAG GGCTAGCTACAACGA CACTGAAA	2784
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4883 CCUUCUAC A UUUGAGGG 1086 CCCTCAAA GGCTAGCTACAACGA GTAGAAGG 2788 4891 AUUUGAGG G CCCAGCCA 1087 TGGCTGGG GGCTAGCTACAACGA CCTCAAAT 2789	4873	CAGCUCUG A CCCUUCUA	1084	TAGAAGGG GGCTAGCTACAACGA CAGAGCTG	2786
4891 AUUUGAGG G CCCAGCCA 1087 TGGCTGGG GGCTAGCTACAACGA CCTCAAAT 2789	4881	ACCCUUCU A CAUUUGAG	1085	CTCAAATG GGCTAGCTACAACGA AGAAGGGT	2787
	4883	CCUUCUAC A UUUGAGGG	1086	CCCTCAAA GGCTAGCTACAACGA GTAGAAGG	2788
4896 AGGGCCCA G CCAGGAGC 1088 GCTCCTGG GGCTAGCTACAACGA TGGGCCCT 2790	4891	AUUUGAGG G CCCAGCCA	1087	TGGCTGGG GGCTAGCTACAACGA CCTCAAAT	2789
	4896	AGGGCCCA G CCAGGAGC	1088	GCTCCTGG GGCTAGCTACAACGA TGGGCCCT	2790

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4936	UUUUCUGG A UUCUGGGA	1096	TCCCAGAA GGCTAGCTACAACGA CCAGAAAA 2798
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5052	GAUUUGUA G CACUGAGG	1119	CCTCAGTG GGCTAGCTACAACGA TACAAATC 2821
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5066	AGGGUGGC A CUCAACUC	1123	GAGTTGAG GGCTAGCTACAACGA GCCACCCT 2825
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5082	CUGAGCCC A UACUUUUG	1126	CAAAAGTA GGCTAGCTACAACGA GGGCTCAG 2828
5084	GAGCCCAU A CUUUUGGC	1127	GCCAAAAG GGCTAGCTACAACGA ATGGGCTC 2829
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5168	CUGAAAAU G UCACAUUC	1145	GAATGTGA GGCTAGCTACAACGA ATTTTCAG	2847
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5224	AUUUCUUG G UAUUAUUC	1159	GAATAATA GGCTAGCTACAACGA CAAGAAAT	2861
5226	UUCUUGGU A UUAUUCUG	1160	CAGAATAA GGCTAGCTACAACGA ACCAAGAA	2862
5229	UUGGUAUU A UUCUGUUU	1161	AAACAGAA GGCTAGCTACAACGA AATACCAA	2863
5234	AUUAUUCU G UUUUGCAC	1162	GTGCAAAA GGCTAGCTACAACGA AGAATAAT	2864
5239	UCUGUUUU G CACAGUUA	1163	TAACTGTG GGCTAGCTACAACGA AAAACAGA	2865
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5279	AUGAAAAU G CAGUCCUG	1171	CAGGACTG GGCTAGCTACAACGA ATTTTCAT	2873
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5343	UCAAUAAG G UCAAGGGA	1181	TCCCTTGA GGCTAGCTACAACGA CTTATTGA	2883
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5359	AAGACCCC G UCUCUAUA	1183	TATAGAGA GGCTAGCTACAACGA GGGGTCTT	
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5371	CUAUACCA A CCAAACCA	1186	TGGTTTGG GGCTAGCTACAACGA TGGTATAG	
5376	CCAACCAA A CCAAUUCA	1187	TGAATTGG GGCTAGCTACAACGA TTGGTTGG	
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<b>50</b> 5 5	<del></del>	1 1 1 1	C11 CT C1	
5388	AUUCACCA A CACAGUUG	1190	CAACTGTG GGCTAGCTACAACGA TGGTGAAT	2892
5388 5390 5393	<del></del>	1190 1191 1192	CAACTGTG GGCTAGCTACAACGA TGGTGAAT CCCAACTG GGCTAGCTACAACGA GTTGGTGA GGTCCCAA GGCTAGCTACAACGA TGTGTTGG	2892 2893 2894

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5419	GGAAGUCA G UCACGUUU	1197	AAACGTGA GGCTAGCTACAACGA TGACTTCC	2899
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5623	UUUCAACU G CUUUGAAA	1242	TTTCAAAG GGCTAGCTACAACGA AGTTGAAA	2944
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5771 GGGUCUAU G UAUUUAGG 1272 CCTAAATA GGC	PAGCTACAACGA ATAGACCC 2974
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5788 AUGCGCCU A CUCUUCAG 1277 CTGAAGAG GGC	TAGCTACAACGA AGGCGCAT 2979
5798 UCUUCAGG G UCUAAAGA 1278 TCTTTAGA GGC	TAGCTACAACGA CCTGAAGA 2980
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5811 AAGAUCAA G UGGGCCUU 1280 AAGGCCCA GGC	TAGCTACAACGA TTGATCTT 2982
	TAGCTACAACGA CCACTTGA 2983
	TAGCTACAACGA CCAAGGCC 2984
5825 CUUGGAUC G CUAAGCUG 1283 CAGCTTAG GGC	TAGCTACAACGA GATCCAAG 2985
5830 AUCGCUAA G CUGGCUCU 1284 AGAGCCAG GGC	TAGCTACAACGA TTAGCGAT 2986
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5839 CUGGCUCU G UUUGAUGC 1286 GCATCAAA GGC	TAGCTACAACGA AGAGCCAG 2988
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5846 UGUUUGAU G CUAUUUAU 1288 ATAAATAG GGC	TAGCTACAACGA ATCAAACA 2990
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5855 CUAUUUAU G CAAGUUAG 1291 CTAACTTG GGC	TAGCTACAACGA ATAAATAG 2993
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6013	CGAAGAAU G UAUGCCUC	1325	GAGGCATA GGCTAGCTACAACGA ATTCTTCG	3027
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6017	GAAUGUAU G CCUCUGUU	1327	AACAGAGG GGCTAGCTACAACGA ATACATTC	3029
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6108	GCCUACUG G CUCCUGGC	1348	GCCAGGAG GGCTAGCTACAACGA CAGTAGGC	

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6812	AUGUGCAA G UCUGUGUC	1494	GACACAGA GGCTAGCTACAACGA TTGCACAT	3196
6816	GCAAGUCU G UGUCUUGU	1495	ACAAGACA GGCTAGCTACAACGA AGACTTGC	
6818	AAGUCUGU G UCUUGUCA	1496	TGACAAGA GGCTAGCTACAACGA ACAGACTT	
6823	UGUGUCUU G UCAGUCCA	1497	TGGACTGA GGCTAGCTACAACGA AAGACACA	
6827	UCUUGUCA G UCCAAGAA	1498	TTCTTGGA GGCTAGCTACAACGA TGACAAGA	
6836	UCCAAGAA G UGACACCG	1499	CGGTGTCA GGCTAGCTACAACGA TTCTTGGA	
6839	AAGAAGUG A CACCGAGA	1500	TCTCGGTG GGCTAGCTACAACGA CACTTCTT	
6841	GAAGUGAC A CCGAGAUG	1501	CATCTCGG GGCTAGCTACAACGA GTCACTTC	
6847	ACACCGAG A UGUUAAUU	1502	AATTAACA GGCTAGCTACAACGA CTCGGTGT	
6849	ACCGAGAU G UUAAUUUU	1503	AAAATTAA GGCTAGCTACAACGA ATCTCGGT	
6853	AGAUGUUA A UUUUAGGG	1504	CCCTAAAA GGCTAGCTACAACGA TAACATCT	
	DOBOUGH A ACCOUNT	1307	SOUTHARN GOLLAGOIACAACGA TAACATCT	3400

			large code organicani di continui l	
6862	UUUUAGGG A CCCGUGCC	1505	GGCACGGG GGCTAGCTACAACGA CCCTAAAA	3207
6866	AGGGACCC G UGCCUUGU	1506	ACAAGGCA GGCTAGCTACAACGA GGGTCCCT	3208
6868	GGACCCGU G CCUUGUUU	1507	AAACAAGG GGCTAGCTACAACGA ACGGGTCC	3209
6873	CGUGCCUU G UUUCCUAG	1508	CTAGGAAA GGCTAGCTACAACGA AAGGCACG	3210
6881	GUUUCCUA G CCCACAAG	1509	CTTGTGGG GGCTAGCTACAACGA TAGGAAAC	3211
6885	CCUAGCCC A CAAGAAUG	1510	CATTCTTG GGCTAGCTACAACGA GGGCTAGG	3212
6891	CCACAAGA A UGCAAACA	1511	TGTTTGCA GGCTAGCTACAACGA TCTTGTGG	3213
6893	ACAAGAAU G CAAACAUC	1512	GATGTTTG GGCTAGCTACAACGA ATTCTTGT	3214
6897	GAAUGCAA A CAUCAAAC	1513	GTTTGATG GGCTAGCTACAACGA TTGCATTC	3215
6899	AUGCAAAC A UCAAACAG	1514	CTGTTTGA GGCTAGCTACAACGA GTTTGCAT	3216
6904	AACAUCAA A CAGAUACU	1515	AGTATCTG GGCTAGCTACAACGA TTGATGTT	3217
6908	UCAAACAG A UACUCGCU	1516	AGCGAGTA GGCTAGCTACAACGA CTGTTTGA	3218
6910	AAACAGAU A CUCGCUAG	1517	CTAGCGAG GGCTAGCTACAACGA ATCTGTTT	3219
6914	AGAUACUC G CUAGCCUC	1518	GAGGCTAG GGCTAGCTACAACGA GAGTATCT	3220
6918	ACUCGCUA G CCUCAUUU	1519	AAATGAGG GGCTAGCTACAACGA TAGCGAGT	3221
6923	CUAGCCUC A UUUAAAUU	1520	AATTTAAA GGCTAGCTACAACGA GAGGCTAG	3222
6929	UCAUUUAA A UUGAUUAA	1521	TTAATCAA GGCTAGCTACAACGA TTAAATGA	3223
6933	UUAAAUUG A UUAAAGGA	1522	TCCTTTAA GGCTAGCTACAACGA CAATTTAA	3224
6945	AAGGAGGA G UGCAUCUU	1523	AAGATGCA GGCTAGCTACAACGA TCCTCCTT	3225
6947	GGAGGAGU G CAUCUUUG	1524	CAAAGATG GGCTAGCTACAACGA ACTCCTCC	3226
6949	AGGAGUGC A UCUUUGGC	1525	GCCAAAGA GGCTAGCTACAACGA GCACTCCT	3227
6956	CAUCUUUG G CCGACAGU	1526	ACTGTCGG GGCTAGCTACAACGA CAAAGATG	3228
6960	UUUGGCCG A CAGUGGUG	1527	CACCACTG GGCTAGCTACAACGA CGGCCAAA	3229
6963	GGCCGACA G UGGUGUAA	1528	TTACACCA GGCTAGCTACAACGA TGTCGGCC	3230
6966	CGACAGUG G UGUAACUG	1529	CAGTTACA GGCTAGCTACAACGA CACTGTCG	3231
6968	ACAGUGGU G UAACUGUG	1530	CACAGTTA GGCTAGCTACAACGA ACCACTGT	3232
6971	GUGGUGUA A CUGUGUGU	1531	ACACACAG GGCTAGCTACAACGA TACACCAC	3233
6974	GUGUAACU G UGUGUGUG	1532	CACACACA GGCTAGCTACAACGA AGTTACAC	3234
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6978	AACUGUGU G UGUGUGUG	1534	CACACACA GGCTAGCTACAACGA ACACAGTT	3236
6980	CUGUGUGU G UGUGUGUG	1535	CACACACA GGCTAGCTACAACGA ACACACAG	3237
6982	GNGNGNGN G NGNGNGNG	1536	CACACACA GGCTAGCTACAACGA ACACACAC	3238
6984	GUGUGUGU G UGUGUGUG	1537	CACACACA GGCTAGCTACAACGA ACACACAC	3239
6986	GUGUGUGU G UGUGUGUG	1538	CACACACA GGCTAGCTACAACGA ACACACAC	3240
6988	GUGUGUGU G UGUGUGUG	1539	CACACACA GGCTAGCTACAACGA ACACACAC	3241
6990	GUGUGUGU G UGUGUGUG	1540	CACACACA GGCTAGCTACAACGA ACACACAC	3242
6992	GNGAGAGA G AGAGAGAGA	1541	CACACACA GGCTAGCTACAACGA ACACACAC	3243
6994	GUGUGUGU G UGUGUGUG	1542	CACACACA GGCTAGCTACAACGA ACACACAC	3244
6996	GUGUGUGU G UGUGUGUG	1543	CACACACA GGCTAGCTACAACGA ACACACAC	3245
6998	GUGUGUGU G UGUGUGUG	1544	CACACACA GGCTAGCTACAACGA ACACACAC	3246
7000	GUGUGUGU G UGUGUGUG	1545	CACACACA GGCTAGCTACAACGA ACACACAC	3247
7002	GUGUGUGU G UGUGUGUG	1546	CACACACA GGCTAGCTACAACGA ACACACAC	3248
7004	GUGUGUGU G UGUGUGUG	1547	CACACACA GGCTAGCTACAACGA ACACACAC	
7006	GUGUGUGU G UGUGUGUG	1548	CACACACA GGCTAGCTACAACGA ACACACAC	3250
7008	GUGUGUGU G UGUGUGGG	1549	CCCACACA GGCTAGCTACAACGA ACACACAC	3251
7010	GUGUGUGU G UGUGGGUG	1550	CACCCACA GGCTAGCTACAACGA ACACACAC	3252
7012	GUGUGUGU G UGGGUGUG	1551	CACACCCA GGCTAGCTACAACGA ACACACAC	3253
7016	GUGUGUGG G UGUGGGUG	1552	CACCCACA GGCTAGCTACAACGA CCACACAC	3254
7018	GUGUGGGU G UGGGUGUA	1553	TACACCCA GGCTAGCTACAACGA ACCCACAC	3255
7022	GGGUGUGG G UGUAUGUG	1554	CACATACA GGCTAGCTACAACGA CCACACCC	3256
7024	GUGUGGGU G UAUGUGUG	1555	CACACATA GGCTAGCTACAACGA ACCCACAC	3257
7026	GUGGGUGU A UGUGUGUU	1556	AACACACA GGCTAGCTACAACGA ACACCCAC	3258
	<del> </del>			

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7028	GGGUGUAU G UGUGUUUU	1557	AAAACACA GGCTAGCTACAACGA ATACACCC	3259
7030	GUGUAUGU G UGUUUUGU	1558	ACAAAACA GGCTAGCTACAACGA ACATACAC	3260
7032	GUAUGUGU G UUUUGUGC	1559	GCACAAAA GGCTAGCTACAACGA ACACATAC	3261
7037	UGUGUUUU G UGCAUAAC	1560	GTTATGCA GGCTAGCTACAACGA AAAACACA	3262
7039	UGUUUUGU G CAUAACUA	1561	TAGTTATG GGCTAGCTACAACGA ACAAAACA	3263
7041	UUUUGUGC A VAACUAUU	1562	AATAGTTA GGCTAGCTACAACGA GCACAAAA	3264
7044	UGUGCAUA A CUAUUUAA	1563	TTAAATAG GGCTAGCTACAACGA TATGCACA	3265
7047	GCAUAACU A UUUAAGGA	1564	TCCTTAAA GGCTAGCTACAACGA AGTTATGC	3266
7057	UUAAGGAA A CUGGAAUU	1565	AATTCCAG GGCTAGCTACAACGA TTCCTTAA	3267
7063	AAACUGGA A UUUUAAAG	1566	CTTTAAAA GGCTAGCTACAACGA TCCAGTTT	3268
7071	AUUUUAAA G UUACUUUU	1567	AAAAGTAA GGCTAGCTACAACGA TTTAAAAT	3269
7074	UUAAAGUU A CUUUUAUA	1568	TATAAAAG GGCTAGCTACAACGA AACTTTAA	3270
7080	UUACUUUU A UACAAACC	1569	GGTTTGTA GGCTAGCTACAACGA AAAAGTAA	3271
7082	ACUUUUAU A CAAACCAA	1570	TTGGTTTG GGCTAGCTACAACGA ATAAAAGT	3272
7086	UUAUACAA A CCAAGAAU	1571	ATTCTTGG GGCTAGCTACAACGA TTGTATAA	3273
7093	AACCAAGA A UAUAUGCU	1572	AGCATATA GGCTAGCTACAACGA TCTTGGTT	3274
7095	CCAAGAAU A UAUGCUAC	1573	GTAGCATA GGCTAGCTACAACGA ATTCTTGG	3275
7097	AAGAAUAU A UGCUACAG	1574	CTGTAGCA GGCTAGCTACAACGA ATATTCTT	3276
7099	GAAUAUAU G CUACAGAU	1575	ATCTGTAG GGCTAGCTACAACGA ATATATTC	3277
7102	UAUAUGCU A CAGAUAUA	1576	TATATCTG GGCTAGCTACAACGA AGCATATA	3278
7106	UGCUACAG A UAUAAGAC	1577	GTCTTATA GGCTAGCTACAACGA CTGTAGCA	3279
7108	CUACAGAU A UAAGACAG	1578	CTGTCTTA GGCTAGCTACAACGA ATCTGTAG	3280
7113	GAUAUAAG A CAGACAUG	1579	CATGTCTG GGCTAGCTACAACGA CTTATATC	3281
7117	UAAGACAG A CAUGGUUU	1580	AAACCATG GGCTAGCTACAACGA CTGTCTTA	3282
7119	AGACAGAC A UGGUUUGG	1581	CCAAACCA GGCTAGCTACAACGA GTCTGTCT	3283
7122	CAGACAUG G UUUGGUCC	1582	GGACCAAA GGCTAGCTACAACGA CATGTCTG	3284
7127	AUGGUUUG G UCCUAUAU	1583	ATATAGGA GGCTAGCTACAACGA CAAACCAT	3285
7132	UUGGUCCU A VAUUUCUA	1584	TAGAAATA GGCTAGCTACAACGA AGGACCAA	3286
7134	GGUCCUAU A UUUCUAGU	1585	ACTAGAAA GGCTAGCTACAACGA ATAGGACC	3287
7141	UAUUUCUA G UCAUGAUG	1586	CATCATGA GGCTAGCTACAACGA TAGAAATA	3288
7144	UUCUAGUC A UGAUGAAU	1587	ATTCATCA GGCTAGCTACAACGA GACTAGAA	3289
7147	UAGUCAUG A UGAAUGUA	1588	TACATTCA GGCTAGCTACAACGA CATGACTA	3290
7151	CAUGAUGA A UGUAUUUU	1589	AAAATACA GGCTAGCTACAACGA TCATCATG	3291
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7155	AUGAAUGU A UUUUGUAU	1591	ATACAAAA GGCTAGCTACAACGA ACATTCAT	3293
7160	UGUAUUUU G UAUACCAU	1592	ATGGTATA GGCTAGCTACAACGA AAAATACA	3294
7162	UAUUUUGU A UACCAUCU	1593	AGATGGTA GGCTAGCTACAACGA ACAAAATA	3295
7164	UUUUGUAU A CCAUCUUC	1594	GAAGATGG GGCTAGCTACAACGA ATACAAAA	3296
7167	UGUAUACC A UCUUCAUA	1595	TATGAAGA GGCTAGCTACAACGA GGTATACA	3296
7173	CCAUCUUC A UAUAAUAU	1596	ATATTATA GGCTAGCTACAACGA GAAGATGG	
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7178	UUCAUAUA A UAUACUUA	1597		3299
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7182				3301
7190	ACUUAAAA A UAUUUCUU	1600	TTTTTAAG GGCTAGCTACAACGA ATATTATA	3302
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		1602	TTAAGAAA GGCTAGCTACAACGA ATTTTTAA	3304
7200	AUUUCUUA A UUGGGAUU	1603	AATCCCAA GGCTAGCTACAACGA TAAGAAAT	3305
7206	UAAUUGGG A UUUGUAAU	1604	ATTACAAA GGCTAGCTACAACGA CCCAATTA	3306
7210	UGGGAUUU G UAAUCGUA	1605	TACGATTA GGCTAGCTACAACGA AAATCCCA	3307
7213	GAUUUGUA A UCGUACCA	1606	TGGTACGA GGCTAGCTACAACGA TACAAATC	
7216	UUGUAAUC G UACCAACU	1607	AGTTGGTA GGCTAGCTACAACGA GATTACAA	3309
7218	GUAAUCGU A CCAACUUA	1608	TAAGTTGG GGCTAGCTACAACGA ACGATTAC	3310

72221         UCGUACCA A CUUNAUUU 1619         CARTHANG GGCTRAGTRACAGGA TAGGTACAG         3311           72231         CUUNAUUG A UNAACUUG 1611         TTATTCAA GGCTRAGTRACAGGA TAGTTAGG         3313           7235         AUUGAIDA A CUUGGCAA         1612         TTATCAGA GGCTRACTRACAGGA CHATTAGA         3313           7240         URAACUUG G CALCUUUU         1613         AGGGTTG GGCTRACTRACAGGA CAGGTTGT         3316           7246         URAACUUG G CUUUUUU         1613         ARAGAGG GGCTRACTRACAGGA AGGTTGT         3316           7246         URAACUUG G CUUUUUU         1615         ARAGACA GGCTRACTRACAGA AAAGCAG         3317           7246         URAACUUU A GUUCUGUU         1618         ARAGACA GGCTRACTRACAGA AAAAGCAG         3318           7252         CUGCUUUC A UCUCCUUC         1618         ARAGACA GGCTRACTRACAGA AGAACATA         3320           7269         CUCCUUC A UAAAUUUU         1619         ARAATTTA GGCTRACTRACAGA TAGATAT         3320           7273         UUCCADAA A UUUUCAA         1621         TTATATAG GGCTRACTRACAGA TAGATATT         3324           7285         UUCAAAAU A CUCAAUU         1621         TAGATTAG GGCTRACTRACAGA TAGATTT         3324           7283         UUCAAAAU A CUCAAUU         1621         TAGATTAG GGCTRACTRACAGA TAGATTTT         3326					
7231         CUUNANUG A UARACUUG         1611         CARGTTTA GGCTAGCTACAGCG CANTTANO         3313           7235         AUUGAURA A CUUGGCAA         1612         TTGCCAAG GGCTAGCTACAGCGA CAAGTTTA         3314           7240         UARACUUG G CARCUGCU         1613         AGAGTTG GGCTAGCAGCAA CAAGTTTA         3315           7243         ACUGGCAACU G CUUUUU         1614         ARAGCAG GGCTAGCTACAAGGA TGCCAAGT         3316           7252         CUGCUUUU A UUGUGGU         1615         CATARAAG GGCTAGCTACAAGGA AGTGCCAAGGA         3318           7252         CUGCUUUU G UUCUGUUC         1616         AGAGAGA GGCTAGCTACAAGGA AAAGACA         3318           7259         UAUGUUCU G UUCUGUUC         1618         AAAATTTA GGCTAGCAAGGA AGAACATA         3320           7269         CUCCUUCC A UAAAUUUU         1620         TTGAAAAA GAAGAAAAA         1620         TTGAAAAA GAACAAAAAAAAAAAAAAAAAAAAAAAAAAA	7222	UCGUACCA A CUUAAUUG	1609	CAATTAAG GGCTAGCTACAACGA TGGTACGA	3311
7235   AUUGAUAA A CUUGGCAA   1612   TTGCCAAG GGCTAGCTACAAGGA TTATCAAT   3314     7244	7227	CCAACUUA A UUGAUAAA			
19240	7231	CUUAAUUG A UAAACUUG	1611	CAAGTTTA GGCTAGCTACAACGA CAATTAAG	3313
7243         ACUUGICA A CUIGUUUU         1614         AAAAGCAG GCTAGCTACACGA TGCCAAGT         3316           7246         UGGCAACU G CUUUUAUG         1615         CATAAAAG GGCTAGCTACACGA AGTTGCCA         3317           7252         CUCCUUUU A UGUUCUUC         1616         ACAGACA GGCTAGCTACAACGA AAAAGCAG         3318           7254         GCUUUUAU G UUCUCUUC         1618         GAAGGAG GGCTAGCTACACGA AAAACAAG         3319           7259         UUCUCUUCA LAAAUU         1619         AAAATTTA GGCTAGCTACACGA GGAAGGAG         3321           7273         UUCCAUAA A UUCUCAAA         1620         TTGAAAAA GCTAGCTACACAGA TTTTGAAAA         3322           7283         UUUCAAAA A UACUAAUU         1621         AATTTGTA GGCTAGCTACACAG ATTTTGAAAA         3324           7289         AAAUACUA A UUCAACAA         1623         TTGTTGAA GGCTAGCTACACGA TTTTTTTT         3326           7395         AAAGAAAAA GUCUUUUU         1625         AAAAAGAG GGCTAGCTACACGA TTATTTTT         3327           7323         UUCCUAAA A UAAACUCA         1626         TTGTTTTA GGCTAGCTAACGA TTTTTTTT         3327           7327         UAAAAUAA A UUAACUCA         1626         TTGTTTAA GGCTAGCTAACGA TTTTTTTT         3327           7333         UACCUAAA         AUAACUCA         1626         TTGTTTAA         GGCTAGCTACACGA	7235	AUUGAUAA A CUUGGCAA	1612	TTGCCAAG GGCTAGCTACAACGA TTATCAAT	3314
7246         UGGCAACU G CUUUUAUG         1615         CATAAAAG GGCTAGCTACACGA AGTTGCCA         3317           7252         CUGCUUUU A UGUUCUGU         1616         ACAGAACA GGCTAGCTACACGA ARAAGCAG         3318           7259         UAUGUUCU G UUCUGUUC         1617         AGAGAGA GGCTAGCTACAACGA ATAAAGGA         3319           7259         UAUGUUCU G UCUCUUC         1618         GAAGGAGA GGCTAGCTACAACGA ATAACGA         3320           7269         CUCCUUCC A UAAAUUUU         1620         TAAAAAAAAAA         AGAGAGA GGTAGCTACAACGA GTATGGAA         3321           7273         UUCAAAAA UAUCUAAUU         1621         AAATTATA GGCTAGCTACAACGA TTATGAAA         3322           7283         UUUCAAAA A UACUAAUA         1622         TAAATTATA GGCTAGCTACAACGA TTATGATA         3322           7289         AAAAACUA A UUCAACAA         1623         TATTGAGA GGCTAGCTACACACA TTATTGAT         3326           7394         CUAAUUCA A CAAAGAAA         1624         TTCTTTG GCTAGCTACACACA TTATTGAT         3326           7327         UAAAAUAA A UUCAACAA         1626         TAGATTTAG GGCTAGCTACACACA TTATTGAT         3328           7327         UAAAAUAA A UUCAUCU         1628         AAGATTAA GGCTAGCTACACACA TTATTTAT         3329           7333         DAACUCAA         UUUAGAC         1629         AACAA	7240	UAAACUUG G CAACUGCU	1613	AGCAGTTG GGCTAGCTACAACGA CAAGTTTA	3315
7252         CUGCUJUU A UGUUCUGU         1616         ACAGAACA GGCTAGCTACACGA AAAAGCA         3318           7254         GCUJULUU G UUCUGUUC         1617         AGACAGAA GGCTAGCTACAACGA ATAAAGC         3319           7259         UALGUUCU G UUCUCUUC         1618         GAAGAGA GGCTAGCTACAACGA AGAACATA         3320           7269         CUCCUUCC A UAAAUUU         1619         AAAATTTA GGCTAGCTACAACGA GGAAGGAG         3321           7273         UUCCAUAA A UUUUUCAA         1620         TGAAAAA GGCTAGCTACAACGA TTATGAAA         3322           7283         UUUCAAAAU A UACAAAUA         1622         TGAATTAG GGCTAGCTACAACGA TTATGAAA         3323           7285         UUCAAAAU A UUCAACAA         1623         TTGTTGAA GGCTAGCTACAACGA TATATTTA         3326           7394         CUAAUUC A CAAAGAAA         1624         TTCTTTG GGCTAGCTACAACGA TTATTTTA         3326           7395         AAGAAAAA CUCAAAUU         1625         AAAAGAGA GGCTAGCTACAACGA TTATTTTA         3327           7327         UAAAACCAA         1626         TATTTTGA GGCTAGCTACAACGA TTATTTTA         3327           7323         UACCAAAA         1627         AATTTGA GGCTAGCTACAACGA TTAGATTTA         3326           7327         UAAAACAA         AUUACCU         1628         AGGATAAA GGCTAGCTACAACGA TATATTTTA         333	7243	ACUUGGCA A CUGCUUUU	1614	AAAAGCAG GGCTAGCTACAACGA TGCCAAGT	3316
7254         GCUUUUAU G UUCUGUCU         1617         AGACAGAA GGCTAGCTACAACGA ATAAAAG         3319           7259         UAUGUUCU G UCUCCUUC         1618         GAAGAGAA GGCTAGCTACAACGA AGAACATA         3320           7269         CUCCUUCC A UAAAUUU         1619         AAAATTA GGCTAGCTACAACGA AGAACATA         3320           7273         UUCCAUAA A UUCUCAA         1620         TTGAAAAA GGCTAGCTACAACGA TTATGAAA         3322           7283         UUUCAAAAU A CUAAUUCA         1621         TTGATAAA GGCTAGCTACAACGA TTTTGAA         3323           7285         UUCAAAAU A CUAAUUCA         1622         TTGATTAA GGCTAGCTACAACGA TTGTAAA         3323           7289         AAAUACUA A UUCAACAA         1623         TTGTTGAA GGCTAGCTACACGA TAGTATTAA         3326           7305         AAGAAAAA G CUCUUUUU         1625         AAAAAGA G GCTAGCTACAACGA TTTTTTTTT         3326           7323         UUCCUAAA A UAAACCCA         1628         AGATATAA GGCTAGCTACACGA TTTGTGAA         3228           7327         UAAAAUAA A UUCUGUUU         1629         AAAGAGAA AUUAACCU         1629         AAGAGAAA AUUAAGAA         1631         TTTCTTG GGCTAGCTACACGA TTTTTTTT         3331           7336         UGUULGAA G CAGAGAAA         1631         TTTCTTG GGCTAGCTACAACGA TTTTTCTT         3334           7350	7246	UGGCAACU G CUUUUAUG	1615	CATAAAAG GGCTAGCTACAACGA AGTTGCCA	3317
7259 UAUGUUCU G UCUCCUUC 1618 GAAGAGA GGCTAGCTACAACGA AGAACATA 3320 7269 CUCCUUCC A UAAAUUUU 1619 AAAATTTA GGCTAGCTACAACGA GGAAGGAC 3321 7273 UUCCADAA A UUUUUCAA 1620 TTGAAAAA GGCTAGCTACAACGA TTATGAAA 3322 7283 UUUUCAAAA A UACUAAUU 1621 AATTAGTA GGCTAGCTACAACGA ATTTGAAA 3322 7285 UUUCAAAAAU A CUAAUUCA 1622 TGAATTAG GGCTAGCTACAACGA ATTTGAAA 3323 7286 UUCAAAAAU A CUAAUUCA 1622 TGAATTAG GGCTAGCTACAACGA ATTTGAAA 3326 7287 CUAAUCCA A CAAAGAAA 1623 TTGTTGAA GGCTAGCTACAACGA TATTTGAA 3326 7288 CUAAAUACU A CAAAGAAA 1624 TTTCTTTG GGCTAGCTACAACGA TATTTTCTA 3326 7390 AAGAAAAA G CUCUUUUU 1625 AAAAAGAG GGCTAGCTACAACGA TTTTTCTT 3327 7323 UUCCUAAA A UAAACUCA 1626 TGAGTTTA GGCTAGCTACAACGA TTTTTCTT 3327 7327 UAAAAUAA A CUCAAAUU 1627 AATTTGAG GGCTAGCTACAACGA TTTTTTCTT 3327 7333 AAACUCAA A UULAACUCA 1628 AGGATAAA GGCTAGCTACAACGA TTTTTTTT 3329 7333 AAACUCAA A UULACUCU 1628 AGGATAAA GGCTAGCTACAACGA TTTTTTTT 3329 7333 UACAAUUU A UCCUUGUU 1629 AACAAGGA GGCTAGCTACAACGA TTTAGGAA 3336 73340 UUAACCUU G UUUAGAGC 1630 GGCTAGATAA GGCTAGCTACAACGA TTTTCTT 3330 73450 UUGUUAGA G CAGAGAAA 1631 TTTCTCTG GGCTAGCTACAACGA TTTTCTCA 3331 73500 UGUUUAGA G CAGAGAAA 1631 TTTCTCTG GGCTAGCTACAACGA TTTCTCT 3334 7370 UAAGAAAA A CUUCAAAAU 1631 TTTCTCTG GGCTAGCTACAACGA TTTCTCT 3334 7370 UAAGAAAA A CUUCAAAA 1633 TTTCTTAA GGCTAGCTACAACGA TTTCTCT 3334 7370 UAAGAAAA A CUUCAAAA 1633 TTTCTAA GGCTAGCTACAACGA TTTCTCT 3334 7371 UCAAAUG G UUCACAAAU 1631 TTTCTCTG GGCTAGCTACAACGA TTTCTCT 3334 7371 UCAAAUG G UUCACAAAA 1633 TTTCTAAG AGGTAGCTACAACGA TTTCTCT 3334 7371 UCAAAUG G UUCACAAAA 1633 TTTCTAAG AGGTAGCTACAACGA TTTCTCT 3334 7371 UCAAAUG G UUCACAAAA 1633 TTTCTAAG AGGTAGCTACAACGA TTTTCTCT 3334 7371 UCAAAUG G UUCAAAUAU 1637 TTTCAAGA GGCTAGCTACAACGA TTTTCTCT 3334 7371 UCAAAUG G UUCAAAUAU 1637 TTTCAAGA GGCTAGCTACAACGA TTTTCAA 3337 7371 UCAAAUG G UUCAAAUAU 1637 TTTCAAGA GGCTAGCTACAACGA TTTTAGA 3337 7371 UCAAAUG G UUCAAAUAU 1637 TATTTAG GGCTAGCTACAACGA TTTAGCAT 3340 7372 UCAAAAUG G UUCAAAUAU 1637 TATTTAG GGCTAGCTACAACGA TTTAGCAT 3340 7373 UCAAAUG G UUCAAAUAU 1637 TATTTAG GGCTAG	7252	CUGCUUUU A UGUUCUGU	1616	ACAGAACA GGCTAGCTACAACGA AAAAGCAG	3318
7269 CUCCUUCC A UAAAUUUU 1619 AAAATTTA GGCTAGCTACAACGA GGAAGGAG 3321 7273 UUCCAUAA A UUUUUCAA 1620 TTGAAAAA GGCTAGCTACAACGA TTATGAAA 3322 7285 UUCCAAAAU A CUAAUUCA 1621 AATTAGTA GGCTAGCTACAACGA TTATGAAA 3323 7286 UUCAAAAU A CUAAUUCA 1622 TGAATTAG GGCTAGCTACAACGA ATTTTGAAA 3324 7289 AAAUACUA A UUCAACAA 1623 TTGTTGAA GGCTAGCTACAACGA TAGTATTT 3325 7294 CUAAUUCA A CAAAGAAA 1623 TTGTTGAA GGCTAGCTACAACGA TAGTATTT 3325 7305 AAGAAAAA G CUCUUUUU 1625 AAAAAGAG GGCTAGCTACAACGA TAGTATTT 3327 7305 AAGAAAAA G CUCUUUUU 1625 AAAAAGAG GGCTAGCTACAACGA TTTTTCTT 3327 7323 UUCCUAAA A UNAACUCA 1626 TGAGTTA GGCTAGCTACAACGA TTTTTTTA 3329 7327 UAAAAUAA A UULAUCCU 1628 AGGATAAA GGCTAGCTACAACGA TTATTTTA 3329 7333 AAACUCAA A UULAUCCU 1628 AGGATAAA GGCTAGCTACAACGA TTATTTTA 3330 7337 UCAAAUUU A UCCUUGUU 1628 AGGATAAA GGCTAGCTACAACGA TTATTTTA 3331 7343 UUAUCCUU G UUUAGACC 1630 GCTCTAAA GGCTAGCTACAACGA TATATTTA 3331 7340 UUAUCCUU G UUUAGACC 1630 GCTCTAAA GGCTAGCTACAACGA AAATTTGA 3331 7350 UGGUAAAA A UUAACGAA 1631 TTTCTCTG GGCTAGCTACAACGA TCTAAACA 3333 7360 AGAGAAAA UUAAGAAA 1632 TTTCTTAA GGCTAGCTACAACGA TCTAAACA 3333 7370 UAAGAAAAA UUGUUAAA 1633 TTTCAAAG GGCTAGCTACAACGA TTTTCTCT 3334 7378 ACUUUGAA A UGGUCUCA 1634 TGAGACCA GGCTAGCTACAACGA TTTTCTCT 3335 7381 UUCAAAUA A UUGUCAAA 1633 TTTCAAAG GGCTAGCTACAACGA TTTTCTCT 3336 7391 CUCAAAAA A UUGUCAAA 1635 TTTTCAGA GGCTAGCTACAACGA TTTTCAA 3337 7391 CUCAAAAA A UUGUCAAA 1636 TTAGAACA GGCTAGCTACAACGA TTTTCAA 3337 7391 CUCAAAAA A UUGUCAAA 1636 TTAGAACA GGCTAGCTACAACGA TTTTCAA 3337 7391 CUCAAAAA A UUGUCAAA 1636 TTAGAACA GGCTAGCTACAACGA ATTTTCAA 3337 7391 CUCAAAAA A UUGUCAAA 1636 TAGAACTA GGCTAGCTACAACGA TTTTCAA 3337 7392 AUUGCUCAAAA 1636 TAGAACTA GGCTAGCTACAACGA ATTTTCAT 3336 7400 UAUGCUCA A UAUUUCCA 1638 TAGAACTA GGCTAGCTACAACGA TTTTCAT 3344 7420 AAAACUAA A UUUUCAAU 1639 ATTATTAA GGCTAGCTACAACGA ATTTTGAT 3340 7401 UGCUAAAU A UUUUCAAU 1639 ATTATTAA GGCTAGCTACAACGA ATTTTGAT 3340 7402 AAAACUAA A UUGUCAA 1664 ACATTAA GGCTAGCTACAACGA ATTTTGAT 3340 7403 AAACUAA A UUGUCAC 1650 ACATTAA GGCTAGCTACAACGA ATTTTGAT 3	7254	GCUUUUAU G UUCUGUCU	1617	AGACAGAA GGCTAGCTACAACGA ATAAAAGC	3319
7273 UUCCAUAA A UUUUUCAA 1620 TTGAAAAA GGCTAGCTACAACGA TTTATGAA 3322 7285 UUUUCAAA A UACUAAUUCA 1621 TATTTTG GGCTAGCTACAACGA TTTGAAAA 3223 7289 AAAUACUA A UUCAACAA 1622 TGAATTAG GGCTAGCTACAACGA TTTTGAAA 3324 7289 AAAUACUA A UUCAACAA 1623 TTGTTGAA GGCTAGCTACAACGA TATTTTATA 3325 7294 CUAAUUCA A CAAAGAAA 1624 TTCTTTG GGCTAGCTACAACGA TATTTTATA 3326 73305 AAGAAAAA G CUCUUUUU 1625 AAAAAGAG GGCTAGCTACAACGA TTTTTCTT 3327 7323 UUCCUAAA A UAAACUCA 1626 TAGGTTTA GGCTAGCTACAACGA TTTTTCTT 3327 7323 UUCCUAAA A UAAACUCA 1626 TAGGTTTA GGCTAGCTACAACGA TTTTTCTT 3329 7333 AAACUCAA A UUUAUCCU 1628 AGATTAAA GGCTAGCTACAACGA TTTAGGAA 3328 7337 UCAAAUUU A UCCUUGUU 1629 AACAAGGA GGCTAGCTACAACGA TTTAGGAA 3329 7333 UUAUCCUU G UUUAGAGC 1630 GGCTAGCTACAACGA TATTAGTTT 3330 7343 UUAUCCUU G UUUAGAGC 1630 GGCTAGCTACAACGA AAGGATAA 3332 7350 UGUUUAGA C CAGAGAAA 1631 TTCTCTG GGCTAGCTACAACGA AAGGATAA 3332 7360 AGAGAAAA UUAACACA 1631 TTCTCTG GGCTAGCTACAACGA TTTTCTT 3334 7370 UAAGAAAA A UUAACAAA 1631 TTCTCTG GGCTAGCTACAACGA TTTTCTCT 3334 7370 UAAGAAAA A CUUUGAAA 1633 TTTCTAA GGCTAGCTACAACGA TTTTCTCT 3336 7378 ACUUUGAA A UUGCULAA 1633 TTTCTAG GGCTAGCTACAACGA TTTTCTTA 3335 7378 ACUUUGAA A UUGCULAA 1633 TTTCTAG GGCTAGCTACAACGA TTTTCTTA 3337 7391 CUCAAAAAU UGCULAAA 1633 TTTTCAAG GGCTAGCTACAACGA TTTTCTTA 3337 7391 CUCAAAAA A UUGCULAAA 1633 TTTTCAGA GGCTAGCTACAACGA TTTTCTTA 3337 7391 CUCAAAAA A UUGCULAAA 1633 TTTTTAGGA GGCTAGCTACAACGA CATTTCAA 3337 7391 AAAAAAUU G CUAAAUAU 1637 ATATTTAG GGCTAGCTACAACGA ATTTTGTA 3337 7392 AUUGCULAA A UUUUCAA 1636 TTTAGGAA GGCTAGCTACAACGA TTTTTTTT 3339 7394 AAAAAAUU G CUAAAUAU 1637 ATATTTAG GGCTAGCTACAACGA ATTTTTTT 3349 7408 UAUUUCAA UGGULAAA 1636 TTTAGCAA GGCTAGCTACAACGA ATTTTTTT 3349 7409 AUUGCULAA UUUUCAAU 1638 TAAAATA GGCTAGCTACAACGA ATTTAGTT 3340 7401 UGCUAAAU G UUUAGACU 1640 TTTTCTA GGCTAGCTACAACGA TTAGACTA 3341 7402 AAACUAA UUUUCAAU 1639 ATTAGAAA GGCTAGCTACAACGA TTAGATT 3340 7403 AAAACUAA UUGCULAAU 1640 TTTTCTA GGCTAGCTACAACGA TTTAGTT 3344 7404 CUGAUUGU G UUGAGUU 1641 ACATTTAG GGCTAGCTACAACGA TTTAGTTT 3344 7405 AAACU	7259	UAUGUUCU G UCUCCUUC	1618	GAAGGAGA GGCTAGCTACAACGA AGAACATA	3320
7283	7269	CUCCUUCC A UAAAUUUU	1619	AAAATTTA GGCTAGCTACAACGA GGAAGGAG	3321
7285         UUCAAAAU A CUAAUUCA         1622         TGAATTAG GGCTAGCTACAAGA ATTTTGAA 3324           7289         AANUACUA A UUCAACAA         1623         TTGTTGAA GGCTAGCTACAAGA TAGTATTT 3325           7294         CUAAUUCA A CAAAGAAA         1624         TTTCTTTG GGCTAGCTACAAGA TGAATTAG 3326           7305         AAGAAAAA G CUCUUUUU         1625         AAAAAGAG GGCTAGCTACAAGA TTAGGAA 3326           7327         UAAAAUAA A UAAACUCA         1626         TGAGTTTA GGCTAGCTACAAGA TTTAGGAA 3328           7327         UAAAAUAA A CUCAAAUU         1627         AATTTGAG GGCTAGCTACAACGA TTAGGTTT         3329           7333         AAACUCAA A UUUAUCCU         1628         AGGATAAA GGCTAGCTACAACGA TTAGGTTT         3330           7337         UCAAAUUU A UCCUUGUU         1628         AGCAAGAA GGCTAGCTACAACGA TTAGACTA         3331           7343         UUAUCCUU G UUUAGAGC         1630         GCTCTAAA GGCTAGCTACAACGA ATTTAGA         3331           7350         UGUUAGA A UUUAGAA         1631         TTTCTCTG GGCTAGCTACAACGA TTTTCTTA         3333           7370         UAAGAAAA A UUGUAAA         1631         TTTCTAA GGCTACCAACGA TTTTCTTA         3336           7381         UUGAABUG G UCUCAAAA         1635         TTTTGAGA GGCTAGCTACAACGA TTTTCAA         3337           7391         CUCAAAAA A UGGUAAA	7273	UUCCAUAA A UUUUUCAA	1620	TTGAAAAA GGCTAGCTACAACGA TTATGGAA	3322
7289         AAAUACUA A UUCAACAA         1623         TTGTTGAA GGCTAGCTACAACGA TAGTATTT         3325           7294         CUAAUUCA A CAAAGAAA         1624         TTTCTTTG GGCTAGCTACAACGA TAAATAG         3326           7305         AAGAAAAA G CUCUUUUU         1625         AAAAAGAG GGCTAGCTACAACGA TTTTTCTT         3327           7323         UUCCUAAA A UAAACUCA         1626         TGAGTTTA GGCTAGCAACGA TTTATTTTA         3327           7337         UAAAAUAA A CUCAAAUU         1627         AATTTGAG GGCTAGCTACAACGA TTTATTTTA         3329           7337         UCAAAUUU A UCCUUGUU         1629         AACAAGGA GGCTAGCTACAACGA TTGAGTT         3330           7337         UCAAAUUU A UCCUUGUU         1629         AACAAGGA GGCTAGCTACAACGA TAGAACA         3331           7343         UUAUCCUU G UUUAGAGC         1630         CTCTAAA GGCTAGCTACAACGA TTTCACACA         3333           7350         UGUUUAGA G CAGAGAA         1631         TTTCTCTG GGCTAGCTACACGA TTTCTCT         3334           7370         UAAAAAAUG G CUUUAGAA         1632         TTTCTAAA GGCTAGCTACAACGA TTTCTCT         3335           7371         UAGAAAAA A UUGUAAA         1635         TTTTGAAG GGCTAGCTACAACGA TTTCTCTA         3337           7381         UUGAAUG G UUAAAAA         1635         TTTTGAGA GGCTAGCTACAACGA TTTTCTA <td< td=""><td>7283</td><td>UUUUCAAA A UACUAAUU</td><td>1621</td><td>AATTAGTA GGCTAGCTACAACGA TTTGAAAA</td><td>3323</td></td<>	7283	UUUUCAAA A UACUAAUU	1621	AATTAGTA GGCTAGCTACAACGA TTTGAAAA	3323
7294         CUAAUUCA A CAAAGAAA         1624         TITCTITG GGCTAGCTACAACGA TGAATTAG         3326           7305         AAGAAAAA G CUCUUUUU         1625         AAAAAGAG GGCTAGCTACAACGA TITTACTA         3327           7323         UUCCUAAA A UAAACUCA         1626         TGAGTTTA GGCTACCAACGA TITTACGAA         3328           7327         UAAAAUAA A CUCAAAUU         1627         AATTGAGG GGCTAGCTACAACGA TITAGGAA         3328           7333         AAACUCAA A UUUAUCCU         1628         AGGATAAA GCTACAACGA AAAGATTTAGA         3331           7333         UCAAAUUU A UCCUUGUU         1629         AACAAGGA GGCTAGCTACAACGA AAAGATTAGA         3331           7343         UUAAUCCU G UUUAGAC         1630         GCTCTAAA GGCTACCAACGA AAAGATTACAACGA         3333           7350         UGUUUAGA G CAGAGAAA         1631         TTTCTTAA GGCTACCAACGA TTTCATACACGA         3333           7360         AGGAAAA A UUAAGAA         1632         TTTCTTAA GGCTACCAACGA TTTCTTCT         3336           7370         UAAGAAAA A CUUUGAAA         1635         TTTTGAAG GGCTACCTACACGA TTTCTTCT         3336           7381         UUGAAAUG G UCUCAAAA         1635         TTTTGAGA GGCTACCTACACGA TTTTTCAA         3337           7391         CUCAAAAA         1636         TTTAGCAA GGCTACCACGA TTTTTGAA         3334	7285	UUCAAAAU A CUAAUUCA	1622	TGAATTAG GGCTAGCTACAACGA ATTTTGAA	3324
7305   AAGAAAAA G CUCUUUUU   1625   AAAAAGAG GGCTAGCTACAACGA TTTTTCTT   3327     7323   UUCCUAAA A UAAACUCA   1626   TGAGTTTA GGCTAGCTACAACGA TTTTAGGAA   3328     7327   UAAAAUNA A CUCAAAUU   1627   AATTTGAG GGCTAGCTACAACGA TTTAGGAA   3329     7333   AAACUCAA A UUUAUCCU   1628   AGGATAAA GGCTAGCTACAACGA TTGAGTTT   3339     7337   UCAAAUUU A UCCUUGUU   1629   AACAAGGA GGCTAGCTACAACGA TTGAGTTT   3330     7343   UUAUCCUU G UUUAGAGC   1630   GCTCTAAA GGCTAGCTACAACGA AAATTTGA   3331     7350   UGUUUAGAG C CAGAGAAA   1631   TTTCTCTG GGCTAGCTACAACGA AAGGATAA   3332     7360   AGGAGAAA A UUAAGAAA   1632   TTTCTTAA GGCTAGCTACAACGA TTTTCTCT   3334     7370   UAAGAAAA A CUCUUGAAA   1633   TTTCAAAG GGCTAGCTACAACGA TTTTCTCT   3335     7378   ACUUUGAA A UGGUCUCA   1634   TGAGACCA GGCTAGCTACAACGA TTTTCTCT   3335     7381   UUGAAAAUG G UCUCAAAA   1635   TTTTGAGA GGCTAGCTACAACGA TTTCTAAAGT   3337     7391   CUCAAAAA A UUGCUAAA   1636   TTTTGCAA GGCTAGCTACAACGA TTTTCTAA   3337     7394   AAAAAUU G CUAAAUAU   1637   ATATTTAG GGCTAGCTACAACGA ATTTTTT   3339     7399   AUUGCUAA A UAUUUUCAA   1638   TGAAAATA GGCTAGCTACAACGA ATTTTTT   3339     7390   AUUGCUAA A UAUUUUCAA   1639   ATTGAAAA GGCTAGCTACAACGA ATTTAGCA   3341     7408   UAUUUCA A UGGAAAAC   1640   GTTTTCCA GGCTAGCTACAACGA ATTTAGCA   3341     7415   AAUGGAAA A UUGAGUU   1642   AACTAACA GGCTAGCTACAACGA ATTTAGCA   3342     7420   AAAACUAA A UUUUGAU   1639   ATTGAAAA GGCTAGCTACAACGA ATTTAGCA   3343     7420   AAAACUAA A UUGUUGUU   1642   AACTAACA GGCTAGCTACAACGA ATTTAGTT   3344     7420   AAAACUAA A UUGUUGUU   1642   AACTAACA GGCTAGCTACAACGA ATTTAGTT   3344     7420   AAAACUAA A UUGUUGUU   1642   AACTAACA GGCTAGCTACAACGA ATTACATT   3345     7420   AAAACUAA A UUUUCACU   1644   CAGCTAAA GGCTAGCTACAACGA ATTACATT   3345     7420   AAACUAA A UUUUCACU   1648   AAACCCA GGCTAGCTACAACGA ATTACATT   3346     7420   AAACUAA A UUUUCACU   1648   AAACCAA GGCTAGCTACAACGA ATAACTAA   3347     7420   AAACUAA UUUUCACU   1648   AAACCCA GGCTAGCTACAACGA ACAATCAG   3357     7450   UUUUGCUG A CCUUUCA	7289	AAAUACUA A UUCAACAA	1623	TTGTTGAA GGCTAGCTACAACGA TAGTATTT	3325
7323         UUCCUAAA A UAAACUCA         1626         TGAGTTTA GGCTAGCTACAACGA TTTAGGAA         3328           7327         UAAAANAA A CUCAANUU         1627         AATTTGAG GGCTAGCTACAACGA TTAGTTT         3329           7333         AAACUCAA A UUUAUCCU         1628         AGGATAAA GGCTAGCTACAACGA TTGAGTT         3330           7337         UCAAADUU A UCCUUGUU         1629         AACAAGGA GGCTAGCTACAACGA AATTTGA         3331           7343         UUAUCCUU G UUUAGAGC         1630         GCTCTAAA GGCTAGCTACAACGA AAGTTGA         3332           7350         UGUUUAGA G CAAGAAA         1631         TTTCTTG GGCTAGCTACAACGA TTTACACA         3333           7360         AGAGAAAA A UUAGAAA         1632         TTTCTAAA GGCTAGCTACAACGA TTTTCTA         3335           7370         UAAGAAAA A CUUGAAA         1634         TGAGACCA GGCTAGCTACAACGA TTTCAAAGT         3336           7381         UUGAAAAA A UUGCUAAA         1635         TTTTGACA GGCTAGCTACAACGA CATTTCAA         3337           7391         CUCAAAAA A UUGCUAAA         1636         TTTAGCAA GGCTAGCTACAACGA TTTTTGAA         3339           7399         AUUGCUAA A UAUUUCAA         1638         TGAAATA GGCTAGCTACAACGA ATTTAGCAA         3340           7401         UGCUAAAUA UUUUCAAU         1639         ATTGAAAA         GGCTAGCTACAACGA ATTACA	7294	CUAAUUCA A CAAAGAAA	1624	TTTCTTTG GGCTAGCTACAACGA TGAATTAG	3326
7327	7305	AAGAAAAA G CUCUUUUU	1625	AAAAAGAG GGCTAGCTACAACGA TTTTTCTT	3327
7333         AAACUCAA A UUUAUCCU         1628         AGGATAAA GGCTAGCTACAACGA TTGAGTTT         3330           7337         UCAAAUUU A UCCUUGUU         1629         AACAAGGA GGCTAGCTACAACGA AAATTTGA         3331           7343         UUAUCCUU G UUUAGAGC         1630         GCTCTAAA GGCTAGCTACAACGA AAGGATAA         3332           7350         UGUUUAGA G CAGAGAAA         1631         TTTCTTG GGCTAGCTACAACGA TTTTCACA         3333           7360         AGAGAAAA A UUAAGAAA         1632         TTTCTTAA GGCTAGCTACAACGA TTTTCTCA         3334           7370         UAAGAAAA A CUUUGAAA         1632         TTTCAAAG GGCTAGCTACAACGA TTTCAAAGT         3336           7381         UUGAAAU G UUCCAAAA         1635         TTTGAGA GGCTAGCTACAACGA CATTTCAA         3337           7391         CUCAAAAA A UUGCUAAA         1636         TTTAGCAA GGCTAGCTACAACGA CATTTTTAG         3338           7394         AAAAAAUU G CUCAAAAA         1637         ATTATTAG GGCTAGCTACAACGA TTTTTTAG         3340           7401         UGCUAAAU A UUUUCAA         1638         TGAAAATA GGCTAGCTACAACGA TTTAGCAA         3341           7408         UAUUUUCA A UGGABAA C 1640         GTTTTCCA GGCTAGCTACAACGA TTTAGCAT         3342           7420         AAACUAAA A UGUUAGUU         1641         ACATTAG GGCTAGCTACAACGA TTAGTTT         3343 <td>7323</td> <td>UUCCUAAA A UAAACUCA</td> <td>1626</td> <td>TGAGTTTA GGCTAGCTACAACGA TTTAGGAA</td> <td>3328</td>	7323	UUCCUAAA A UAAACUCA	1626	TGAGTTTA GGCTAGCTACAACGA TTTAGGAA	3328
7337         UCAAAUUU A UCCUUGU         1629         AACAAGGA GGCTACCTACAACGA AAATTTGA 3331           7343         UUAUCCUU G UUUAGAGC         1630         GCTCTAAA GGCTACCTACAACGA AAGGATAA 3332           7350         UGUUUAGA G CAGAGAAA 1631         TTTCTTG GGCTACCTACACGA TCTAAACA 3333           7360         AGAGAAAA A UUAAGAAA 1632         TTTCTTAA GGCTACCTACAACGA TTTCTCT 3334           7370         UAAGAAAA A CUUUGAAA 1633         TTTCTAAG GGCTAGCTACAACGA TTTCTAAG 3335           7378         ACUUUGAA A UGGUCUCA 1634         TGAGACCA GGCTAGCTACAACGA TTTCTAAG 3336           7381         UUCAAAAA A UUGCUAAA 1635         TTTTGAGA GGCTAGCTACAACGA TTTCTAAG 3337           7391         CUCAAAAA A UUGCUAAA 1636         TTTTAGCA GGCTACCAACGA TTTTTGAG 3338           7394         AAAAAAUU G CUAAAUAU 1637         ATATTTAG GGCTACCAACGA ATTTTTTAG 3339           7399         AUUGCUAA A UUUUCAAU 1638         TGAAAAATA GGCTACCAACGA ATTTAGCA 3341           7401         UGCUAAAU A UUUUCAAU 1639         ATTGAAAA GGCTACCAACGA TTTAGCAT 3342           7415         AAUGGAAA A CUAAAUGU 1640         ACATTTAG GGCTACCAACGA TTTCATT 3343           7420         AAACUAA A UGUUAGUU 1642         AACTTACA GGCTACCAACGA TTTCATT 3344           7422         AACUAAAU G UUAGCUG 1644         CAGCTAAA GGCTACCAACGA TTACATTT 3345           7426         AAAUGUAG G UUAGCUG 1643         CACATCA	7327	UAAAAUAA A CUCAAAUU	1627	AATTTGAG GGCTAGCTACAACGA TTATTTTA	3329
7343 UUAUCCUU G UUUAGAGC 1630 GCTCTAAA GGCTACCAACGA AAGGATAA 3332 7350 UGUUUAGA G CAGAGAAA 1631 TTCTCTG GGCTACCAACGA TCTAAACA 3333 7360 AGAGAAAA A UUAAGAAA 1632 TTTCTTAA GGCTAGCTACAACGA TCTAAACA 3333 7370 UAAGAAAA A CUUUGAAA 1633 TTTCAAAG GGCTAGCTACAACGA TTTCTCTT 3334 7378 ACUUUGAA A UGUUCAAA 1633 TTTCAAAG GGCTAGCTACAACGA TTTCTCTA 3335 7381 UUGAAAGG G UCUCAAAA 1635 TTTTGAGA GGCTAGCTACAACGA TTCAAAGT 3336 7391 CUCAAAAA A UUGCUAAA 1635 TTTTGAGA GGCTAGCTACAACGA TTCTAAAGT 3337 7391 CUCAAAAA A UUGCUAAA 1636 TTTAGCAA GGCTAGCTACAACGA TTTTTGAG 3338 7394 AAAAAAUU G CUAAAUAU 1637 ATATTTAG GGCTAGCTACAACGA ATTTTTTA 3339 7399 AUUGCUAA A UAUUUCAA 1638 TGAAAATA GGCTAGCTACAACGA ATTTTTTA 3339 7401 UGCUAAAU A UUUUCAAU 1639 ATTGAAAA GGCTAGCTACAACGA ATTTTTAGA 3341 7401 UGCUAAAU A UUUUCAAU 1639 ATTGAAAA GGCTAGCTACAACGA TTAGCAAT 3340 7402 AAACUAAA A UGUUAGUU 1641 ACATTTAG GGCTAGCTACAACGA TTTAGCAA 3341 7420 AAAACUAA A UGUAGUUU 1642 AACTAACA GGCTAGCTACAACGA TTTCCCTT 3343 7420 AAACUAAA U UUUAGUUU 1642 AACTAACA GGCTAGCTACAACGA TTTCCCTT 3343 7420 AAACUAAA U UUUAGUUU 1642 AACTAACA GGCTAGCTACAACGA TTTTCTTT 3345 7422 AACUAAAU G UUAGUUU 1642 AACTAACA GGCTAGCTACAACGA TTTTGTTT 3345 7426 AAAUGUAA G UUAGUUU 1643 TAAACTAA GGCTAGCTACAACGA TTTAGTTT 3346 7431 UUAGUUUA G CUGAUUGU 1645 ACATCAG GGCTAGCTACAACGA TAACCATT 3346 7433 UUUAGCUG A UUGUUGU 1645 ACATCAG GGCTAGCTACAACGA TAAACTATA 3347 7434 UUAGUUUA G UUAUGCUG 1644 ACCCCATA GGCTAGCTACAACGA TAAACTAA 3347 7435 GUUUUCGA A UGUGUGUU 1648 AAACCCCA GGCTAGCTACAACGA TAAACTAA 3349 7440 CUGAUUUG A UGGGGUUU 1648 AAACCCCA GGCTAGCTACAACGA ACAACTAA 3351 7445 UGUAUGGG G UUUUCGAA 1649 TTCGAAAA GGCTAGCTACAACGA ACAACTAA 3351 7460 AACCUUUU G UUUGCAA 1650 GTGAAAAG GGCTAGCTACAACGA ACAACAA 33551 7461 UGUUUCGA A CCUUUCCA 1650 AAACAAA GGCTAGCTACAACGA ACAACAA 33551 7460 AACCUUU G UUUGCAA 1650 GTGAAAAG GGCTAGCTACAACGA AAAAAAA 33551 7461 UUUUACCU A UUACCUU 1653 AGGTAAAA GGCTAGCTACAACGA AAAAAAA 33551 7460 UUUUACCU A UUUCCAA 1650 AAACAAA GGCTAGCTACAACGA AAAAAAA 33551 7460 UUUUACCU A UUACCUU 1653 AGGTAAAA GGCTAGCTACAACGA AAACAAA	7333	AAACUCAA A UUUAUCCU	1628	AGGATAAA GGCTAGCTACAACGA TTGAGTTT	3330
7350 UGUUUAGA G CAGAGAAA 1631 TITCTCTG GGCTAGCTACAACGA TCTAAACA 3333 7360 AGAGAAAA A UUAAGAAA 1632 TITCTTAA GGCTAGCTACAACGA TTTTCTCT 3334 7370 UAAGAAAA A CUUUGAAA 1633 TITCAAAG GGCTAGCTACAACGA TITTCTCT 3334 7378 ACUUUGAA A UGGUCUCA 1634 TGAGACCA GGCTAGCTACAACGA TTTTCTTA 3335 7381 UUGAAAUG G UCUCAAAA 1635 TITTGAAAG GGCTAGCTACAACGA TTTTAAAGT 3336 7381 CUCAAAAA A UUGCUAAA 1635 TITTGAGA GGCTAGCTACAACGA TTTTAGA 3337 7391 CUCAAAAA A UUGCUAAA 1635 TITTGAGA GGCTAGCTACAACGA TTTTTAGA 3337 7394 AAAAAUU G CUAAAUAU 1637 ATATTTTAG GGCTAGCTACAACGA TTTTTGAG 3338 7399 AUUGCUAA A UAUUUCA 1638 TGAAAATA GGCTAGCTACAACGA ATTTTTT 3339 7399 AUUGCUAAAU A UUUUCAAU 1639 ATTGAAAA GGCTAGCTACAACGA ATTTAGCA 3341 7401 UGCUAAAU A UUUUCAAU 1639 ATTGAAAA GGCTAGCTACAACGA ATTTAGCA 3341 7408 UAUUUUCA A UGGAAAAC 1640 GTTTTCCA GGCTAGCTACAACGA ATTTAGCA 3341 7415 AAUGGAAA A CUUAAUGU 1641 ACATTTAG GGCTAGCTACAACGA TTTAGCA 3342 7420 AAAACUAA A UGUUAGUU 1642 AACTAACA GGCTAGCTACAACGA TTTCCATT 3344 7422 AACUAAAU G UUAGUUUA 1643 TAAACTAA GGCTAGCTACAACGA ATTTAGTTT 3344 7426 AAAUGUUA G UUUAGCUG 1644 CAGCTAAA GGCTAGCTACAACGA TTAACATTT 3346 7431 UUAGUUUA G CUGAUUGU 1643 TAAACTAA GGCTAGCTACAACGA TAACATTT 3346 7431 UUAGUUUA G CUGAUUGU 1645 ACAATCAG GGCTAGCTACAACGA TAACATTT 3346 7431 UUAGUUUA G CUGAUUGU 1645 ACAATCAG GGCTAGCTACAACGA TAACATTT 3346 7433 AGCUGAU G UUGGGGU 1647 ACCCCATA GGCTAGCTACAACGA ATCAGCT 3349 7440 CUGAUUGU A UGGGGGU 1647 ACCCCATA GGCTAGCTACAACGA ACAATCAG 3350 7445 UGUAUGGG UUUUCGAA 1649 TCGAAAA GGCTAGCTACAACGA ACAATCAG 3350 7460 AACCUUUC A CUUUUGU 1651 ACAAAAAG GGCTAGCTACAACGA ACAATCAG 3351 7467 CACUUUU G UUUGCAA 1659 GTAAACAAA GGCTAGCTACAACGA ACAACAA 3355 7467 CACUUUU G UUUUCACAA 1659 TTGAAAAG GGCTAGCTACAACGA AAAAAAGTG 3356 7460 AACCUUU A CUUUUCA 1651 ACAAAAAG GGCTAGCTACAACGA AAAACAAA 3355 7467 CACUUUU G UUUUCACAA 1659 TTGAAAAG GGCTAGCTACAACGA AAAACAAA 3355 7460 AACCUUU A CUUUCACA 1655 TTACACAG GGCTAGCTACAACGA AAAACAAA 3355 7460 CACUUUC A CAACUGUG 1654 AAACAAA GGCTAGCTACAACGA AAAACAAA 3355 7460 UUUUACCU A UUUCACAA 1655 TTGAAAAG GGCTAGCTACAACGA AA	7337	UCAAAUUU A UCCUUGUU	1629	AACAAGGA GGCTAGCTACAACGA AAATTTGA	3331
7360         AGAGAAAA A UUAAGAAA         1632         TITCTTAA GGCTAGCTACAACGA TITTCTCT         3334           7370         UAAGAAAA A CUUUGAAA         1633         TITCAAAG GGCTAGCTACAACGA TITTCTTA         3335           7378         ACUUUGAAA A UGGUCUCA         1634         TGAGACCA GGCTAGCTACAACGA TTCAAAGT         3336           7381         UUGAAAUG G UCUCAAAA         1635         TITTGAGA GGCTAGCTACAACGA CATTCCAA         3337           7391         CUCAAAAA A UAUUUCA         1636         TITAGCAA GGCTAGCTACAACGA CATTTCTAA         3338           7394         AAAAAAUU G CUAAUUU         1637         ATATTTAG GGCTAGCTACAACGA ATTTTTT         3339           7399         AUUGCUAA A UAUUUCA         1638         TGAAAATA GGCTAGCTACAACGA TTTAGCAA         3341           7401         UGCUAAAU A UUUUCAAU         1639         ATTGAAAA GGCTAGCTACAACGA TTTAGCAA         3341           7408         UAUUUCA A UGGAAAAC         1640         GTTTTCCA GGCTAGCTACAACGA TTAGCTT         3344           7420         AAAACUAA A UGUUAGUU         1641         ACATTAG GGCTAGCTACAACGA TTAGTTT         3345           7422         AACUAAAU G UUAGUUU         1643         TAAACTAA GGCTAGCTACAACGA TTAGTTT         3346           7431         UUAGUUA G CUGAUGU         1645         ACAATCAG GGCTAGCTACAACGA TAACCATTT         <	7343	UUAUCCUU G UUUAGAGC	1630	GCTCTAAA GGCTAGCTACAACGA AAGGATAA	3332
7370         UAAGAAAA A CUUUGAAA         1633         TTTCAAAG GCTAGCTACAACGA TTTCTTA         3335           7378         ACUUUGAA A UGGUCUCA         1634         TGAGACCA GGCTAGCTACAACGA TTCAAAGT         3336           7381         UUGAAAAG G UCUCAAAA         1635         TTTTGAGA GGCTAGCTACAACGA CATTTCAA         3337           7391         CUCAAAAA A UUGCUAAA         1636         TTTAGCAA GGCTAGCTACAACGA TTTTTGAG         3338           7394         AAAAAAUU G CUAAAUAU         1637         ATATTTAG GGCTAGCTACAACGA ATTTTTT         3339           7399         AUUGCUAAA A UUUUCAAU         1639         ATTGAAAA GGCTAGCTACAACGA ATTTGCA         3341           7401         UGCUAAAU A UUUUCAAU         1639         ATTGAAAA GGCTAGCTACAACGA ATTTAGCA         3341           7408         UAUUUUCA A UGGAAAC         1640         GTTTTCCA GGCTAGCTACAACGA ATTAGCA         3342           7415         AAUGGAAA A CUAAAUGU         1641         ACATTACA GGCTAGCTACAACGA TTAGTTT         3343           7420         AAACUAA A UGUUGUU         1642         AACTAACA GGCTAGCTACAACGA ATTAGTTT         3345           7426         AAAUGUUA G UUUGUUU         1643         TAAACTAA GGCTAGCTACAACGA TAACATTT         3346           7431         UUUAGUUG A UUGGGGU         1645         ACAACAA GGCTAGCTAACAGA AACAATAA	7350	UGUUUAGA G CAGAGAAA	1631	TTTCTCTG GGCTAGCTACAACGA TCTAAACA	3333
7378         ACUUUGAA A UGGUCUCA         1634         TGAGACCA GGCTAGCTACAACGA TTCAAAGT         3336           7381         UUGAAAUG G UCUCAAAA         1635         TTTTGAGA GGCTAGCTACAACGA CATTTCAA         3337           7391         CUCAAAAA A UUGCUAAA         1636         TTTAGCAA GGCTAGCTACAACGA TTTTTGAG         3338           7394         AAAAAAUU G CUAAAUAU         1637         ATATTTAG GGCTAGCTACAACGA ATTTTTT         3339           7399         AUUGCUAA A UAUUUCA         1638         TGAAAATA GGCTAGCTACAACGA ATTTAGCA         3341           7401         UGCUAAAU A UUUUCAAU         1639         ATTGAAAA GGCTAGCTACAACGA ATTTAGCA         3341           7408         UAUUUCA A UGGAAAAC         1640         GTTTTCCA GGCTACACACGA TTTAGCA         3342           7415         AAUGGAAA A CUAAAUGU         1641         ACATTTAG GGCTACCACCAC ATTAGTTT         3343           7420         AAAACUAA A UGUUAGUU         1642         AACTAACA GGCTACCAACGA TTTAGTT         3345           7422         AACUAAAU G UUUAGCUG         1644         CAGCTAAA GGCTACCAACGA TTACATTT         3346           7431         UUAGCUG A UUGGGGU         1644         CAGCTAAA GGCTACCAACGA TAACATTA         3347           7438         AGCUGAUU G UUGGGGU         1646         CCATACAA GGCTACCAACGA AACAACGA         3350	7360	AGAGAAAA A UUAAGAAA	1632	TTTCTTAA GGCTAGCTACAACGA TTTTCTCT	3334
7381         UUGAAAUG G UCUCAAAA         1635         TTTTGAGA GGCTAGCTACAACGA CATTTCAA         3337           7391         CUCAAAAA A UUGCUAAA         1636         TTTAGCAA GGCTAGCTACAACGA TTTTGAG         3338           7394         AAAAAAUU G CUAAAUAU         1637         ATATTTAG GGCTAGCTACAACGA AATTTTT         3339           7399         AUUGCUAA A UAUUUCA         1638         TGAAAATA GGCTAGCTACAACGA ATTTAGCA         3341           7401         UGCUAAAU A UUUUCAAU         1639         ATTGAAAA GGCTAGCTACAACGA ATTTAGCA         3341           7408         UAUUUUCA A UGGAAAAC         1640         GTTTTCCA GGCTAGCTACAACGA TTTAGCTT         3342           7415         AAUGGAAA A CUAAAUGU         1641         ACATTAG GGCTAGCTACAACGA TTTCCATT         3343           7420         AAAACUAA A UGUUAGUU         1642         AACTAACA GGCTAGCTACAACGA TTTAGTTT         3345           7422         AACUAAAU G UUAGCUG         1643         TAAACTAA GGCTACCAACGA TAACATTT         3346           7431         UUAGCUG A UUGUGUG         1645         ACAATCAG GGCTACCAACGA TAACATTA         3347           7438         AGCUGAUU G UAUGGGGU         1646         CCATACAA GGCTACCAACGA AATCAGC         3349           7440         CUGAUGUA A UGGGGGUU         1648         AAACCCCA GGCTACCAACGA ACAATCAG         3350 <td>7370</td> <td>UAAGAAAA A CUUUGAAA</td> <td>1633</td> <td>TTTCAAAG GGCTAGCTACAACGA TTTTCTTA</td> <td>3335</td>	7370	UAAGAAAA A CUUUGAAA	1633	TTTCAAAG GGCTAGCTACAACGA TTTTCTTA	3335
7391         CUCAAAAA A UUGCUAAA         1636         TTTAGCAA GGCTAGCTACAACGA TTTTTGAG         3338           7394         AAAAAAUU G CUAAAUAU         1637         ATATTTAG GGCTAGCTACAACGA AATTTTT         3339           7399         AUUGCUAA A UAUUUUCA         1638         TGAAAATA GGCTAGCTACAACGA TTAGCAAT         3340           7401         UGCUAAAU A UUUUCAAU         1639         ATTGAAAA GGCTAGCTACAACGA ATTTAGCA         3341           7408         UAUUUUCA A UGGAAAAC         1640         GTTTTCCA GGCTAGCTACAACGA TTAGATT         3342           7415         AAUGGAAA A CUAAAUGU         1641         ACATTAG GGCTAGCTACAACGA TTAGTTTT         3343           7420         AAAACUAA A UGUUAGUU         1642         AACTAACA GGCTAGCTACAACGA TTAGTTTT         3344           7422         AACUAAAU G UUAGUUUA         1643         TAAACTAA GGCTAGCTACAACGA ATTAGTT         3346           7431         UUAGCUG A UUGUUUA         1644         CACATCAG GGCTAGCTACAACGA TAAACTAA         3347           7435         UUUAGCUG A UUGUAUUG         1646         CCATACAA GGCTACAACGA AATCAGC         3349           7440         CUGAUUGU A UGGGGUU         1648         AAACCCCA GGCTACAACGA ACAATCAG         3350           7445         UGUAUGGA A CCUUUCAC         1650         GTGAAAAG GGCTACAACGA ACAATCAG         3351 <td>7378</td> <td>ACUUUGAA A UGGUCUCA</td> <td>1634</td> <td>TGAGACCA GGCTAGCTACAACGA TTCAAAGT</td> <td>3336</td>	7378	ACUUUGAA A UGGUCUCA	1634	TGAGACCA GGCTAGCTACAACGA TTCAAAGT	3336
7394         AAAAAAUU G CUAAAUAU         1637         ATATTTAG GGCTAGCTACAACGA AATTTTT         3339           7399         AUUGCUAA A UAUUUUCA         1638         TGAAAATA GGCTAGCTACAACGA TTAGCAAT         3340           7401         UGCUAAAU A UUUUCAAU         1639         ATTGAAAA GGCTAGCTACAACGA ATTTAGCA         3341           7408         UAUUUUCA A UGGAAAAC         1640         GTTTTCCA GGCTAGCTACAACGA TGAAAATA         3342           7415         AAUGGAAA A CUAAAUGU         1641         ACATTTAG GGCTAGCTACAACGA TTTCCATT         3343           7420         AAAACUAA A UGUUAGUU         1642         AACTAACA GGCTAGCTACAACGA TTTAGTTT         3344           7422         AACUAAAU G UUUAGUUA         1643         TAAACTAA GGCTAGCTACAACGA ATTTAGTT         3345           7426         AAAUGUUA G UUUAGUUG         1644         CAGCTAAA GGCTAGCTACAACGA TAAACATT         3346           7431         UUAGCUG A UUGUAUGG         1646         CCATACAA GGCTAGCTACAACGA CAGCTAAA         3347           7438         AGCUGAUUG U GUAGGGGU         1647         ACCCCATA GGCTAGCTACAACGA ACAACAC         3350           7445         UGUAUGGA A CUUUCGA         1649         TTCGAAAA         GGCTAGCTACAACGA ACAACAAC         3351           7453         GUUUUCGA A CUUUUCC         1650         GTGAAAGG GGCTAGCTACAACGA A	7381	UUGAAAUG G UCUCAAAA	1635	TTTTGAGA GGCTAGCTACAACGA CATTTCAA	3337
7399         AUUGCUAA A UAUUUCA         1638         TGAAAATA GGCTAGCTACAACGA TTAGCAAT         3340           7401         UGCUAAAU A UUUUCAAU         1639         ATTGAAAA GGCTAGCTACAACGA ATTTAGCA         3341           7408         UAUUUUCA A UGGAAAAC         1640         GTTTTCCA GGCTAGCTACAACGA TGAAAATA         3342           7415         AAUGGAAA A CUAAAUGU         1641         ACATTTAG GGCTAGCTACAACGA TTTCCATT         3343           7420         AAAACUAA A UGUUAGUU         1642         AACTAACA GGCTAGCTACAACGA TTTAGTT         3345           7422         AACUAAAU G UUUAGCUG         1644         CAGCTAAA GGCTAGCTACAACGA ATTTAGTT         3346           7431         UUAGUUUA G CUGAUUGU         1645         ACAATCAG GGCTAGCTACAACGA TAAACTAA         3347           7435         UUUAGCUG A UUGUAUGG         1646         CCATACAA GGCTAGCTACAACGA CAGCTAAA         3349           7440         CUGAUUGU A UGGGGUU         1648         AAACCCCA GGCTAGCTACAACGA ACAATCAG         3350           7445         UGUAUGGG G UUUUCGAA         1649         TTCGAAAA GGCTAGCTACAACGA CCATACA         3351           7453         GUUUUCGA A CCUUUUCA         1650         GTGAAAGG GGCTAGCTACAACGA ACAACGA ACAACGA CCATACA         3351           7445         UGUAUUUG A CUUUUGUUU         1651         ACAAAAAG GGCTAGCTACAACGA AA	7391	CUCAAAAA A UUGCUAAA	1636	TTTAGCAA GGCTAGCTACAACGA TTTTTGAG	3338
7401         UGCUAAAU A UUUUCAU         1639         ATTGAAAA GGCTAGCTACAACGA ATTTAGCA         3341           7408         UAUUUUCA A UGGAAAAC         1640         GTTTTCCA GGCTAGCTACAACGA TGAAAATA         3342           7415         AAUGGAAA A CUAAAUGU         1641         ACATTAG GGCTAGCTACAACGA TTACATT         3343           7420         AAAACUAA A UGUUAGUU         1642         AACTAACA GGCTAGCTACAACGA TTAGTTT         3344           7422         AACUAAAU G UUUAGCUG         1644         CAGCTAAA GGCTACAACGA ATTAGTT         3345           7426         AAAUGUUA G CUGAUUGU         1645         ACAATCAG GGCTACCTACAACGA TAAACTT         3346           7431         UUAGCUG A UUGUAUGG         1646         CCATACAA GGCTACAACGA TAAACTAA         3347           7435         UUUAGCUG A UUGUAUGG         1647         ACCCCATA GGCTACAACGA ATCAGCA         3349           7440         CUGAUUGU A UGGGGUU         1648         AAACCCCA GGCTAGCTACAACGA ACAATCAG         3350           7445         UGUAUGGG G UUUUCGAA         1649         TTCGAAAA GGCTACCAACGA ACAATCAG         3351           7453         GUUUUCGA A CCUUUCAC         1650         GTGAAAGG GGCTAGCTACAACGA TCGAACGA         3352           7460         AACCUUU A CUUUUGUU         1651         ACAAAAAG GGCTAGCTACAACGA AAAAAGTG         3353	7394	AAAAAAUU G CUAAAUAU	1637	ATATTTAG GGCTAGCTACAACGA AATTTTTT	3339
7408 UAUUUUCA A UGGAAAAC 1640 GTTTTCCA GGCTAGCTACAACGA TGAAAATA 3342 7415 AAUGGAAA A CUAAAUGU 1641 ACATTTAG GGCTAGCTACAACGA TTTCCATT 3343 7420 AAAACUAA A UGUUAGUU 1642 AACTAACA GGCTAGCTACAACGA TTTCCATT 3344 7422 AACUAAAU G UUAGUUUA 1643 TAAACTAA GGCTAGCTACAACGA ATTTAGTT 3344 7422 AACUAAAU G UUAGCUG 1644 CAGCTAAA GGCTAGCTACAACGA ATTTAGTT 3346 7431 UUAGUUUA G CUGAUUGU 1645 ACAATCAG GGCTAGCTACAACGA TAAACTTA 3347 7435 UUUAGCUG A UUGUAUGG 1646 CCATACAA GGCTACAACGA TAAACTAA 3347 7438 AGCUGAUU G UAUGGGGU 1647 ACCCCATA GGCTACAACGA CAGCTAAA 3349 7440 CUGAUUGU A UGGGGUUU 1648 AAACCCCA GGCTAGCTACAACGA AATCAGC 3350 7445 UGUAUGGG G UUUUCGAA 1649 TTCGAAAA GGCTAGCTACAACGA ACAATCAG 3351 7453 GUUUUCGA A CCUUUCAC 1650 GTGAAAGG GGCTAGCTACAACGA CCCATACA 3351 7460 AACCUUUC A CUUUUUGU 1651 ACAAAAAG GGCTAGCTACAACGA GAAAGGTT 3353 7467 CACUUUU G UUUGUUUU 1652 AAAACAAA GGCTAGCTACAACGA AAAAAGGG 3354 7471 UUUUGUUU G UUUUACCU 1653 AGGTAAAA GGCTAGCTACAACGA AAAAAGGG 3356 7476 UUUGUUUU A CCUAUUUC 1654 GAAATAGG GGCTAGCTACAACGA AAAACAAA 3355 7476 UUUGUUUU A CCUAUUUC 1654 GAAATAGG GGCTAGCTACAACGA AAAACAAA 3356 7480 UUUUACCU A UUUCACAA 1655 TTGTGAAA GGCTAGCTACAACGA AAAACAAA 3357 7485 CCUAUUUC A CAACUGUG 1656 CACAGTTG GGCTAGCTACAACGA AGAACAAA 3357 7486 AUUUCACAA CUGUGUAA 1657 TTACACAG GGCTAGCTACAACGA GAAATAGG 3358 7488 AUUUCACAA CUGUGUAA 1657 TTACACAG GGCTAGCTACAACGA AGAATAGG 3358 7491 UCACAACU G UGUAAAUU 1658 AATTTACA GGCTAGCTACAACGA AGAATAGG 3360 7493 ACAACUGU G UAAAUUGC 1659 GCAATTTA GGCTAGCTACAACGA ACAGTTGT 3361	7399	AUUGCUAA A UAUUUUCA	1638	TGAAAATA GGCTAGCTACAACGA TTAGCAAT	3340
7415         AAUGGAAA A CUAAAUGU         1641         ACATTTAG GGCTAGCTACAACGA TTTCCATT         3343           7420         AAAACUAA A UGUUAGUU         1642         AACTAACA GGCTAGCTACAACGA TTAGTTT         3344           7422         AACUAAAU G UUAGUUUA         1643         TAAACTAA GGCTAGCTACAACGA ATTTAGTT         3345           7426         AAAUGUUA G UUUAGCUG         1644         CAGCTAAA GGCTAGCTACAACGA TAAACTAA         3347           7431         UUAGCUG A UUGUAUGG         1645         ACAATCAG GGCTAGCTACAACGA TAAACTAA         3347           7435         UUUAGCUG A UUGUAUGG         1646         CCATACAA GGCTAGCTACAACGA CAGCTAAA         3348           7438         AGCUGAUU G UAUGGGGU         1647         ACCCCATA GGCTAGCTACAACGA ATCAGCT         3349           7440         CUGAUUGU A UGGGGUUU         1648         AAACCCCA GGCTAGCTACAACGA ACAATCAG         3350           7445         UGUAUGGG G UUUUCGAA         1649         TTCGAAAA GGCTAGCTACAACGA CCCATACA         3351           7453         GUUUUCGA A CCUUUCAC         1650         GTGAAAGG GGCTAGCTACAACGA CCAAAAC         3352           7460         AACCUUU A CUUUUUUU         1651         ACAAAAAG GGCTAGCTACAACGA AAAAAAA         3353           7471         UUUUGUUU A CUUUUUUU         1652         AAAACAAA GGCTAGCTACAACGA AAAACAAA	7401	UGCUAAAU A UUUUCAAU	1639	ATTGAAAA GGCTAGCTACAACGA ATTTAGCA	3341
AAAACUAA A UGUUAGUU 1642 AACTAACA GGCTAGCTACAACGA TTAGTTTT 3344  7422 AACUAAAU G UUAGUUUA 1643 TAAACTAA GGCTAGCTACAACGA ATTTAGTT 3345  7426 AAAUGUUA G UUUAGCUG 1644 CAGCTAAA GGCTAGCTACAACGA ATTTAGTT 3346  7431 UUAGUUUA G CUGAUUGU 1645 ACAATCAG GGCTAGCTACAACGA TAAACTAA 3347  7435 UUUAGCUG A UUGUAUGG 1646 CCATACAA GGCTAGCTACAACGA CAGCTAAA 3348  7438 AGCUGAUU G UAUGGGGU 1647 ACCCCATA GGCTAGCTACAACGA AATCAGCT 3349  7440 CUGAUUGU A UGGGGUUU 1648 AAACCCCA GGCTAGCTACAACGA ACAATCAG 3350  7445 UGUAUGGG G UUUUCGAA 1649 TTCGAAAA GGCTAGCTACAACGA CCCATACA 3351  7453 GUUUUCGA A CCUUUCAC 1650 GTGAAAGG GGCTAGCTACAACGA CCCATACA 3352  7460 AACCUUUC A CUUUUUGU 1651 ACAAAAAG GGCTAGCTACAACGA GAAAGGTT 3353  7467 CACUUUUU G UUUGUUUU 1652 AAAACAAA GGCTAGCTACAACGA AAAAAGTG 3354  7471 UUUUGUUU G UUUUACCU 1653 AGGTAAAA GGCTAGCTACAACGA AAAAAAGTG 3356  7476 UUUGUUUU A CCUAUUUC 1654 GAAATAGG GGCTAGCTACAACGA AAACAAAA 3355  7476 UUUGUUU A CCUAUUUC 1654 GAAATAGG GGCTAGCTACAACGA AAACAAAA 3355  7476 UUUGUUU A CCUAUUUC 1654 GAAATAGG GGCTAGCTACAACGA AAACAAAA 3356  7480 UUUUACCU A UUUCACAA 1655 TTGTGAAA GGCTAGCTACAACGA AAACAAAA 3357  7485 CCUAUUUC A CAACUGUG 1656 CACAGTTG GGCTAGCTACAACGA AGGTAAAA 3357  7488 AUUUCACA A CUGUGUAA 1657 TTACACAG GGCTAGCTACAACGA AGGTAAAA 3359  7491 UCACAACU G UGUAAAUU 1658 AATTTACA GGCTAGCTACAACGA AGTTGTA 3360  7493 ACAACUGU G UAAAUUGC 1659 GCAATTTA GGCTAGCTACAACGA ACAGTTGT 3361	7408	UAUUUUCA A UGGAAAAC	1640	GTTTTCCA GGCTAGCTACAACGA TGAAAATA	3342
7422 AACUAAAU G UUAGUUUA 1643 TAAACTAA GGCTAGCTACAACGA ATTTAGTT 3345 7426 AAAUGUUA G UUUAGCUG 1644 CAGCTAAA GGCTAGCTACAACGA TAACATTT 3346 7431 UUAGUUUA G CUGAUUGU 1645 ACAATCAG GGCTAGCTACAACGA TAAACTAA 3347 7435 UUUAGCUG A UUGUAUGG 1646 CCATACAA GGCTAGCTACAACGA CAGCTAAA 3348 7438 AGCUGAUU G UAUGGGGU 1647 ACCCCATA GGCTAGCTACAACGA AATCAGCT 3349 7440 CUGAUUGU A UGGGGUUU 1648 AAACCCCA GGCTAGCTACAACGA ACAATCAG 3350 7445 UGUAUGGG G UUUUCGAA 1649 TTCGAAAA GGCTAGCTACAACGA ACAATCAG 3351 7453 GUUUUCGA A CCUUUCAC 1650 GTGAAAGG GGCTAGCTACAACGA TCGAAAC 3352 7460 AACCUUUC A CUUUUUGU 1651 ACAAAAAG GGCTAGCTACAACGA GAAAGGTT 3353 7467 CACUUUUU G UUUGUUUU 1652 AAAACAAA GGCTAGCTACAACGA AAAAAGTG 3354 7471 UUUUGUUU G UUUUACCU 1653 AGGTAAAA GGCTAGCTACAACGA AAAAAGTG 3356 7476 UUUGUUUU A CCUAUUUC 1654 GAAATAGG GGCTAGCTACAACGA AAACAAAA 3355 7476 UUUGUUUU A CCUAUUUC 1654 GAAATAGG GGCTAGCTACAACGA AAACAAAA 3357 7480 UUUUACCU A UUUCACAA 1655 TTGTGAAA GGCTAGCTACAACGA AAACAAAA 3356 7480 UUUUACCU A UUUCACAA 1655 TTGTGAAA GGCTAGCTACAACGA AGGTAAAA 3357 7485 CCUAUUUC A CAACUGUG 1656 CACAGTTG GGCTAGCTACAACGA AGGTAAAA 3357 7488 AUUUCACA A CUGUGUAA 1657 TTACACAG GGCTAGCTACAACGA AGATAGG 3356 7491 UCACAACU G UGUAAAUU 1658 AATTTACA GGCTAGCTACAACGA AGTTGTGA 3360 7493 ACAACUGU G UAAAUUGC 1659 GCAATTTA GGCTAGCTACAACGA ACGTTGT 3361	7415	AAUGGAAA A CUAAAUGU	1641	ACATTTAG GGCTAGCTACAACGA TTTCCATT	3343
7426 AAAUGUUA G UUUAGCUG 1644 CAGCTAAA GGCTAGCTACAACGA TAACATTT 3346 7431 UUAGUUUA G CUGAUUGU 1645 ACAATCAG GGCTAGCTACAACGA TAAACTAA 3347 7435 UUUAGCUG A UUGUAUGG 1646 CCATACAA GGCTAGCTACAACGA CAGCTAAA 3348 7438 AGCUGAUU G UAUGGGGU 1647 ACCCCATA GGCTAGCTACAACGA AATCAGCT 3349 7440 CUGAUUGU A UGGGGUUU 1648 AAACCCCA GGCTAGCTACAACGA ACAATCAG 3350 7445 UGUAUGGG G UUUUCGAA 1649 TTCGAAAA GGCTAGCTACAACGA CCCATACA 3351 7453 GUUUUCGA A CCUUUCAC 1650 GTGAAAGG GGCTAGCTACAACGA CCCATACA 3351 7460 AACCUUUC A CUUUUUGU 1651 ACAAAAAG GGCTAGCTACAACGA GAAAGGTT 3353 7467 CACUUUU G UUUGUUUU 1652 AAAACAAA GGCTAGCTACAACGA AAAAAAGTG 3354 7471 UUUUGUUU G UUUUACCU 1653 AGGTAAAA GGCTAGCTACAACGA AAACAAA 3355 7476 UUUGUUUU A CCUAUUUC 1654 GAAATAGG GGCTAGCTACAACGA AAACAAA 3356 7476 UUUGUUU A CCUAUUUC 1654 GAAATAGG GGCTAGCTACAACGA AAACAAA 3356 7480 UUUUACCU A UUUCACAA 1655 TTGTGAAA GGCTAGCTACAACGA AGAACAAA 3357 7485 CCUAUUUC A CAACUGUG 1656 CACAGTTG GGCTAGCTACAACGA GAAATAGG 3358 7488 AUUUCACA A CUGUGUAA 1657 TTACACAG GGCTAGCTACAACGA AGATAAG 3359 7491 UCACAACU G UGUAAAUU 1658 AATTTACA GGCTAGCTACAACGA ACAGTTGT 3361 7493 ACAACUGU G UAAAUUGC 1659 GCAATTTA GGCTAGCTACAACGA ACAGTTGT 3361	7420	AAAACUAA A UGUUAGUU	1642	AACTAACA GGCTAGCTACAACGA TTAGTTTT	3344
7431UUAGUUUA G CUGAUUGU1645ACAATCAG GGCTAGCTACAACGA TAAACTAA33477435UUUAGCUG A UUGUAUGG1646CCATACAA GGCTAGCTACAACGA CAGCTAAA33487438AGCUGAUU G UAUGGGGU1647ACCCCATA GGCTAGCTACAACGA AATCAGCT33497440CUGAUUGU A UGGGGUUU1648AAACCCCA GGCTAGCTACAACGA ACAATCAG33507445UGUAUGGG G UUUUCGAA1649TTCGAAAA GGCTAGCTACAACGA CCCATACA33517453GUUUUCGA A CCUUUCAC1650GTGAAAGG GGCTAGCTACAACGA TCGAAAAC33527460AACCUUUC A CUUUUUGU1651ACAAAAAG GGCTAGCTACAACGA GAAAGGTT33537467CACUUUUU G UUUGUUUU1652AAAACAAA GGCTAGCTACAACGA AAAAAAGTG33547471UUUUGUUU G UUUUACCU1653AGGTAAAA GGCTAGCTACAACGA AAACAAA33557476UUUGUUUU A CCUAUUUC1654GAAATAGG GGCTAGCTACAACGA AAACAAA33567480UUUUACCU A UUUCACAA1655TTGTGAAA GGCTAGCTACAACGA AGGTAAAA33577485CCUAUUUC A CAACUGUG1656CACAGTTG GGCTAGCTACAACGA GAAATAGG33587488AUUUCACA A CUGUGUAA1657TTACACAG GGCTAGCTACAACGA AGTTGAAAT33597491UCACAACU G UGUAAAUU1658AATTTACA GGCTAGCTACAACGA AGTTGTGA33607493ACAACUGU G UAAAUUGC1659GCAATTTA GGCTAGCTACAACGA ACAGTTGT3361	7422	AACUAAAU G UUAGUUUA	1643	TAAACTAA GGCTAGCTACAACGA ATTTAGTT	3345
T435 UUUAGCUG A UUGUAUGG 1646 CCATACAA GGCTAGCTACAACGA CAGCTAAA 3348  7438 AGCUGAUU G UAUGGGGU 1647 ACCCCATA GGCTAGCTACAACGA AATCAGCT 3349  7440 CUGAUUGU A UGGGGUUU 1648 AAACCCCA GGCTAGCTACAACGA ACAATCAG 3350  7445 UGUAUGGG G UUUUCGAA 1649 TTCGAAAA GGCTAGCTACAACGA CCCATACA 3351  7453 GUUUUCGA A CCUUUCAC 1650 GTGAAAGG GGCTAGCTACAACGA TCGAAAAC 3352  7460 AACCUUUC A CUUUUUGU 1651 ACAAAAAG GGCTAGCTACAACGA GAAAGGTT 3353  7467 CACUUUUU G UUUGUUUU 1652 AAAACAAA GGCTAGCTACAACGA AAAAAGTG 3354  7471 UUUUGUUU G UUUUACCU 1653 AGGTAAAA GGCTAGCTACAACGA AAACAAA 3355  7476 UUUGUUUU A CCUAUUUC 1654 GAAATAGG GGCTAGCTACAACGA AAACAAA 3356  7480 UUUUACCU A UUUCACAA 1655 TTGTGAAA GGCTAGCTACAACGA AGGTAAAA 3357  7485 CCUAUUUC A CAACUGUG 1656 CACAGTTG GGCTAGCTACAACGA GAAATAGG 3358  7488 AUUUCACA A CUGUGUAA 1657 TTACACAG GGCTAGCTACAACGA TGTGAAAT 3359  7491 UCACAACU G UGUAAAUU 1658 AATTTACA GGCTAGCTACAACGA ACAGTTGT 3361			1644		3346
7438 AGCUGAUU G UAUGGGGU 1647 ACCCCATA GGCTAGCTACAACGA AATCAGCT 3349 7440 CUGAUUGU A UGGGGUUU 1648 AAACCCCA GGCTAGCTACAACGA ACAATCAG 3350 7445 UGUAUGGG G UUUUCGAA 1649 TTCGAAAA GGCTAGCTACAACGA CCCATACA 3351 7453 GUUUUCGA A CCUUUCAC 1650 GTGAAAGG GGCTAGCTACAACGA TCGAAAAC 3352 7460 AACCUUUC A CUUUUUGU 1651 ACAAAAAG GGCTAGCTACAACGA GAAAGGTT 3353 7467 CACUUUUU G UUUGUUUU 1652 AAAACAAA GGCTAGCTACAACGA AAAAAGTG 3354 7471 UUUUGUUU G UUUUACCU 1653 AGGTAAAA GGCTAGCTACAACGA AAACAAA 3355 7476 UUUGUUUU A CCUAUUUC 1654 GAAATAGG GGCTAGCTACAACGA AAACAAA 3356 7480 UUUUACCU A UUUCACAA 1655 TTGTGAAA GGCTAGCTACAACGA AGGTAAAA 3357 7485 CCUAUUUC A CAACUGUG 1656 CACAGTTG GGCTAGCTACAACGA GAAATAGG 3358 7488 AUUUCACA A CUGUGUAA 1657 TTACACAG GGCTAGCTACAACGA TGTGAAAT 3359 7491 UCACAACU G UGUAAAUU 1658 AATTTACA GGCTAGCTACAACGA ACAGTTGT 3360 7493 ACAACUGU G UAAAUUGC 1659 GCAATTTA GGCTAGCTACAACGA ACAGTTGT 3361	7431	UUAGUUUA G CUGAUUGU	1645	ACAATCAG GGCTAGCTACAACGA TAAACTAA	3347
7440 CUGAUUGU A UGGGGUUU 1648 AAACCCCA GGCTAGCTACAACGA ACAATCAG 3350 7445 UGUAUGGG G UUUUCGAA 1649 TTCGAAAA GGCTAGCTACAACGA CCCATACA 3351 7453 GUUUUCGA A CCUUUCAC 1650 GTGAAAGG GGCTAGCTACAACGA TCGAAAAC 3352 7460 AACCUUUC A CUUUUUGU 1651 ACAAAAAG GGCTAGCTACAACGA GAAAGGTT 3353 7467 CACUUUUU G UUUGUUUU 1652 AAAACAAA GGCTAGCTACAACGA AAAAAGTG 3354 7471 UUUUGUUU G UUUUACCU 1653 AGGTAAAA GGCTAGCTACAACGA AAACAAAA 3355 7476 UUUGUUUU A CCUAUUUC 1654 GAAATAGG GGCTAGCTACAACGA AAACAAA 3356 7480 UUUUACCU A UUUCACAA 1655 TTGTGAAA GGCTAGCTACAACGA AGGTAAAA 3357 7485 CCUAUUUC A CAACUGUG 1656 CACAGTTG GGCTAGCTACAACGA GAAATAGG 3358 7488 AUUUCACA A CUGUGUAA 1657 TTACACAG GGCTAGCTACAACGA TGTGAAAT 3359 7491 UCACAACU G UGUAAAUU 1658 AATTTACA GGCTAGCTACAACGA ACAGTTGTA 3360 7493 ACAACUGU G UAAAUUGC 1659 GCAATTTA GGCTAGCTACAACGA ACAGTTGT 3361			1646	CCATACAA GGCTAGCTACAACGA CAGCTAAA	3348
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7467 CACUUUUU G UUUGUUUU 1652 AAAACAAA GGCTAGCTACAACGA AAAAAGTG 3354 7471 UUUUGUUU G UUUUACCU 1653 AGGTAAAA GGCTAGCTACAACGA AAACAAAA 3355 7476 UUUGUUUU A CCUAUUUC 1654 GAAATAGG GGCTAGCTACAACGA AAACAAAA 3356 7480 UUUUACCU A UUUCACAA 1655 TTGTGAAA GGCTAGCTACAACGA AGGTAAAA 3357 7485 CCUAUUUC A CAACUGUG 1656 CACAGTTG GGCTAGCTACAACGA GAAATAGG 3358 7488 AUUUCACA A CUGUGUAA 1657 TTACACAG GGCTAGCTACAACGA TGTGAAAT 3359 7491 UCACAACU G UGUAAAUU 1658 AATTTACA GGCTAGCTACAACGA AGTTGTGA 3360 7493 ACAACUGU G UAAAUUGC 1659 GCAATTTA GGCTAGCTACAACGA ACAGTTGT 3361					3352
7471 UUUUGUUU G UUUUACCU 1653 AGGTAAAA GGCTAGCTACAACGA AAACAAAA 3355 7476 UUUGUUUU A CCUAUUUC 1654 GAAATAGG GGCTAGCTACAACGA AAACAAAA 3356 7480 UUUUACCU A UUUCACAA 1655 TTGTGAAA GGCTAGCTACAACGA AGGTAAAA 3357 7485 CCUAUUUC A CAACUGUG 1656 CACAGTTG GGCTAGCTACAACGA GAAATAGG 3358 7488 AUUUCACA A CUGUGUAA 1657 TTACACAG GGCTAGCTACAACGA TGTGAAAT 3359 7491 UCACAACU G UGUAAAUU 1658 AATTTACA GGCTAGCTACAACGA AGTTGTGA 3360 7493 ACAACUGU G UAAAUUGC 1659 GCAATTTA GGCTAGCTACAACGA ACAGTTGT 3361					3353
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7480 UUUUACCU A UUUCACAA 1655 TTGTGAAA GGCTAGCTACAACGA AGGTAAAA 3357 7485 CCUAUUUC A CAACUGUG 1656 CACAGTTG GGCTAGCTACAACGA GAAATAGG 3358 7488 AUUUCACA A CUGUGUAA 1657 TTACACAG GGCTAGCTACAACGA TGTGAAAT 3359 7491 UCACAACU G UGUAAAUU 1658 AATTTACA GGCTAGCTACAACGA AGTTGTGA 3360 7493 ACAACUGU G UAAAUUGC 1659 GCAATTTA GGCTAGCTACAACGA ACAGTTGT 3361					3355
7485 CCUAUUUC A CAACUGUG 1656 CACAGTTG GGCTAGCTACAACGA GAAATAGG 3358 7488 AUUUCACA A CUGUGUAA 1657 TTACACAG GGCTAGCTACAACGA TGTGAAAT 3359 7491 UCACAACU G UGUAAAUU 1658 AATTTACA GGCTAGCTACAACGA AGTTGTGA 3360 7493 ACAACUGU G UAAAUUGC 1659 GCAATTTA GGCTAGCTACAACGA ACAGTTGT 3361					3356
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7497   CUGUGUAA A UUGCCAAU   1660   ATTGGCAA GGCTAGCTACAACGA TTACACAG 3362					3361
	7497	CUGUGUAA A UUGCCAAU	1660	ATTGGCAA GGCTAGCTACAACGA TTACACAG	3362

7500 UGUAAAUU G CCAAUAAU 1661 ATTATTGG GGCTAGCTACAACGA AATTTACA 33 7504 AAUUGCCA A UAAUUCCU 1662 AGGAATTA GGCTAGCTACAACGA TGGCAATT 33 7507 UGCCAAUA A UUCCUGUC 1663 GACAGGAA GGCTAGCTACAACGA TATTGGCA 33 7513 UAAUUCCU G UCCAUGAA 1664 TTCATGGA GGCTAGCTACAACGA AGGAATTA 33 7517 UCCUGUCC A UGAAAAUG 1665 CATTTCA GGCTAGCTACAACGA GGACAGGA 33 7523 CCAUGAAA A UGCAAAUU 1666 AATTTGCA GGCTAGCTACAACGA TTTCATGG 33 7525 AUGAAAAU G CAAAUUAU 1667 ATAATTTG GGCTAGCTACAACGA ATTTCAT 33 7529 AAAUGCAA A UUAUCCAG 1668 CTGGATAA GGCTAGCTACAACGA TTGCATTT 33	64 65 66 67 68
7507 UGCCAAUA A UUCCUGUC 1663 GACAGGAA GGCTAGCTACAACGA TATTGGCA 33 7513 UAAUUCCU G UCCAUGAA 1664 TTCATGGA GGCTAGCTACAACGA AGGAATTA 33 7517 UCCUGUCC A UGAAAAUG 1665 CATTTCA GGCTAGCTACAACGA GGACAGGA 33 7523 CCAUGAAA A UGCAAAUU 1666 AATTTGCA GGCTAGCTACAACGA TTTCATGG 33 7525 AUGAAAAU G CAAAUUAU 1667 ATAATTTG GGCTAGCTACAACGA ATTTCAT 33	65 66 67 68 69
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7525 AUGAAAAU G CAAAUUAU 1667 ATAATTTG GGCTAGCTACAACGA ATTTTCAT 33	69
7529 AAAUGCAA A UUAUCCAG 1668 CTGGATAA GGCTAGCTACAACGA TTGCATTT 33	70
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7532 UGCAAAUU A UCCAGUGU 1669 ACACTGGA GGCTAGCTACAACGA AATTTGCA 33	71
7537 AUUAUCCA G UGUAGAUA 1670 TATCTACA GGCTAGCTACAACGA TGGATAAT 33	72
7539 UAUCCAGU G UAGAUAUA 1671 TATATCTA GGCTAGCTACAACGA ACTGGATA 33	73
7543 CAGUGUAG A UAUAUUUG 1672 CAAATATA GGCTAGCTACAACGA CTACACTG 33	74
7545 GUGUAGAU A UAUUUGAC 1673 GTCAAATA GGCTAGCTACAACGA ATCTACAC 33	75
7547 GUAGAUAU A UUUGACCA 1674 TGGTCAAA GGCTAGCTACAACGA ATATCTAC 33	76
7552 UAUAUUUG A CCAUCACC 1675 GGTGATGG GGCTAGCTACAACGA CAAATATA 33	77
7555 AUUUGACC A UCACCCUA 1676 TAGGGTGA GGCTAGCTACAACGA GGTCAAAT 33	78
7558 UGACCAUC A CCCUAUGG 1677 CCATAGGG GGCTAGCTACAACGA GATGGTCA 33	79
7563 AUCACCCU A UGGAUAUU 1678 AATATCCA GGCTAGCTACAACGA AGGGTGAT 33	80
7567 CCCUAUGG A UAUUGGCU 1679 AGCCAATA GGCTAGCTACAACGA CCATAGGG 33	81
7569 CUAUGGAU A UUGGCUAG 1680 CTAGCCAA GGCTAGCTACAACGA ATCCATAG 33	82
7573 GGAUAUUG G CUAGUUUU 1681 AAAACTAG GGCTAGCTACAACGA CAATATCC 33	83
7577 AUUGGCUA G UUUUGCCU 1682 AGGCAAAA GGCTAGCTACAACGA TAGCCAAT 33	84
7582 CUAGUUUU G CCUUUAUU 1683 AATAAAGG GGCTAGCTACAACGA AAAACTAG 33	85 ·
7588 UUGCCUUU A UUAAGCAA 1684 TTGCTTAA GGCTAGCTACAACGA AAAGGCAA 33	86
7593 UUUAUUAA G CAAAUUCA 1685 TGAATTTG GGCTAGCTACAACGA TTAATAAA 33	87
7597 UUAAGCAA A UUCAUUUC   1686   GAAATGAA GGCTAGCTACAACGA TTGCTTAA 33	88
7601 GCAAAUUC A UUUCAGCC 1687 GGCTGAAA GGCTAGCTACAACGA GAATTTGC 33	89
7607 UCAUUUCA G CCUGAAUG 1688 CATTCAGG GGCTAGCTACAACGA TGAAATGA 33	90
7613 CAGCCUGA A UGUCUGCC 1689 GGCAGACA GGCTAGCTACAACGA TCAGGCTG 33	91
7615 GCCUGAAU G UCUGCCUA 1690 TAGGCAGA GGCTAGCTACAACGA ATTCAGGC 33	92
7619 GAAUGUCU G CCUAUAUA 1691 TATATAGG GGCTAGCTACAACGA AGACATTC 33	93
7623 GUCUGCCU A UAUAUUCU 1692 AGAATATA GGCTAGCTACAACGA AGGCAGAC 33	94
7625 CUGCCUAU A UAUUCUCU 1693 AGAGAATA GGCTAGCTACAACGA ATAGGCAG 33	95
7627 GCCUAUAU A UUCUCUGC 1694 GCAGAGAA GGCTAGCTACAACGA ATATAGGC 33	96
7634 UAUUCUCU G CUCUUUGU 1695 ACAAAGAG GGCTAGCTACAACGA AGAGAATA 33	97
7641 UGCUCUUU G UAUUCUCC 1696 GGAGAATA GGCTAGCTACAACGA AAAGAGCA 33	98
7643 CUCUUUGU A UUCUCCUU 1697 AAGGAGAA GGCTAGCTACAACGA ACAAAGAG 33	99
7655 UCCUUUGA A CCCGUUAA 1698 TTAACGGG GGCTAGCTACAACGA TCAAAGGA 34	00
7659 UUGAACCC G UUAAAACA 1699 TGTTTTAA GGCTAGCTACAACGA GGGTTCAA 34	01
7665 CCGUUAAA A CAUCCUGU 1700 ACAGGATG GGCTAGCTACAACGA TTTAACGG 34	02
7667 GUUAAAAC A UCCUGUGG 1701 CCACAGGA GGCTAGCTACAACGA GTTTTAAC 34	03
7672 AACAUCCU G UGGCACUC 1702 GAGTGCCA GGCTAGCTACAACGA AGGATGTT 34	04

Input Sequence = HSFLT. Cut Site = R/Y

Arm Length = 8. Core Sequence = GGCTAGCTACAACGA

HSFLT (Human flt mRNA for receptor-related tyrosine kinase.; Acc# X51602; 7680 bp)

Table VI: Human KDR DNAzyme and Substrate sequence

Pos	Substrate	Seq ID	DNAzyme	Seq ID
	Dabbaate	No	Diving me	No
14	GUCCCGGG A CCCCGGGA	3405	TCCCGGGG GGCTAGCTACAACGA CCCGGGAC	4691
25	CCGGGAGA G CGGUCAGU	3406	ACTGACCG GGCTAGCTACAACGA TCTCCCGG	4692
28	GGAGAGCG G UCAGUGUG	3407	CACACTGA GGCTAGCTACAACGA CGCTCTCC	4693
32	AGCGGUCA G UGUGUGGU	3408	ACCACACA GGCTAGCTACAACGA TGACCGCT	4694
34	CGGUCAGU G UGUGGUCG	3409	CGACCACA GGCTAGCTACAACGA ACTGACCG	4695
36	GUCAGUGU G UGGUCGCU	3410	AGCGACCA GGCTAGCTACAACGA ACACTGAC	4696
39	AGUGUGUG G UCGCUGCG	3411	CGCAGCGA GGCTAGCTACAACGA CACACACT	4697
42	GUGUGGUC G CUGCGUUU	3412	AAACGCAG GGCTAGCTACAACGA GACCACAC	4698
45	UGGUCGCU G CGUUUCCU	3413	AGGAAACG GGCTAGCTACAACGA AGCGACCA	4699
47	GUCGCUGC G UUUCCUCU	3414	AGAGGAAA GGCTAGCTACAACGA GCAGCGAC	4700
56	UUUCCUCU G CCUGCGCC	3415	GGCGCAGG GGCTAGCTACAACGA AGAGGAAA	4701
60	CUCUGCCU G CGCCGGGC	3416	GCCCGGCG GGCTAGCTACAACGA AGGCAGAG	4702
62	CUGCCUGC G CCGGGCAU	3417	ATGCCCGG GGCTAGCTACAACGA GCAGGCAG	4703
67	UGCGCCGG G CAUCACUU	3418	AAGTGATG GGCTAGCTACAACGA CCGGCGCA	4704
69	CGCCGGGC A UCACUUGC	3419	GCAAGTGA GGCTAGCTACAACGA GCCCGGCG	4705
72	CGGGCAUC A CUUGCGCG	3420	CGCGCAAG GGCTAGCTACAACGA GATGCCCG	4706
7€,	AUCACUU G CGCGCCGC	3421	GCGGCGCG GGCTAGCTACAACGA AAGTGATG	4707
78	UCACUUGC G CGCCGCAG	3422	CTGCGGCG GGCTAGCTACAACGA GCAAGTGA	4708
80	ACUUGCGC G CCGCAGAA	3423	TTCTGCGG GGCTAGCTACAACGA GCGCAAGT	4709
83	UGCGCGCC G CAGAAAGU	3424	ACTITCTG GGCTAGCTACAACGA GGCGCGCA	4710
90	CGCAGAAA G UCCGUCUG	3425	CAGACGGA GGCTAGCTACAACGA TTTCTGCG	4711
94	GAAAGUCC G UCUGGCAG	3426	CTGCCAGA GGCTAGCTACAACGA GGACTTTC	4712
99	UCCGUCUG G CAGCCUGG	3427	CCAGGCTG GGCTAGCTACAACGA CAGACGGA	4713
102	GUCUGGCA G CCUGGAUA	3428	TATCCAGG GGCTAGCTACAACGA TGCCAGAC	4714
108	CAGCCUGG A UAUCCUCU	3429	AGAGGATA GGCTAGCTACAACGA CCAGGCTG	4715
110	GCCUGGAU A UCCUCUCC	3430	GGAGAGGA GGCTAGCTACAACGA ATCCAGGC	4716
120	CCUCUCCU A CCGGCACC	3431	GGTGCCGG GGCTAGCTACAACGA AGGAGAGG	4717
124	UCCUACCG G CACCCGCA	3432	TGCGGGTG GGCTAGCTACAACGA CGGTAGGA	4718
126	CUACCGGC A CCCGCAGA	3433	TCTGCGGG GGCTAGCTACAACGA GCCGGTAG	4719
130	CGGCACCC G CAGACGCC	3434	GGCGTCTG GGCTAGCTACAACGA GGGTGCCG	4720
134	ACCCGCAG A CGCCCCUG	3435	CAGGGGCG GGCTAGCTACAACGA CTGCGGGT	4721
136	CCGCAGAC G CCCCUGCA	3436	TGCAGGGG GGCTAGCTACAACGA GTCTGCGG	4722
142	ACGCCCCU G CAGCCGCC	3437	GGCGGCTG GGCTAGCTACAACGA AGGGGCGT	4723
145	CCCCUGCA G CCGCCGGU	3438	ACCGGCGG GGCTAGCTACAACGA TGCAGGGG	4724
148	CUGCAGCC G CCGGUCGG	3439	CCGACCGG GGCTAGCTACAACGA GGCTGCAG	4725
152	AGCCGCCG G UCGGCGCC	3440	GGCGCCGA GGCTAGCTACAACGA CGGCGGCT	4726
156	ecceence e ceccceee	3441	CCCGGGCG GGCTAGCTACAACGA CGACCGGC	4727
158	cegucege e ceeegeeu	3442	AGCCCGGG GGCTAGCTACAACGA GCCGACCG	4728
164	GCGCCCGG G CUCCCUAG	3443	CTAGGGAG GGCTAGCTACAACGA CCGGGCGC	4729
172	GCUCCCUA G CCCUGUGC	3444	GCACAGGG GGCTAGCTACAACGA TAGGGAGC	4730
177	CUAGCCCU G UGCGCUCA		TGAGCGCA GGCTAGCTACAACGA AGGGCTAG	4731
179	AGCCCUGU G CGCUCAAC	3446	GTTGAGCG GGCTAGCTACAACGA ACAGGGCT	4732
181	CCCUGUGC G CUCAACUG		CAGTTGAG GGCTAGCTACAACGA GCACAGGG	4733
	UGCGCUCA A CUGUCCUG		CAGGACAG GGCTAGCTACAACGA TGAGCGCA	4734
	GCUCAACU G UCCUGCGC		GCGCAGGA GGCTAGCTACAACGA AGTTGAGC	4735
	ACUGUCCU G CGCUGCGG		CCGCAGCG GGCTAGCTACAACGA AGGACAGT	4736
196	nancanea e caeceeee	3451	CCCCGCAG GGCTAGCTACAACGA GCAGGACA	4737
199	CCUGCGCU G CGGGGUGC	3452	GCACCCCG GGCTAGCTACAACGA AGCGCAGG	4738
204	GCUGCGGG G UGCCGCGA	3453	TCGCGGCA GGCTAGCTACAACGA CCCGCAGC	4739

206	UGCGGGGU G CCGCGAGU	3454	ACTCGCGG GGCTAGCTACAACGA ACCCCGCA	4740
209	GGGGUGCC G CGAGUUCC	3455	GGAACTCG GGCTAGCTACAACGA GGCACCCC	4741
213	UGCCGCGA G UUCCACCU	3456	AGGTGGAA GGCTAGCTACAACGA TCGCGGCA	4742
218	CGAGUUCC A CCUCCGCG	3457	CGCGGAGG GGCTAGCTACAACGA GGAACTCG	4743
224	CCACCUCC G CGCCUCCU	3458	AGGAGGCG GGCTAGCTACAACGA GGAGGTGG	4744
226	ACCUCCGC G CCUCCUUC	3459	GAAGGAGG GGCTAGCTACAACGA GCGGAGGT	4745
240	UUCUCUAG A CAGGCGCU	3460	AGCGCCTG GGCTAGCTACAACGA CTAGAGAA	4746
244	CUAGACAG G CGCUGGGA	3461	TCCCAGCG GGCTAGCTACAACGA CTGTCTAG	4747
246	AGACAGGC G CUGGGAGA	3462	TCTCCCAG GGCTAGCTACAACGA GCCTGTCT	4748
259	GAGAAAGA A CCGGCUCC	3463	GGAGCCGG GGCTAGCTACAACGA TCTTTCTC	4749
263	AAGAACCG G CUCCCGAG	3464	CTCGGGAG GGCTAGCTACAACGA CGGTTCTT	4750
271	GCUCCCGA G UUCUGGGC	3465	GCCCAGAA GGCTAGCTACAACGA TCGGGAGC	4751
278	AGUUCUGG G CAUUUCGC	3466	GCGAAATG GGCTAGCTACAACGA CCAGAACT	4752
280	UUCUGGC A UUUCGCCC	3467	GGGCGAAA GGCTAGCTACAACGA GCCCAGAA	4753
285	GGCAUUUC G CCCGGCUC		GAGCCGGG GGCTAGCTACAACGA GAAATGCC	4754
	UUCGCCCG G CUCGAGGU		ACCTCGAG GGCTAGCTACAACGA CGGGCGAA	4755
297	GGCUCGAG G UGCAGGAU		ATCCTGCA GGCTAGCTACAACGA CTCGAGCC	4756
299	CUCGAGGU G CAGGAUGC		GCATCCTG GGCTAGCTACAACGA ACCTCGAG	4757
304	GGUGCAGG A UGCAGAGC		GCTCTGCA GGCTAGCTACAACGA CCTGCACC	4758
	UGCAGGAU G CAGAGCAA	3473	TTGCTCTG GGCTAGCTACAACGA ATCCTGCA	4759
311	GAUGCAGA G CAAGGUGC		GCACCTTG GGCTAGCTACAACGA TCTGCATC	4760
	AGAGCAAG G UGCUGCUG		CAGCAGCA GGCTAGCTACAACGA CTTGCTCT	4761
	AGCAAGGU G CUGCUGGC		GCCAGCAG GGCTAGCTACAACGA ACCTTGCT	
-	AAGGUGCU G CUGGCCGU			4762
	NGCNGCAG G CCGNCGCC		ACGGCCAG GGCTAGCTAGAACGA AGCACCTT	4763
	nacneace a reacease		GGCGACGG GGCTAGCTACAACGA CAGCAGCA	4764
331	neeccanc a cccnence		CAGGGCGA GGCTAGCTACAACGA GGCCAGCA	4765
336	GUCGCCCA G CCCAGAGA		CCACAGGG GGCTAGCTACAACGA GACGGCCA	4766
339	<del></del>		CAGAGCCA GGCTAGCTACAACGA AGGGCGAC	4767
344	GCCCUGUG G CUCUGCGU	3482	ACGCAGAG GGCTAGCTACAACGA CACAGGGC	4768
346	GUGGCUCU G CGUGGAGA		TCTCCACG GGCTAGCTACAACGA AGAGCCAC	4769
<del></del>	GCCUCUGC G UGGAGACC GCGUGGAG A CCCGGGCC		GGTCTCCA GGCTAGCTACAACGA GCAGAGCC	4770
	AGACCCGG G CCGCCUCU		GGCCCGGG GGCTAGCTACAACGA CTCCACGC	4771
361	CCCGGGCC G CCUCUGUG		AGAGGCGG GGCTAGCTACAACGA CCGGGTCT	4772
367	cceccucu e needning	3487	CARAGAGG GGCTAGCTACAACGA GGCCCGGG	4773
	CUCUGUGG G UUUGCCUA		CAAACCCA GGCTAGCTACAACGA AGAGGCGG	4774
371		3489	TAGGCAAA GGCTAGCTACAACGA CCACAGAG	4775
	GUGGGUUU G CCUAGUGU		ACACTAGG GGCTAGCTACAACGA AAACCCAC	4776
380	UUUGCCUA G UGUUUCUC		GAGAAACA GGCTAGCTACAACGA TAGGCAAA	4777
	UGCCUAGU G UUUCUCUU		AAGAGAAA GGCTAGCTACAACGA ACTAGGCA	4778
_	CUIGAUCH C CCCACCU		TGGGCAGA GGCTAGCTACAACGA CAAGAGAA	4779
<b>—</b> —	CUUGAUCU G CCCAGGCU		AGCCTGGG GGCTAGCTACAACGA AGATCAAG	4780
_	CUGCCCAG G CUCAGCAU		ATGCTGAG GGCTAGCTACAACGA CTGGGCAG	4781
407	CAGGUCAG CAUACAAA	3496	TTTGTATG GGCTAGCTACAACGA TGAGCCTG	4782
409	GGCUCAGC A UACAAAAA	3497	TTTTTGTA GGCTAGCTACAACGA GCTGAGCC	4783
411	CUCAGCAU A CAAAAAGA	3498	TCTTTTTG GGCTAGCTACAACGA ATGCTGAG	4784
	ACAAAAAG A CAUACUUA	3499	TAAGTATG GGCTAGCTACAACGA CTTTTTGT	4785
	AAAAAGAC A UACUUACA	3500	TGTAAGTA GGCTAGCTACAACGA GTCTTTTT	4786
	AAAGACAU A CUUACAAU	3501	ATTGTAAG GGCTAGCTACAACGA ATGTCTTT	4787
	ACAUACUU A CAAUUAAG		CTTAATTG GGCTAGCTACAACGA AAGTATGT	4788
	UACUUACA A UUAAGGCU		AGCCTTAA GGCTAGCTACAACGA TGTAAGTA	4789
⊢–	CAAUUAAG G CUAAUACA	3504 .	TGTATTAG GGCTAGCTACAACGA CTTAATTG	4790
	UAAGGCUA A UACAACUC	3505	GAGTTGTA GGCTAGCTACAACGA TAGCCTTA	4791
442	AGGCUAAU A CAACUCUU	3506	AAGAGTTG GGCTAGCTACAACGA ATTAGCCT	4792

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445	CUAAUACA A CUCUUCAA	3507	TTGAAGAG GGCTAGCTACAACGA TGTATTAG 479	3
454	CUCUUCAA A UUACUUGC	3508	GCAAGTAA GGCTAGCTACAACGA TTGAAGAG 479	94
457	UUCAAAUU A CUUGCAGG	3509	CCTGCAAG GGCTAGCTACAACGA AATTTGAA 479	5
461	AAUUACUU G CAGGGGAC	3510	GTCCCCTG GGCTAGCTACAACGA AAGTAATT 479	96
468	UGCAGGGG A CAGAGGGA	3511	TCCCTCTG GGCTAGCTACAACGA CCCCTGCA 479	97
476	ACAGAGGG A CUUGGACU	3512	AGTCCAAG GGCTAGCTACAACGA CCCTCTGT 479	8
482	GGACUUGG A CUGGCUUU	3513	AAAGCCAG GGCTAGCTACAACGA CCAAGTCC 479	9
486	UUGGACUG G CUUUGGCC	3514	GGCCAAAG GGCTAGCTACAACGA CAGTCCAA 480	0
	UGGCUUUG G CCCAAUAA	3515	TTATTGGG GGCTAGCTACAACGA CAAAGCCA 480	
497	UUGGCCCA A UAAUCAGA	3516	TCTGATTA GGCTAGCTACAACGA TGGGCCAA 480	
500	GCCCAAUA A UCAGAGUG	3517	CACTCTGA GGCTAGCTACAACGA TATTGGGC 480	
506	UAAUCAGA G UGGCAGUG	3518	CACTGCCA GGCTAGCTACAACGA TCTGATTA 480	
509	UCAGAGUG G CAGUGAGC	3519	GCTCACTG GGCTAGCTACAACGA CACTCTGA 480	
512	GAGUGGCA G UGAGCAAA	3520	TTTGCTCA GGCTAGCTACAACGA TGCCACTC 480	
516	GGCAGUGA G CAAAGGGU	3521	ACCOTTEG GGCTAGCTACAACGA TCACTGCC 480	
523	AGCAAAGG G UGGAGGUG	3522	CACCTCCA GGCTAGCTACAACGA CCTTTGCT 480	
529	GGGUGGAG G UGACUGAG	3523	CTCAGTCA GGCTAGCTACAACGA CTCCACCC 480	
532	UGGAGGUG A CUGAGUGC	3524	GCACTCAG GGCTAGCTACAACGA CACCTCCA 481	
537	GUGACUGA G UGCAGCGA	3525	TCGCTGCA GGCTAGCTACAACGA TCAGTCAC 481	
539	GACUGAGU G CAGCGAUG	3526	CATCGCTG GGCTAGCTACAACGA ACTCAGTC 481	
542	UGAGUGCA G CGAUGGCC	3527	GGCCATCG GGCTAGCTACAACGA TGCACTCA 481	13
545	GUGCAGCG A UGGCCUCU	3528	AGAGGCCA GGCTAGCTACAACGA CGCTGCAC 481	L4
548	CAGCGAUG G CCUCUUCU	3529	AGAAGAGG GGCTAGCTACAACGA CATCGCTG 481	15
557	CCUCUUCU G UAAGACAC	3530	GTGTCTTA GGCTAGCTACAACGA AGAAGAGG 481	16
562	UCUGUAAG A CACUCACA	3531	TGTGAGTG GGCTAGCTACAACGA CTTACAGA 481	۱7
564	UGUAAGAC A CUCACAAU	3532	ATTGTGAG GGCTAGCTACAACGA GTCTTACA 481	18
568	AGACACUC A CAAUUCCA	3533	TGGAATTG GGCTAGCTACAACGA GAGTGTCT 481	L <b>9</b>
571	CACUCACA A UUCCAAAA	3534	TTTTGGAA GGCTAGCTACAACGA TGTGAGTG 482	20
580	UUCCAAAA G UGAUCGGA	3535	TCCGATCA GGCTAGCTACAACGA TTTTGGAA 482	21
583	CAAAAGUG A UCGGAAAU	3536	ATTTCCGA GGCTAGCTACAACGA CACTTTTG 482	22
590	GAUCGGAA A UGACACUG	3537	CAGTGTCA GGCTAGCTACAACGA TTCCGATC 482	23
593	CGGAAAUG A CACUGGAG	3538	CTCCAGTG GGCTAGCTACAACGA CATTTCCG 482	24
595	GAAAUGAC A CUGGAGCC	3539	GGCTCCAG GGCTAGCTACAACGA GTCATTTC 482	25
601	ACACUGGA G CCUACAAG	3540	CTTGTAGG GGCTAGCTACAACGA TCCAGTGT 482	26
605	UGGAGCCU A CAAGUGCU	3541	AGCACTTG GGCTAGCTACAACGA AGGCTCCA 482	27
609	GCCUACAA G UGCUUCUA	3542	TAGAAGCA GGCTAGCTACAACGA TTGTAGGC 482	28
611	CUACAAGU G CUUCUACC	3543	GGTAGAAG GGCTAGCTACAACGA ACTTGTAG 482	29
617	GUGCUUCU A CCGGGAAA	3544	TTTCCCGG GGCTAGCTACAACGA AGAAGCAC 483	
<u> </u>	ACCGGGAA A CUGACUTIG	3545	CAAGTCAG GGCTAGCTACAACGA TTCCCGGT 483	
_	GGAAACUG A CUUGGCCU		AGGCCAAG GGCTAGCTACAACGA CAGTTTCC 483	
634	CUGACUUG G CCUCGGUC	3547	GACCGAGG GGCTAGCTACAACGA CAAGTCAG 483	
640	UGGCCUCG G UCAUUUAU	3548	ATAAATGA GGCTAGCTACAACGA CGAGGCCA 483	
643	CCUCGGUC A UUUAUGUC	3549	GACATAAA GGCTAGCTACAACGA GACCGAGG 483	
647	GGUCAUUU A UGUCUAUG	3550	CATAGACA GGCTAGCTACAACGA AAATGACC 483	
649	UCAUUUAU G UCUAUGUU	3551		
653	UUAUGUCU A UGUUCAAG	3552		
655	AUGUCUAU G UUCAAGAU	3553	ATCTTGAA GGCTAGCTACAACGA ATAGACAT 483	
	UGUUCAAG A UUACAGAU	3554	ATCTGTAA GGCTAGCTACAACGA CTTGAACA 484	
665	UCAAGAUU A CAGAUCUC	3555	GAGATCTG GGCTAGCTACAACGA AATCTTGA 484	
669	GAUUACAG A UCUCCAUU	3556	AATGGAGA GGCTAGCTACAACGA CTGTAATC 484	
675	AGAUCUCC A UUUAUUGC	3557	GCAATAAA GGCTAGCTACAACGA GGAGATCT 484	
679	CUCCAUUU A UUGCUUCU	3558 .	AGAAGCAA GGCTAGCTACAACGA AAATGGAG 484	
682	CAUUUAUU G CUUCUGUU	3559	AACAGAAG GGCTAGCTACAACGA AATAAATG 484	15

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688	UUGCUUCU G UUAGUGAC	3560	GTCACTAA GGCTAGCTACAACGA AGAAGCAA 4846
692	UUCUGUUA G UGACCAAC	3561	GTTGGTCA GGCTAGCTACAACGA TAACAGAA 4847
695	UGUUAGUG A CCAACAUG	3562	CATGTTGG GGCTAGCTACAACGA CACTAACA 4848
699	AGUGACCA A CAUGGAGU	3563	ACTCCATG GGCTAGCTACAACGA TGGTCACT 4849
701	UGACCAAC A UGGAGUCG	3564	CGACTCCA GGCTAGCTACAACGA GTTGGTCA 4850
706	AACAUGGA G UCGUGUAC	3565	GTACACGA GGCTAGCTACAACGA TCCATGTT 4851
	AUGGAGUC G UGUACAUU	3566	AATGTACA GGCTAGCTACAACGA GACTCCAT 4852
711	GGAGUCGU G UACAUUAC	3567	GTAATGTA GGCTAGCTACAACGA ACGACTCC 4853
713	AGUCGUGU A CAUUACUG	3568	CAGTAATG GGCTAGCTACAACGA ACACGACT 4854
715	UCGUGUAC A UUACUGAG	3569	CTCAGTAA GGCTAGCTACAACGA GTACACGA 4855
718	UGUACAUU A CUGAGAAC	3570	GTTCTCAG GGCTAGCTACAACGA AATGTACA 4856
725	UACUGAGA A CAAAAACA	3571	TGTTTTTG GGCTAGCTACAACGA TCTCAGTA 4857
731	GAACAAAA A CAAAACUG	3572	CAGTTTTG GGCTAGCTACAACGA TTTTGTTC 4858
736	AAAACAAA A CUGUGGUG	3573	CACCACAG GGCTAGCTACAACGA TTTGTTTT 4859
739	ACAAAACU G UGGUGAUU	3574	
<del></del>			<del></del>
742	AAACUGUG G UGAUUCCA	3575	TGGAATCA GGCTAGCTACAACGA CACAGTTT 4861
745	CUGUGGUG A UUCCAUGU	3576	ACATGGAA GGCTAGCTACAACGA CACCACAG 4862
750	GUGAUUCC A UGUCUCGG	3577	CCGAGACA GGCTAGCTACAACGA GGAATCAC 4863
752	GAUUCCAU G UCUCGGGU	3578	ACCCGAGA GGCTAGCTACAACGA ATGGAATC 4864
759	UGUCUCGG G UCCAUUUC	3579	GAAATGGA GGCTAGCTACAACGA CCGAGACA 4865
763	UCGGGUCC A UUUCAAAU	3580	ATTTGAAA GGCTAGCTACAACGA GGACCCGA 4866
770	CAUUUCAA A UCUCAACG	3581	CGTTGAGA GGCTAGCTACAACGA TTGAAATG 4867
776	AAAUCUCA A CGUGUCAC	3582	GTGACACG GGCTAGCTACAACGA TGAGATTT 4868
778	AUCUCAAC G UGUCACUU	3583	AAGTGACA GGCTAGCTACAACGA GTTGAGAT 4869
780	CUCAACGU G UCACUUUG	3584	CAAAGTGA GGCTAGCTACAACGA ACGTTGAG 4870
783	AACGUGUC A CUUUGUGC	3585	GCACAAAG GGCTAGCTACAACGA GACACGTT 4871
788	GUCACUUU G UGCAAGAU	3586	ATCTTGCA GGCTAGCTACAACGA AAAGTGAC 4872
790	CACUUUGU G CAAGAUAC	3587	GTATCTTG GGCTAGCTACAACGA ACAAAGTG 4873
795	UGUGCAAG A UACCCAGA	3588	TCTGGGTA GGCTAGCTACAACGA CTTGCACA 4874
797	UGCAAGAU A CCCAGAAA	3589	TTTCTGGG GGCTAGCTACAACGA ATCTTGCA 4875
810	GAAAAGAG A UUUGUUCC	3590	GGAACAAA GGCTAGCTACAACGA CTCTTTTC 4876
814	AGAGAUUU G UUCCUGAU	3591	ATCAGGAA GGCTAGCTACAACGA AAATCTCT 4877
821	UGUUCCUG A UGGUAACA	3592	TGTTACCA GGCTAGCTACAACGA CAGGAACA 4878
824	UCCUGAUG G UAACAGAA	3593	TTCTGTTA GGCTAGCTACAACGA CATCAGGA 4879
827	UGAUGGUA A CAGAAUUU	3594	AAATTCTG GGCTAGCTACAACGA TACCATCA 4880
832	GUAACAGA A UUUCCUGG	3595	CCAGGAAA GGCTAGCTACAACGA TCTGTTAC 4881
842	UUCCUGGG A CAGCAAGA	3596	TCTTGCTG GGCTAGCTACAACGA CCCAGGAA 4882
845	CUGGGACA G CAAGAAGG	3597	CCTTCTTG GGCTAGCTACAACGA TGTCCCAG 4883
854	CAAGAAGG G CUUUACUA	3598	TAGTAAAG GGCTAGCTACAACGA CCTTCTTG 4884
-	AGGGCUUU A CUAUUCCC	3599	GGGAATAG GGCTAGCTACAACGA AAAGCCCT 4885
862	GCUUUACU A UUCCCAGC	3600	GCTGGGAA GGCTAGCTACAACGA AGTAAAGC 4886
869	UAUUCCCA G CUACAUGA	3601	TCATGTAG GGCTAGCTACAACGA TGGGAATA 4887
872	UCCCAGCU A CAUGAUCA	3602	TGATCATG GGCTAGCTACAACGA AGCTGGGA 4888
874	CCAGCUAC A UGAUCAGC	3603	GCTGATCA GGCTAGCTACAACGA GTAGCTGG 4889
877	GCUACAUG A UCAGCUAU	3604	ATAGCTGA GGCTAGCTACAACGA CATGTAGC 4890
881	CAUGAUCA G CUAUGCUG	3605	CAGCATAG GGCTAGCTACAACGA TGATCATG 4891
884	GAUCAGCU A UGCUGGCA	3606	TGCCAGCA GGCTAGCTACAACGA AGCTGATC 4892
886	UCAGCUAU G CUGGCAUG	3607	CATGCCAG GGCTAGCTACAACGA ATAGCTGA 4893
890	CUAUGCUG G CAUGGUCU	3608	AGACCATG GGCTAGCTACAACGA CAGCATAG 4894
892	AUGCUGGC A UGGUCUUC	3609	GAAGACCA GGCTAGCTACAACGA GCCAGCAT 4895
895	CUGGCAUG G UCUUCUGU	3610	ACAGAAGA GGCTAGCTACAACGA CATGCCAG 4896
902	GGUCUUCU G UGAAGCAA	3611	TTGCTTCA GGCTAGCTACAACGA AGAAGACC 4897
907	UCUGUGAA G CAAAAAUU	3612	AATTTTTG GGCTAGCTACAACGA TTCACAGA 4898
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			151	
913	AAGCAAAA A UUAAUGAU	3613	ATCATTAA GGCTAGCTACAACGA TTTTGCTT	4899
917	AAAAAUUA A UGAUGAAA	3614	TTTCATCA GGCTAGCTACAACGA TAATTTTT	4900
920	AAUUAAUG A UGAAAGUU	3615	AACTTTCA GGCTAGCTACAACGA CATTAATT	4901
926	UGAUGAAA G UUACCAGU	3616	ACTGGTAA GGCTAGCTACAACGA TTTCATCA	4902
929	UGAAAGUU A CCAGUCUA	3617	TAGACTGG GGCTAGCTACAACGA AACTTTCA	4903
933	AGUUACCA G UCUAUUAU	3618	ATAATAGA GGCTAGCTACAACGA TGGTAACT	4904
937	ACCAGUCU A UUAUGUAC	3619	GTACATAA GGCTAGCTACAACGA AGACTGGT	4905
940	AGUCUAUU A UGUACAUA	3620	TATGTACA GGCTAGCTACAACGA AATAGACT	4906
942	UCUAUUAU G UACAUAGU	3621	ACTATGTA GGCTAGCTACAACGA ATAATAGA	4907
944	UAUUAUGU A CAUAGUUG	3622	CAACTATG GGCTAGCTACAACGA ACATAATA	4908
946	UUAUGUAC A UAGUUGUC	3623	GACAACTA GGCTAGCTACAACGA GTACATAA	4909
949	UGUACAUA G UUGUCGUU	3624	AACGACAA GGCTAGCTACAACGA TATGTACA	4910
952	ACAUAGUU G UCGUUGUA	3625	TACAACGA GGCTAGCTACAACGA AACTATGT	4911
955	UAGUUGUC G UUGUAGGG	3626	CCCTACAA GGCTAGCTACAACGA GACAACTA	4912
958	UUGUCGUU G UAGGGUAU	3627	ATACCCTA GGCTAGCTACAACGA AACGACAA	4913
963	GUUGUAGG G UAUAGGAU	3628	ATCCTATA GGCTAGCTACAACGA CCTACAAC	4914
965	UGUAGGGU A UAGGAUUU	3629	AAATCCTA GGCTAGCTACAACGA ACCCTACA	4915
970	GGUAUAGG A UUUAUGAU	3630	ATCATAAA GGCTAGCTACAACGA CCTATACC	4916
974	UAGGAUUU A UGAUGUGG	3631	CCACATCA GGCTAGCTACAACGA AAATCCTA	4917
977	GAUUUAUG A UGUGGUUC	3632	GAACCACA GGCTAGCTACAACGA CATAAATC	4918
979	UUUAUGAU G UGGUUCUG	3633	CAGAACCA GGCTAGCTACAACGA ATCATAAA	4919
982	AUGAUGUG G UUCUGAGU	3634	ACTCAGAA GGCTAGCTACAACGA CACATCAT	4920
989	GGUUCUGA G UCCGUCUC	3635	GAGACGGA GGCTAGCTACAACGA TCAGAACC	4921
993	CUGAGUCC G UCUCAUGG	3636		
998			CCATGAGA GGCTAGCTACAACGA GGACTCAG	4922
	UCCGUCUC A UGGAAUUG	3637	CAATTCCA GGCTAGCTACAACGA GAGACGGA	4923
1003		3638	TAGTTCAA GGCTAGCTACAACGA TCCATGAG	4924
<b></b>	GGAAUUGA A CUAUCUGU	3639	ACAGATAG GGCTAGCTACAACGA TCAATTCC	4925
<b>—</b>	AUUGAACU A UCUGUUGG	3640	CCAACAGA GGCTAGCTACAACGA AGTTCAAT	4926
	AACUAUCU G UUGGAGAA	3641	TTCTCCAA GGCTAGCTACAACGA AGATAGTT	4927
	GGAGAAAA G CUUGUCUU	3642	AAGACAAG GGCTAGCTACAACGA TTTTCTCC	4928
<u> </u>	AAAAGCUU G UCUUAAAU	3643	ATTTAAGA GGCTAGCTACAACGA AAGCTTTT	4929
H: -	UGUCUUAA A UUGUACAG	3644	CTGTACAA GGCTAGCTACAACGA TTAAGACA	4930
	CUUAAAUU G UACAGCAA	3645	TTGCTGTA GGCTAGCTACAACGA AATTTAAG	4931
	UAAAUUGU A CAGCAAGA	3646	TCTTGCTG GGCTAGCTACAACGA ACAATTTA	4932
	AUUGUACA G CAAGAACU	3647	AGTTCTTG GGCTAGCTACAACGA TGTACAAT	4933
	CAGCAAGA A CUGAACUA	3648	TAGTTCAG GGCTAGCTACAACGA TCTTGCTG	4934
	AGAACUGA A CUAAAUGU	3649	ACATTTAG GGCTAGCTACAACGA TCAGTTCT	4935
	UGAACUAA A UGUGGGGA	3650	TCCCCACA GGCTAGCTACAACGA TTAGTTCA	4936
$\overline{}$	AACUAAAU G UGGGGAUU	3651	AATCCCCA GGCTAGCTACAACGA ATTTAGTT	4937
	AUGUGGGG A UUGACUUC		GAAGTCAA GGCTAGCTACAACGA CCCCACAT	4938
	GGGGAUUG A CUUCAACU		AGITGAAG GGCTAGCTACAACGA CAATCCCC	4939
	UGACUUCA A CUGGGAAU	3654	ATTCCCAG GGCTAGCTACAACGA TGAAGTCA	4940
	AACUGGGA A UACCCUUC		GAAGGGTA GGCTAGCTACAACGA TCCCAGTT	4941
-	CUGGGAAU A CCCUUCUU	3656	AAGAAGGG GGCTAGCTACAACGA ATTCCCAG	4942
	UCUUCGAA G CAUCAGCA	3657	TGCTGATG GGCTAGCTACAACGA TTCGAAGA	4943
_	UUCGAAGC A UCAGCAUA	3658	TATGCTGA GGCTAGCTACAACGA GCTTCGAA	4944
1107	AAGCAUCA G CAUAAGAA	3659	TTCTTATG GGCTAGCTACAACGA TGATGCTT	4945
1109	GCAUCAGC A UAAGAAAC	3660	GTTTCTTA GGCTAGCTACAACGA GCTGATGC	4946
1116	CAUAAGAA A CUUGUAAA	3661	TTTACAAG GGCTAGCTACAACGA TTCTTATG	4947
1120	AGAAACUU G UAAACCGA	3662	TCGGTTTA GGCTAGCTACAACGA AAGTTTCT	4948
1124	ACUUGUAA A CCGAGACC	3663	GGTCTCGG GGCTAGCTACAACGA TTACAAGT	4949
1130	AAACCGAG A CCUAAAAA	3664	TTTTTAGG GGCTAGCTACAACGA CTCGGTTT	4950
1138	ACCUAAAA A CCCAGUCU	3665	AGACTGGG GGCTAGCTACAACGA TTTTAGGT	4951
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1143   ANARCCC & UCUGGGAS   3666   CTCCCCAR GGCTAGCTACCAACGA TCCCARGC   4953					
1156 GOAGUGAG A UGAAGAAA 3668 TTCTTTCA GGCTAGCTACAACGA CTCACTCC 4954 1164 AUGAAGAA A UUUUUGAG 3669 CTCAAAAA GGCTAGCTACAACGA TTCTTCAT 4955 1174 UUUUGAG C ACCUUAA 3670 TTAAAGTG GGCTAGCTACAACGA TCAAAAAT 4956 1174 UUUUGAG C ACCUUAA 3670 TTAAAGTG GGCTAGCTACAACGA TCAAAAAT 4956 1180 GCACCUUA A CUAUAAGU 3671 AGTTAAGG GGCTAGCTACAACGA GCTAAAAAT 4956 1183 CCUUAACU A UAGAUGGU 3673 ACCATCTA GGCTAGCTACAACGA ATTAAGG 4958 1187 AACUAUAG A UGGUGUAA 3672 ATTACACCA GGCTAGCTACAACGA ATTAAGG 4958 1187 AACUAUAG A UGGUGUAA 3674 TTACACCA GGCTAGCTACAACGA ATTAAGG 4958 1189 CUUAAGUG A UGGUGUAA 3674 TTACACCA GGCTAGCTACAACGA ATTAAGG 4958 1199 UAUAGAUG A UGGUGUAA 3674 TTACACCA GGCTAGCTACAACGA ATTAAGG 4958 1199 UAUAGAUG G UGUACACC 3675 GGGTTACA GGCTAGCTACAACGA ACTATATA 4961 1192 UAGAGUG A CCAGGAGU 3677 ACTCCGGG GGCTAGCTACAACGA ACCACTT 4962 1195 AUGGUGUA A CCCGGAGU 3677 ACTCCGGG GGCTAGCTACAACGA ACCACTT 4963 1202 AACCCGGA G UGACCAAC 3678 TCTTGGTCA GGCTAGCTACAACGA ACCACTT 4963 1202 CACCAGGA A UGACCAAC 3678 ACCCTGGGTA GGCTAGCTACAACGA ACCACCT 4963 1212 GACCAAGG A UGACCAAC 3660 GTGTACAA GGCTAGCTACAACGA ACCACCAT 4964 1215 CAACGAUG A CCAAGGAU 3678 ACCCTGGGTA GGCTAGCTACAACGA ACCCTGCGG 4965 1212 GACCAAGG A UGACACCU 3661 GTGTACAA GGCTAGCTACAACGA ACACCCT 4966 1212 GACCAAGG A CCAGGGTA 3661 GTGTACAA GGCTAGCTACAACGA ACACCCT 4967 1212 GACCAGGG A CCAGGGTA 3661 TCACACGG GGCTAGCTACAACGA ACACCCT 4967 1212 GAUCACCU G UGCAGCU 3661 TCACACGG GGCTAGCTACAACGA ACACCCT 4967 1223 GUCACCCU G UGCAGCU 3661 TCACACGG GGCTAGCTACAACGA ACACCCT 4969 1223 GUCACCCU G CACCACCCG 3661 TCACACCGG GGCTAGCTACAACGA ACACCCT 4969 1223 GUCACCCU G CACCACCCG 3661 TCACACGG GGCTAGCTACAACGA ACACCCT 4971 1228 CCUUUGCA G CAUCACAG 3661 TCACACGG GGCTAGCTACAACGA ACACCGT 4971 1228 CCUUUGCA GCACCCCACGG GGCTAGCTACAACGA TCCACCGG 4972 1230 UUCACCC G UGAGGCGA GCACCCC GGCTAGCTACAACGA TCCACCGG GGCTAGCTACAACGA TCCACCGG 4972 1230 UUCACCC G UGAGGCGA GCACCCC GGCTAGCTACAACGA TCCACCGG GGCTAGCTACAACGA TCCACCCC 4971 1230 UUCAGGC A UCCACCAG GGCTAGCTACAACGA TCCACCAC 4971 1230 UUCAGAC A CCACGGG GGCTAGCTACAACGA ACACACC A C	1143	AAAACCCA G UCUGGGAG	3666	CTCCCAGA GGCTAGCTACAACGA TGGGTTTT	4952
1164 AUGANGAA A UUUUUGAG 1679 CTCARARA GGCTAGCTACAACGA TTCTTCAT 4955 1172 AUUUUUGA G CACCUUAA 3670 TTARGGT GGCTAGCTACAACGA CTCARARA 4957 1180 GCACCUUA C CUNUAGAU 3671 AGTTARGG GGCTAGCTACAACGA GCTCARAA 4957 1180 GCACCUUA C CUNUAGAU 3672 ATCTATAG GGCTAGCTACAACGA GCTCARAA 4957 1181 COUTAACU A UAGAUGGU 3673 ACCATCTA GGCTAGCTACAACGA AGTTAAGG 4959 1183 CCUUAACU A UAGAUGGU 3673 ACCATCTA GGCTAGCTACAACGA AGTTAAGG 4959 1184 IARCUUAGAU G UGUAACCC 3675 GGGTTACA GGCTAGCTACAACGA CATCTATA 4951 1195 UAGAUGGU G UAACCCG 3675 GGGTTACA GGCTAGCTACAACGA CATCTATA 4951 1195 LAUGGUGUA A CCCAGAGU 3677 ACTCCGGG GGCTAGCTACAACGA CATCTATA 4951 1205 CACCAGAG G UGACCCA 3678 CTTGGTCA GGCTAGCTACAACGA TCCACCAT 4961 1205 CACCAGAG G UGACCACA 3678 CTTGGTCA GGCTAGCTACAACGA TCCACCAT 4961 1205 CACAGAUG A CCCAGAGU 3679 ATCCTTCG GGCTAGCTACAACGA TCCCGGGTT 4964 1205 CCGGARGU A CCCAGAGU 3679 ATCCTTGG GGCTAGCTACAACGA TCCCGGGT 4964 1215 CAACGAUG A UGACCCC 3681 CACCAGGA GCTACCACAGA ACCACCT 4963 1212 GACCAGAG A UUGACCC 3680 TGTGACA GCCACCTACAACGA ACCACCT 4967 1217 AGGAUUGU A CACCUGUG 3681 CAGGTGTA GGCTAGCTACAACGA ACCACCT 4967 1217 AGGAUUGU A CACCUGUG 3681 CAGGTGTA GGCTAGCTACAACGA ACCACCT 4968 1221 GACACCUG G UGCACCU 3681 ATCCTCGG GGCTAGCTACAACGA ACAACCT 4968 1222 GACACCUG G UGCACCU 3684 ATCCTCT 4967 1223 GUACACCU G UGCACCU 3685 CACAGGTG GGCTAGCTACAACGA ACAACCT 4968 1223 GUACACCU G UGCACCU 3685 CACAGGTG GGCTAGCTACAACGA ACCACGG 4971 1224 CACCUGUG G CAGCAUC 3685 CACAGGTG GGCTAGCTACAACGA ACCACGG 4972 1225 CACACCUG G UGCACCAU 3684 ATCCTCT 4968 1226 CACAGAGA AUGACCAU 3684 ATCCTCT 4967 1227 CAGGGUGA GACCACC 3685 CACAGGTG GGCTAGCTACAACGA TCCACCG 4973 1228 CCCUGUCA G CACACCAU 3684 ATCCTCAC GGCTAGCTACAACGA TCCACCG 4973 1239 UCCACAG A UCCAGAGU 3689 TCCACCA GGCTAGCTACAACGA TCCACCG 4971 1239 UCCAGAGA A CACACCAGA 3689 TCCACCA GGCTAGCTACAACGA TCCACCG 4971 1239 UCCAGAGA A CACACCAGA 3689 TCCACCA GGCTAGCTACAACGA TCCACCG 4971 1246 GCUGAGA A UCCACCAG 3669 TCCACCA GGCTAGCTACAACGA TCCACCA 4973 1251 GACACCUG G UCCACCAG 3690 TCCACCA GGCTAGCTACAACGA TCCACCA 4972 1252 GACACCUG G UCCACA	1151	GUCUGGGA G UGAGAUGA	3667	TCATCTCA GGCTAGCTACAACGA TCCCAGAC	4953
1172 AUUUUUGA G CACCUUAAU 3670 TTAAGGTG GGCTAGCTACAAGA TCAAAAAT 4956 1180 GGCACCUUA A CUUAAGAU 3671 AGTTAAGG GGCTAGCTACAAGA GCTCAAAA 4957 1183 CCUUAACU A UAGAUGGU 3673 ACCATCTA GGCTAGCTACAACGA TAAGGTCC 4958 1183 CCUUAACU A UAGAUGGU 3673 ACCATCTA GGCTAGCTACAACGA AGTTAAGG 4959 1184 AACUATAG A UAGAUGGU 3673 ACCATCTA GGCTAGCTACAACGA AGTTAAGG 4959 1185 CAUUAACU A UAGAUGGU 3674 TTACACCA GGCTAGCTACAACGA AGTTAAGG 4959 1195 UAAGAUGG U GUAACCC 3675 GGGTTAC GGCTAGCTACAACGA CATCTATA 4961 1190 UAUAGAUG G UGUAACC 3675 GGGTTACA GGCTAGCTACAACGA ACCATCTA 4962 1195 UAGAUGGU G UAACCCGG 3676 CCGGGTTA GGCTAGCTACAACGA ACCATCTA 4962 1195 UAGAUGGU A CCCAGAGU 3677 ACCCCGG GGCTAGCTACAACGA ACCATCTA 4962 1202 AACCCGGA G UAACCACAG 3678 CTCCGGG GGCTAGCTACAACGA TACACCAT 4962 12102 AACCCGGA G UAGACCAG 3660 CTGTACAA GGCTAGCTACAACGA TACACCAT 4963 1212 GACCAAGG A UUGUACAC 3660 CTGTACAA GGCTAGCTACAACGA ACCTCCGG 4965 1212 GACCAAGG A UUGUACAC 3661 CAGGTTAG GGCTAGCTACAACGA ACCATCCTG 4967 1213 GAUUGUA A CACCUGUG 3661 CAGGTTAG GGCTAGCTACAACGA ACCATCCTG 4967 1214 GAUUGUAC A CACCUGUG 3662 CACAGGTG GGCTAGCTACAACGA ACCATCCTG 4967 1215 GAAGAGUU G UACCACCU 3661 CAGGTTAG GGCTAGCTACAACGA ACCATCCTG 4968 1212 GAUUGUAC A CACCUGUG 3662 CACAGGTG GGCTAGCTACAACGA ACCATCCTG 4968 1213 GAUUGUAC A CACCUGUG 3662 CACAGGTG GGCTAGCTACAACGA ACCATCCTG 4969 1214 GAUUGUAC A CACCUGUG 3668 GGAGGTGGCTACAACGA ACCATCCTG 4969 1225 ACACCUGU G UGCAGCAU 3668 GGAGGTGGGGTAGCTACAACGA ACCATCCT 4969 1225 ACACCUGU G UGCAGCAU 3668 GGAGGTGGGGGTAGCTACAACGA ACCAGTGAC 4971 1226 CCUGUGCA G CAUCCAGU 3668 GCATGCTGGCTACAACGA ACCAGGTTAC 4972 1239 UCCAGUGG G UGAGCAU 3668 ACTGGAG GGCTAGCTCAACGA ACCAGGTTAC 4972 1239 UCCAGUGG G UGAGCAU 3668 ACTGGAG GGCTAGCTCAACGA ACAGGTTC 4971 1246 GAUGAGAU A CACAGGAU 3669 GTCAGCTG AGCTACAACGA ACAGGTTC 4971 1259 GAAGAACA G CACAUUCG 3669 GTCAGCTACAACGA CACCACC 4976 1246 GGCUGAUGA A CACAGGAU 3669 GTCAGCTACAACGA CACCACC 4976 1246 GGCUGAUGA A CCAAGGAU 3669 GTCAGCTACAACGA CACCACC 4976 1246 GGCUGAUGA A CCAAGGAU 3669 GTCAGCTACAACGA CACCACC 4976 1247 GUGUCAGA A CCACAGGAU 3669 GTCA	1156	GGAGUGAG A UGAAGAAA	3668	TTTCTTCA GGCTAGCTACAACGA CTCACTCC	4954
1174   UUUUGAGC A CCUUAACU 3671   AGTTARGG GGCTAGCTACAACGA GCTCAANA 4957   1180   GCACCUUA A CUALINGAD 3672   ATCTATAG GGCTAGCTACAACGA TAAGGTGG 4958   1187   AACUAUAG A UAGAUGGU 3673   ACCATCTA GGCTAGCTACAACGA CATTARGG 4959   1187   AACUAUAG A UGGUGUAA 3674   TTACACCA GGCTAGCTACAACGA CATCTATGT 4960   1190   UAUAGAUG G UGUAACCC 3675   GGGTTACA GGCTAGCTACAACGA CATCTATA 4961   1192   UAGAUGGU G UACACCGG 3676   CCGGGGTTA GGCTAGCTACAACGA CATCTATA 4961   1192   UAGAUGGU G UACACCGG 3676   CCGGGGTTA GGCTAGCTACAACGA CACCTCTA 4963   1193   AUGGUGUA A CCCGGAGU 3677   ACTCCGGG GGCTAGCTACAACGA TACACCAT 4963   1202   AACCCGGA G UGACCAGA 3678   CTTGGTCA GGCTAGCTACAACGA TACACCAT 4963   1205   CCGGGGU A CCAAGGAU 3679   ATCCTTGA GGCTAGCTACAACGA CACTCCGG 4965   1212   GACCAAGG A UUGUACAC 3680   GTGTACAA GGCTAGCTACAACGA CACTCCGG 4965   1212   GACCAAGG A UUGUACAC 3680   GTGTACAA GGCTAGCTACAACGA CACTCCGG 4965   1213   GAUGUUAC A CCCUGUG 3681   CAGGTGTA GGCTAGCTACAACGA CACTCCGG 4967   1214   GAUUGUAC A CCCUGUG 3682   CACAGGTG GGCTAGCTACAACGA CACTCCTG 4967   1215   GAUGUUAC A CCCUGUG 3683   TGCACAGG GGCTAGCTACAACGA CACTCCTG 4967   1216   GALUCUAGU A CACCUGUG 3684   ATGCTGCA GGCTAGCTACAACGA CACTCCTG 4967   1217   AGAUUGUA A CACCUGUG 3684   ATGCTGCA GGCTAGCTACAACGA CAGTCCT 4969   1218   CUCUGUGCA G CAUCCAGG 3684   ATGCTGCA GGCTAGCTACAACGA CAGGTGTACATCA 4969   1223   CUCUGUGCA G CAUCCAGG 3686   ACTGGATG GGCTAGCTACAACGA CAGGTGTA 4971   1225   CACCUGU G CAGCAUC 3688   GATGGTG GGCTAGCTACAACGA CAGGTGTA 4971   1226   CUCUGUGCA G CUCCAGGUG 3687   CACCTGGA GGCTAGCTACAACGA CAGGTGTA 4971   1227   CAGGGGCGA GGCAGCAU 3688   TCAGCCCA GGCTAGCTACAACGA CAGCGCCA 4972   1228   CUCUGUGCA G CUCCAGGG 3689   CTCATCAG GGCTAGCTACAACGA CAGCCCC 4976   1226   GCCACUU G UGGGCUGA 3689   CTCATCAG GGCTAGCTACAACGA CAGCCCC 4976   1226   GCCACUU G UGGGCUGA 3689   CTCATCAG GGCTAGCTACAACGA CAGCCCC 4976   1226   GAGAACA A CCAGCACU 3691   CTCTCTG GGCTAGCTACAACGA CATCAGCC 4976   1226   GAGAACA A CCAAGAGA 3691   CTCTCTG GGCTAGCTACAACGA CATCAGCC 4976   1227   CAGGGGGG G UGGGCG	1164	AUGAAGAA A UUUUUGAG	3669	CTCAAAAA GGCTAGCTACAACGA TTCTTCAT	4955
1180 GCACCUUA A CUAUAGAU 3672 ATCTATAG GGCTAGCTACAACGA TAAGGTGC 4958 1183 CCUUAACU A UAGAUGGU 3673 ACCATCTA GGCTAGCTACAACGA AGTTAAGGT 4959 1191 UAUAGAUGG UGUAACCC 3675 GGGTTACA GGCTAGCTACAACGA CTATAGTT 4961 1192 UAUAGAUG G UGUAACCC 3675 GGGTTACA GGCTAGCTACAACGA CTATAGTT 4961 1192 UAUAGAUG G UGUAACCC 3675 GGGTTACA GGCTAGCTACAACGA CATCTATA 4961 1192 UAGAUGGU G UAACCCGG 3676 CCGGGTTA GGCTAGCTACAACGA CATCTATA 4961 1192 UAGAUGGU G UAACCCGG 3676 CCGGGTTA GGCTAGCTACAACGA CACCATCTA 4962 1192 DAGAUGGU A CCCGGAGU 3677 ACTCCGGG GGCTAGCTACAACGA TACACCAT 4963 1202 FACCCAGGA G UGACCAAG 3678 CTRGGTCA GGCTAGCTACAACGA TACACCAT 4963 1202 FACCAGGA G UGACCAAG 3679 ATCCTGGG GGCTAGCTACAACGA TACACCAT 4964 1205 CCGGAGUG A CCAAGGAU 3679 ATCCTGG GGCTAGCTACAACGA CCTTGGTC 4966 1212 GACCAAGG A UUGUACC 3680 GTTACAA GGCTAGCTACAACGA ACTCCTGG 4965 1212 GACCAAGG A UUGUACC 3680 GTTACAA GGCTAGCTACAACGA ACTCCTGG 4967 1213 GAUUGUAC A CCCUGUGG 3682 CACAGGTG GGCTAGCTACAACGA ACTCCTTG 4967 1213 GAUUGUAC A CCUGUGCA 3683 TGCACAGG GGCTAGCTACAACGA ACTCCTTG 4968 1213 GAUGUAC A CCUGUGCA 3683 TGCACAGG GGCTAGCTACAACGA ACTCCTTG 4968 1223 GUACCACCU G UGCAGCAU 3684 ATGCTGCA GGCTAGCTACAACGA ACTCCTTG 4970 1225 ACACCUGU G CAGCAUCC 3685 GGATGCTG GGCTAGCTACAACGA ACGGTTGTACACGA 4970 1228 CCUGUGCA G CACCAGGG 3687 CCACTGGG GGCTAGCTACAACGA ACGGTTGTACACGA 4970 1228 GUACCAGCA G CACCAGGG 3688 TCAGCACG GGCTAGCTACAACGA ACGGTTGTACACGA 4970 1228 GUACCAGCA G CACCAGGG 3688 TCAGCACG GGCTAGCTACAACGA CACGGCGA 4971 1228 GUACCAGCA G CACCAGGG 3688 TCAGCCAC GGCTAGCTACAACGA ACGGCTACA 4970 1228 GUACCAGCA G CACCAGGG 3689 CCACTGGG AGCTACAACGA CACGCCAC 4971 1239 UCCAGGCA G CCACGGGG 3688 TCAGCCAC GGCTAGCTACAACGA CACCCAC 4971 1239 UCCAGGCG A CCACGGG 3689 CCACTGG GGCTAGCTACAACGA CACCCAC 4971 1239 UCCAGCAG A CACUUGC 3689 CTTGGTCA GGCTAGCTACAACGA CACCCAC 4971 1246 GCUGAGA A CCACGGG 3693 CTTGGTCA GGCTAGCTACAACGA CACCCAC 4976 1246 GCUGAGA A CCACGGG 3693 CTTGGTCA GGCTAGCTACAACGA CACCCAC 4976 1246 GCUGAGAC A CUUUGCA 3699 CTTGGTCA GGCTAGCTACAACGA CACCAC 4980 1247 CACCGGG A CACCCGGG 3690 CTTGGTCA GGCTAG	1172	AUUUUUGA G CACCUUAA	3670	TTAAGGTG GGCTAGCTACAACGA TCAAAAAT	4956
1183 CCUUAACU A UAGAUGGU 3673 ACCATCTA GGCTAGCTACAACGA AGTTAAGG 4959 1187 AACUNJAG A UGGUGUAA 3674 TACACCA GGCTAGCTACAACGA CTATAGGT 4960 1190 UAJAGAUGG G UGAACCC 3675 GGGTTACA GGCTAGCTACAACGA CATCTATA 4961 1192 UAGAUGGU G UAACCCGG 3676 CCGGGTTA GGCTAGCTACAACGA CATCTATA 4961 1192 UAGAUGGU G UAACCCGG 3676 CCGGGTTA GGCTAGCTACAACGA ACCATCTA 4962 1195 AUGGUGUA A CCCGGAGU 3677 ACTCCGGG GGCTAGCTACAACGA ACCATCTA 4963 1202 AACCCGGA G UGACCAAG 3678 CTTGGTCA GGCTAGCTACAACGA TCCGGGTT 4964 1205 CCGGAGUG A CCAGGAU 3679 ACTCTGG GGCTAGCTACAACGA TCCGGGTT 4964 1212 GACCAAGG A UUGUACAC 3680 GTGTACAA GGCTAGCTACAACGA CATCCGG 4965 1212 GACCAAGG A UUGUACAC 3680 GTGTACAA GGCTAGCTACAACGA CATCCGG 4966 1212 GACCAAGG A UUGUACAC 3680 GTGTACAA GGCTAGCTACAACGA ACTCCTG 4967 1215 CAAGGAUU G UACACCUG 3681 CAGGTGTG GGCTAGCTACAACGA ACCATCCTG 4967 1217 AGGAUUGUA A CCCUGUGCA 3683 TGCACAGG GGCTAGCTACAACGA ACCATCCTG 4967 1218 GAUCUGUA A CCCUGUGCA 3683 TGCACAGG GGCTAGCTACAACGA ACACTCCTG 4969 1219 GAUCUGUA A CCUGUGCA 3684 ATGCTGCA GGCTAGCTACAACGA ACACTCTC 4969 1223 GUACACCU G UGCAGCAU 3684 ATGCTGCA GGCTAGCTACAACGA ACAGGTGTA C4970 1228 CCUGUGCA G CUCCAGUU 3686 ACTGGATG GGCTAGCTACAACGA ACAGGTGT 4971 1228 CCUGUGCA G CUCCAGUU 3686 ACTGGATG GGCTAGCTACAACGA ACAGGTGT 4971 1228 UGUGCAG C UCCAGUG 3687 TCACTGGA GGCTAGCTACAACGA ACAGGTGT 4974 1239 UCCAGUGCA G UGCAGCAA 3689 GTCATCGA GGCTAGCTACAACGA TGCACAG 4975 1243 GUGCGAGC A UCCAGUG 3689 GTCATCGA GGCTAGCTACAACGA TGCACAG 4975 1243 GUGCGAGC A UCCAGUG 3689 TCATCGA GGCTAGCTACAACGA TGCACAG 4975 1243 GUGCGAGC A UUCAGUGA 3691 TCATCGG GGCTAGCTACAACGA TGCACAG 4976 1243 GUGCGAGC A UCCAGUG 3692 ATGTGTC GGCTAGCTACAACGA TGCACCA 4976 1243 GUGCGAGC A UUCAGUGA 3699 TCATCGG GGCTAGCTACAACGA TGCACCA 4976 1243 GUGCGAGC A CUUUGUG 3699 TCATCGG GGCTAGCTACAACGA TCGACC 4976 1256 CAAGAAGA A CAGCACAG 3690 TTCATCG GGCTAGCTACAACGA TCATCAGC 4976 1256 CAAGAAGA A CAGCACAG 3690 TCATCGAG GGCTAGCTACAACGA TCTCTCT 4978 1256 CAAGAAGA A CAGCACAG 3690 TCATCGAG GGCTAGCTACAACGA TCTCTCT 4991 1257 CAGGGUC A UGAAAAC 3691 TCATCGG GGCTAGCTACAACGA TCTCTCT 4991	1174	UUUUGAGC A CCUUAACU	3671	AGTTAAGG GGCTAGCTACAACGA GCTCAAAA	4957
1187   AACUAUAG A UGGUGUAA 3674   TTACACCA GGCTAGCTACAACGA CTATAGTT   4960   1192   UAUAGAUG G UGUAACCC 3675   GGGTTAC GGCTAGCTACAACGA CATCTATA   4961   1192   UAGAUGGU G UAACCCGG 3676   CCGGGTTA GGCTAGCTACAACGA ACCATCTA   4961   1192   UAGAUGGU G UAACCCGG 3676   CCGGGTTA GGCTAGCTACAACGA ACCATCTA   4962   1195   ANGGUGUA A CCGGGATG   3677   ACTCCGGG GGCTAGCTACAACGA ACCACCAT   4963   1202   AACCCGGA G UGACCAAG   3678   CTTGGTCA GGCTAGCTACAACGA ACCACCAT   4964   1205   CCGGAGUG A CCAAGGAU   3679   ATCCTTGG GGCTAGCTACAACGA CACTCCGG   4965   1212   GACCAAGG A UUGUACAC   3680   GTGTACAA GGCTAGCTACAACGA CCTTGGTC   4966   1215   CAAGGAUU G UACACCUG   3681   CAGGTGTA GGCTAGCTACAACGA CCTTGGTC   4966   1215   CAAGGAUU G UACACCUG   3681   CAGGTGTA GGCTAGCTACAACGA ACTCCTG   4967   1217   AGGAUUGUA A CCCUGUGA   3683   TGCACAGG GGCTAGCTACAACGA ACTCCTC   4969   1229   GAUUGUAC A CCUGUGUA   3684   ATGCTGCA GGCTAGCTACAACGA ACTCCAT   4969   1229   GAUUGUAC A CCUGUGUA   3684   ATGCTGCA GGCTAGCTACAACGA ACGTGTTA   4970   1228   CCUGUGCA   6036   GATGGTG GGCTAGCTACAACGA ACGGTGTA   4971   1228   CCUGUGGA   6040	1180	GCACCUUA A CUAUAGAU	3672	ATCTATAG GGCTAGCTACAACGA TAAGGTGC	4958
1190   UAUAGAUG G UGUAACCC   3675   GGGTTACA GGCTAGCTACAACGA CATCTATA   4961   1192   UAGAUGGU G UAACCCGG   3676   CCGGGTTA GGCTAGCTACAACGA ACCATCTA   4962   1195   AUGGUGUA A CCCGGAGU   3677   ACTCCGGG GGCTAGCTACAACGA TACACCAT   4963   1202   AACCCGGA G UGACCAAG   3679   ATCCTTGG GGCTAGCTACAACGA TACACCAT   4964   1205   CAGGAGU A CCAAGGAU   3679   ATCCTTGG GGCTAGCTACAACGA CACTCCGG   4965   1212   GACCAAGG A UUGUACAC   3680   GTGTACAA GGCTAGCTACAACGA CACTCCGG   4965   1212   GACCAAGG A UUGUACAC   3680   CAGGAGUU G UACACCUG   3681   CAGGTGTA GGCTAGCTACAACGA ACCATCCT   4967   1215   CAAGGAUU G UACACCUG   3681   CAGGTGTA GGCTAGCTACAACGA ACCATCCT   4968   1219   GAUUSUAC A CCUUGUGA   3681   CAGGTGTA GGCTAGCTACAACGA ACAATCCT   4968   1219   GAUUSUAC A CCUUGUGA   3684   ATGCTGCA GGCTAGCTACAACGA ACAATCCT   4968   1229   GAUCACU G UGCAGCAU   3685   GGATGCTG GGCTAGCTACAACGA ACGGTGTAC   4970   1228   CACCUGU G CAGCAUC   3685   GGATGCTG GGCTAGCTACAACGA ACGGTGTAC   4970   1228   CCUGUGCA   CACCUGUG   3686   ACTGGATG GGCTAGCTACAACGA ACGGTGTAC   4971   1228   CCUGUGCA   CUCAGUUG   3686   ACTGGATG GGCTAGCTACAACGA ACGGTGTAC   4971   1228   CCUGUGCA   CUCAGUUG   3688   TCACCCCA GGCTAGCTACAACGA CGTGCACA   4972   1223   UCCAGUG   UCCAGUUG   3688   TCACCCCA GGCTAGCTACAACGA CGTGCACA   4974   1224   CUCAGUUG A UCCAGUUG   3689   CTCATCAG GGCTAGCTACAACGA CAGCCCAC   4976   1224   CUCAGUUG A UCACAGA   3691   CTTCTTG GGCTAGCTACAACGA CAGCCCAC   4976   1224   CUCAGUUG A UCACAGA   3691   CTTCTTG GGCTAGCTACAACGA CAGCCCAC   4976   1225   AACACACA A UUGUCA   3692   ATGTGCTA GGCTACAACGA CATCAGCCA   4976   1225   AACACACA CACCAACA   3691   CTTCTTG GGCTAGCTACAACGA CATCAGCCAC   4978   1225   AACACACA CACCAACA   3691   CTTCTTG GGCTAGCTACAACGA CATCAGCCAC   4978   1225   AACACACA CACCAACA   3691   CTTCTTG GGCTAGCTACAACGA CATCAGCCAC   4978   1226   AAAACAACA A CAUUUUG   3692   ATGTGCTA GGCTACAACGA CATCAGCA CACCAACA   3692   ATGTGCTA GGCTACAACGA CATCAGCA CACCAACA   3691   CTTCATCAA GGCTACAACGA CATCAGCA CACCAACAACAA   3691   CTTCATCAA GGCTACCAACGA CAT	1183	CCUUAACU A UAGAUGGU	3673	ACCATCTA GGCTAGCTACAACGA AGTTAAGG	4959
1192   UAGAUGGU   GUAACCCGG 3676   CCGGGTTA GGCTAGCTACAACGA ACCATCTA 4962   1957   AUGCUGG GGCTAGCTACAACGA TACACCAT 4963   1202   AACCCGGA G UGACCAAG 3678   CTTGGTCA GGCTAGCTACAACGA TACACCAT 4964   1205   CCGGAGUG A CCAAGGAU 3679   ATCCTTGG GGCTAGCTACAACGA CACTCCGG 4965   1212   GACCAAGG A UUGUACAC 3680   GTGTACAA GGCTAGCTACAACGA CACTCCGG 4966   1215   CAAGGAUU G UACACCUG 3681   CAGGTTAG GGCTAGCTACAACGA CACTCTGG 4966   1215   CAAGGAUU G UACACCUG 3681   CAGGTTAG GGCTAGCTACAACGA AATCCTTG 4966   1217   AGGAUUGU A CACCUGUG 3681   CAGGTTAG GGCTAGCTACAACGA ACTACCTT 4968   1219   GAUUGUAC A CCUGUGCA 3683   TGCACAGG GGCTAGCTACAACGA ACAACCT 4968   1223   GUACACCU G UGCAGCAU 3685   GAGTGCTG GGCTAGCTACAACGA ACAATCCT 4969   1223   GUACACCU G UGCAGCAU 3685   GAGTGCTG GGCTAGCTACAACGA ACAATCCT 4969   1223   CACCUGUG G CACCC 3685   GGATGCTG GGCTAGCTACAACGA ACAGTTAC 4971   1228   CCUGUGCA G CAUCCAGU 3685   GAGTGCTG GGCTAGCTACAACGA ACAGTTAC 4971   1228   CCUGUGCA G CAUCCAGU 3686   ACTGGAT GGCTAGCTACAACGA ACAGTTAC 4971   1228   CCUGUGCA G CUGAUGA 3688   CCACTGGA GGCTAGCTACAACGA ACAGTTAC 4971   1228   CCUGUGCA G UGGCCUGA 3688   CCACTGGA GGCTAGCTACAACGA CCACCAGGA 4973   1239   UCCAGUGG G CUGAUGA 3688   CTACTCAG GGCTAGCTACAACGA CCACTGGA 4975   1239   UCCAGUGG G CUGAUGA 3689   CTTCTTGG GGCTAGCTACAACGA CCACTGGA 4975   1246   GGCUCAUUG A CCAAGGAG 3690   CTTCGGTCA GGCTAGCTACAACGA CACCCAC 4976   1246   GGCUCAUUG A CCAAGGAG 3691   CTTCTTGG GGCTAGCTACAACGA CACCACC 4976   1226   AAGGAACA A CACCACUU 3692   ATGTGCTG GGCTAGCTACAACGA CACTACGC 4976   1226   AAGGAACA CACCAUUG 3693   CAAATGG GGCTAGCTACAACGA CACTAGCC 4976   1226   AAGGAACA CACCAUUG 3693   CAAATGG GGCTAGCTACAACGA CACTCTCT 4978   1226   AAGAACAG A CACUUGUA 3693   CAAATGG GGCTAGCTACAACGA CACTCTC 4978   1226   AAGAACAG A CACUUGUA 3693   CAAATGG GGCTAGCTACAACGA CACTCTC 4978   1226   AAGAACAG A CACUUGUA 3693   CAAATGG GGCTAGCTACAACGA CACTTCC 4991   1226   AAGAACAG A CACUUGUA 3695   CTGACAAA GGCTAGCTACAACGA ACATACACGA CACUUGUA 3702   CAAGGCCA GGCTAGCTACAACGA ACACAAA CACAACAA CAGAACAA CA	1187	AACUAUAG A UGGUGUAA	3674 ·	TTACACCA GGCTAGCTACAACGA CTATAGTT	4960
1195 AUGGUGUA A CCCGGAGU 3677 ACTCCGGG GGCTAGCTACAACGA TACACCAT 4963 1202 AACCCGGA G UGACCAAG 3678 CTTGGTCA GGCTAGCTACAACGA TCCGGGGTT 4964 1212 GACCAAGG A UUGUACAC 3680 GTGTACAA GGCTAGCTACAACGA CCTCCGGG 4965 1212 GACCAAGG A UUGUACAC 3680 GTGTACAA GGCTAGCTACAACGA CACTCCGG 4966 1215 CAAGGAUU G UACACCUG 3681 CAGGTGTA GGCTAGCTACAACGA CACTCCGG 4967 1217 AGGAUUGU A CACCUGUG 3681 CAGGTGTA GGCTAGCTACAACGA ACATCCTT 4967 1218 GAUGUACA C CUUGUGCA 3683 TGCCACAG GGCTAGCTACAACGA ACATCCT 4968 1229 GAUGUACA C CUUGUGCA 3683 TGCCACAG GGCTAGCTACAACGA ACATCCT 4969 1223 GUACACCU G UGCAGCAU 3684 ATGCTGCA GGCTAGCTACAACGA ACATCCT 4969 1223 GUACACCU G UGCAGCAU 3685 GGATGCTG GGCTAGCTACAACGA ACATCCT 4970 1225 CCUGUGCA G CAUCCAGU 3685 GGATGCTG GGCTAGCTACAACGA ACAGTGT 4971 1228 CCUGUGCA G CAUCCAGU 3686 GCTAGCTACAACGA ACAGGTGT 4971 1228 CCUGUGCA G CAUCCAGU 3687 CCACTGGA GGCTAGCTACAACGA ACAGGTGT 4971 1229 UCCAGUGG G CUGAUGAC 3688 TCAGCCCA GGCTAGCTACAACGA TGCACCAG 4972 1230 UUGUCAGU A UGACCAG 3689 CCACTGGA GGCTAGCTACAACGA CCACTGGA 4973 1231 UUCCAGUG A UGACCAAG 3690 CTTGGTCA GGCTAGCTACAACGA CCACTGGA 4973 1243 GUGGCUG A UGACCAAG 3690 CTTGGTCA GGCTAGCTACAACGA CCACTGGA 4976 1246 GGCUGAUG A CCAAGGAG 3690 CTTGTTG GGCTAGCTACAACGA CCACTGGA 4976 1246 GGCUGAUG A CCAAGGAG 3690 CTTGTTG GGCTAGCTACAACGA CATCAGCC 4976 1246 GACCAGC A CAUUUGG 3691 CTTCTTGG GGCTAGCTACAACGA CATCAGCC 4976 1256 CAAGAAGA A CAGCACAU 3692 ATGTGCTG GGCTAGCTACAACGA CATCAGCC 4976 1256 CAAGAAGA C CACUUUG 3693 ACAAATG GGCTACAACGA CTCTTCTT 4978 1256 AACAGCAC A UUUGUCA 3694 GACCATGA GGCTACAACGA TCTTCTTC 4978 1257 CAGGUCC A UAAAAAA 3697 TTCATGA GGCTACAACGA TCTTCTTC 4980 1267 GAACAGC A CAUUUGU 3694 GACCATGA GGCTACAACGA GTGCTTT 4980 1267 GACCAUUU G UCAGGGUC 3694 GACCATGA GGCTACAACGA CATCTAGCC 4981 1271 CAGGGUCC A UGAAAAAC 3698 GTTTTTCA GGCTAGCTACAACGA CATCTTCC 4980 1267 GCACAUUU G UCAGGGUC 3694 GACCATGA GGCTACAACGA CATCTACCA GGCTACAACGA CATCTACCA GGCTACAACGA CATCTACCA GGCTACAACGA CATCTACCA GGCTACAACGA CATCTACCA GGCTACAACGA CATCTACCA GGCTACAACGA CATCTACACGA CATCTACACGA CATCTACACGA CATCTACACGA	1190	UAUAGAUG G UGUAACCC	3675	GGGTTACA GGCTAGCTACAACGA CATCTATA	4961
1202   AACCCGGG G UGACCAAG 3678   CTTGGTCA GGCTAGCTACAACGA TCCGGGTT 4964   1205   CCGGAGUG A CCAAGGAU 3679   ATCCTTGG GGCTAGCTACAACGA CACTCCGG 4965   1212   GACCAAGG A UUGUACAC 3680   GTGTACAA GGCTAGCTACAACGA CACTCCGG 4965   1215   CAAGGANU G UACACCUG 3681   CAGGTGTA GGCTAGCTACAACGA AATCCTT 4967   1217   AGGAUUGU A CACCUGUG 3681   CAGGTGTA GGCTAGCTACAACGA AATCCTT 4968   1219   GAUUGUACA C CCUGUGCA 3683   TGCACAGG GGCTAGCTACAACGA AATCCTT 4968   1219   GAUUGUACA C CCUGUGCA 3683   TGCACAGG GGCTAGCTACAACGA ACAATCCT 4968   1229   GAUUGUACA C CCUGUGCA 3683   TGCACAGG GGCTAGCTACAACGA ACGGTGTAC 4970   1225   ACACCUGU G CAGCAUC 3685   GGATGCTG GGCTAGCTACAACGA ACGGTGTAC 4971   1228   CCUGUGCA G CAUCCAGU 3686   ACTGGTG GGCTAGCTACAACGA ACAGGTGT 4971   1228   CCUGUGCA G CUCCAGU 3686   ACTGGTG GGCTAGCTACAACGA ACAGGTGT 4971   1228   CCUGUGCA G CUCCAGUG 3687   CCACTGGA GGCTAGCTACAACGA ACAGGTGT 4971   1228   ACCAUCCA G UGGGCUGA 3688   CCACTGGA GGCTAGCTACAACGA CCACCAGG 4972   1229   UCCAGUGG G CUGAUGAC 3689   GTCATCAG GGCTAGCTACAACGA CCACTGGA 4975   1224   GUGGGCUG A UGACCAAG 3690   CTTGGTG GGCTAGCTACAACGA CCACTGGA 4975   1226   CAAGAAGA A CAGCACAU 3692   ATGTGCTG GGCTAGCTACAACGA CACCACCA 4976   1226   CAAGAAGA A CAGCACAU 3692   ATGTGCTG GGCTAGCTACAACGA CATCAGCC 4976   1226   CAAGAAGA A CAGCACAU 3692   ATGTGCTG GGCTAGCTACAACGA CATCAGCC 4976   1225   AAGAACAC A CAUUUGU 3694   CAAATATG GGCTAGCTACAACGA CATCAGCC 4976   1226   AAGAACAC A CAUUUGU 3694   CAAAATG GGCTAGCTACAACGA CATCAGCC 4977   1226   AAGAACAC A CAUUUGU 3694   CAAAATG GGCTAGCTACAACGA CTCTTCTT 4978   1227   CAGGGUC A UUGAGGGU 3696   GACCATGA GGCTAGCTACAACGA CTCTTCTT 4980   1227   CAGGGUC A UGAGGGU 3696   GACCATGA GGCTAGCTACAACGA CTCTACAACGA CTGTTCT 4980   1227   CAGGGUC A UGAGGGU 3696   GACCATGA GGCTAGCTACAACGA CTTTCTA 4981   1227   CAGGGUC G UGAGGAU 3700   AAAAGCAA GGCTAGCTACAACGA CTTTCCAA 4981   1227   CAGGGUC G UGAGAACCA A GAGGAGA GGCTAGCTACAACGA CACTAGCAA A 4983   1227   UGUUGGAA A UCCAUGG 3700   AGAACCACA GGCTAGCTACAACGA AACAGAA CACTAGA GGCTAGCTACAACGA ACACAACA GG	1192	UAGAUGGU G UAACCCGG	3676	CCGGGTTA GGCTAGCTACAACGA ACCATCTA	4962
1215   CCGGAGUG A CCAAGGAU   3679   ATCCTTGG GGCTAGCTACAACGA CACTCCGG   4965   1212   GACCAAGG A UUGUACAC   3680   GTGTACAA GGCTAGCTACAACGA CACTTGGTC   4966   1215   CAAGGAUU G UACACCUG   3681   CAGGTGTA GGCTAGCTACAACGA AATCCTTG   4967   1217   AGGAUUGU A CACCUGUG   3682   CACAGGTG GGCTAGCTACAACGA ACATCCTTG   4968   1219   GAUUGUAC A CCUGUGCA   3683   TGCACAGG GGCTAGCTACAACGA ACAATCCT   4969   1223   GUACACCU G UGCAGCAU   3684   ATGCTGCA GGCTAGCTACAACGA ACAATCCT   4969   1225   ACACCUGU G CAGCAUCC   3685   GGATGCTG GGCTAGCTACAACGA ACAGTGT   4971   1228   CCUGUGCA G CAUCCAGU   3686   ACTGGATG GGCTAGCTACAACGA ACAGTGT   4971   1228   CCUGUGCA G CAUCCAGU   3686   ACTGGATG GGCTAGCTACAACGA ACAGTGT   4971   1228   ACCAUGUA G CAUCCAGU   3686   ACTGGATG GGCTAGCTACAACGA ACAGTGT   4971   1228   ACCAUGCA G UGGGCUGA   3687   CCACTGGA GGCTAGCTACAACGA ACAGTGT   4971   1229   UCCAGUGG G UGGAUGAC   3688   TCAGCCCA GGCTAGCTACAACGA CAGCACA   4973   1225   AGCAUCCA G UGGGCUGA   3689   TCATCAG GGCTAGCTACAACGA CAGCCACA   4975   1224   GUGGUGG A UGACCAAG   3690   CTTGGTCA GGCTAGCTACAACGA CAGCCGCA   4975   1224   GUGGUGA A CAAGAAA   3690   CTTGGTCA GGCTAGCTACAACGA CAGCCACA   4976   1226   GAGGAACA A CAGCACAU   3693   CATATGG GGCTAGCTACAACGA CATCAGCC   4977   1256   CAAGAAAG A CAGCACAU   3693   CAAATGTG GGCTAGCTACAACGA CTTCTCTT   4979   1251   AGACAGCA C UUUGUCC   3694   GACAATG GGCTAGCTACAACGA CTTCTCTT   4979   1251   AGACAGCA C UUUGUCC   3695   CTGACAA GGCTAGCTACAACGA CTTCTCTT   4980   1224   AGACAGCA C UUUGUCC   3695   CTGACAA GGCTAGCTACAACGA CTTCTCT   4980   1224   ACUUUGU G UCAGGGUC   3696   GACCCTGA GGCTAGCTACAACGA CTTCTCT   4981   1224   ACUUUGU G UCAGGAU   3699   ACAAAGG GGCTAGCTACAACGA CTTCTCT   4981   1224   ACUUUGU G UUCAGGA   3701   TCCAGAA GGCTAGCTACAACGA CTTCCAAA   4983   1277   CAGGGUC A UGAAAAAC   3699   ACAAAGG GGCTAGCTACAACGA AAATGGTC   4984   1294   ACUUUGU G UUCAGGA   3702   CCAGGGA GGCTAGCTACAACGA CCTACAAA   4983   1294   ACUUUGU G UUCAGGA   3702   ACACCAG GGCTAGCTACAACGA CCTACCAA   4986   1294   ACUUUGU G UUCAGG	1195	AUGGUGUA A CCCGGAGU	3677	ACTCCGGG GGCTAGCTACAACGA TACACCAT	4963
1215   CCGGAGUG A CCAAGGAU   3679   ATCCTTGG GGCTAGCTACAACGA CACTCCGG   4965   1212   GACCAAGG A UUGUACAC   3680   GTGTACAA GGCTAGCTACAACGA CACTTGGTC   4966   1215   CAAGGAUU G UACACCUG   3681   CAGGTGTA GGCTAGCTACAACGA AATCCTTG   4967   1217   AGGAUUGU A CACCUGUG   3682   CACAGGTG GGCTAGCTACAACGA ACAATCCT   4968   1219   GAUUGUAC A CCUGUGCA   3683   TGCACAGG GGCTAGCTACAACGA ACAATCCT   4969   1223   GUACACCU G UGCAGCAU   3684   ATGCTGCA GGCTAGCTACAACGA ACAATCCT   4969   1225   ACACCUGU G CAGCAUCC   3685   GGATGCTG GGCTAGCTACAACGA ACAGTGT   4971   1228   CCUGUGCA G CAUCCAGU   3686   ACTGGATG GGCTAGCTACAACGA ACAGTGT   4971   1228   CCUGUGCA G CAUCCAGU   3686   ACTGGATG GGCTAGCTACAACGA ACAGTGT   4971   1228   ACCAUGUA G CAUCCAGU   3686   ACTGGATG GGCTAGCTACAACGA ACAGTGT   4971   1228   ACCAUGCA G UGGGCUGA   3688   TCAGCCCA GGCTAGCTACAACGA ACAGTGT   4971   1229   UCCAGUGG G UGGAUGAC   3689   TCAGCCCA GGCTAGCTACAACGA CCACTGGA   4973   1225   AGCAUCCA G UGGGCUGA   3689   TCAGCCCA GGCTAGCTACAACGA CACCTGGA   4975   1224   GUGGGUG A UGACCAAG   3690   CTTGGTCA GGCTAGCTACAACGA CACCTGGA   4975   1224   GUGGUGA A CAAGAAA   3690   CTTGGTCA GGCTAGCTACAACGA CACCAGCA   4976   4976   4976   4976   4976   4976   4976   4976   4976   4976   4976   4976   4976   4976   4976   4976   4977   4979   4977   4977   4977   4979   4977	1202	AACCCGGA G UGACCAAG	3678	CTTGGTCA GGCTAGCTACAACGA TCCGGGTT	4964
1212   GACCAAGG A UUGUACAC   3680   GTGTACAA GGCTAGCTACAACGA ACTCGTG   4966   1215   CAAGGAUU G UACACCUG   3681   CAGGTGTA GGCTAGCTACAACGA AATCCTTG   4967   1217   AGGAUGUA A CACCUGUG   3683   CACAGGTG GGCTAGCTACAACGA ACAATCCT   4968   1219   GAUUGUAC A CCUGUGCA   3683   TGCACAGG GGCTAGCTACAACGA ACGATCCT   4969   1223   GUACACCU G UGCAGCAU   3684   ATGCTGCA GGCTAGCTACAACGA ACGAGTGT   4970   1225   ACACUGU G CAGCAUCC   3685   GGATGGTG GGCTAGCTACAACGA ACGAGTGT   4971   1228   CCUGUGCA G CAUCCAGU   3686   ACTGGTAG GGCTAGCTACAACGA ACGAGTGT   4971   1228   CUGUGCA G CAUCCAGU   3686   ACTGGTAG GGCTAGCTACAACGA ACGAGTGT   4971   1228   UGUGCAGC A UCCAGUGG   3687   CCACTGGA GGCTAGCTACAACGA ACGACACA   4973   1229   UCCAGUGG G CUGAUGAC   3688   TCAGCCCA GGCTAGCTACAACGA TGCACAG   4973   1229   UCCAGUGG G CUGAUGAC   3689   GTCATCAG GGCTAGCTACAACGA TGGATGCT   4974   1229   UCCAGUGG G CUGAUGAC   3689   GTCATCAG GGCTAGCTACAACGA TGGATGCT   4974   1226   GGCUGAUGA C CACAGGAG   3690   CTTGGTCA GGCTAGCTACAACGA CACCACCAC   4975   1226   GGCUGAUG A CCAAGAAG   3691   CTTCTTGG GGCTAGCTACAACGA CACCACCAC   4976   1226   CAGGAGAG A CAGACACU   3669   ATGTGCT GGCTAGCTACAACGA TCTTCTT   4978   1226   CAGGAGAG A CACUUUUG   3693   CAAATGTG GGCTAGCTACAACGA TCTTCTT   4979   1226   AGACACAC A CAUUUUG   3693   CAAATGTG GGCTAGCTACAACGA TCTTCTT   4979   1226   AGACACAC A CAUUUUG   3695   CAAAATGT GGCTAGCTACAACGA CTCTTCT   4981   1226   AACAGCAC A UUUGUCAG   3695   CTGACAAA GGCTAGCTACAACGA CTCTTCT   4981   1226   AACAGCAC A UUUGUCAG   3695   CTGACAAA GGCTAGCTACAACGA CTCTTCT   4981   1226   CACAUUU G UUAGGGUC   3696   GACCCTGA GGCTAGCTACAACGA CTCTTCT   4981   1226   CACAUUU G UUAGGGUC   3696   GACCCTGA GGCTAGCTACAACGA CTCTTCTC   4981   1224   CUUUUGU G UUGCUUU   3699   ACAAAAG GGCTAGCTACAACGA CCTTACAACA   4983   1277   CAGGUCC A UGAAAAAC   3697   TCATGAGA GGCTAGCTACAACGA CCTTCCAAA   4981   1291   AACCUUU G UUGCAGA   3701   TCCAAAA GGCTAGCTACAACGA ACAAAAG   4981   1294   CUUUUGUAG GCTAGAGA   3701   TCCAAAA GGCTAGCTACAACGA ACAAAAGG CCTACTCCA   4991	<b></b>				
1215 CAAGGADU G UACACCUG 3681 CAGGTGTA GGCTAGCTACAACGA AATCCTTG 4967 1217 AGGAUUGU A CACCUGUG 3682 CACAGGTG GGCTAGCTACAACGA ACAATCCT 4968 1219 GAUUGUAC A CCUGUGCA 3683 TGCACAGG GGCTAGCTACAACGA ACAATCCT 4968 1223 GUACACCU G UGCAGCAU 3684 ATGCTGCA GGCTAGCTACAACGA AGGTGTACA 4970 1225 CACCUGU G CAGCAUCC 3685 GGATGCTG GGCTAGCTACAACGA AGGTGTACA 4970 1225 CCUGUGCA G CAUCCAGU 3686 ACTGGATG GGCTAGCTACAACGA ACAGGTGT 4971 1228 CCUGUGCA G CAUCCAGU 3686 ACTGGATG GGCTAGCTACAACGA ACAGGTGT 4971 1228 CCUGUGCA G CAUCCAGU 3686 ACTGGATG GGCTAGCTACAACGA CACAGGTGT 4971 1228 CCUGUGCA G UGGCCUGA 3688 TCAGCCCA GGCTAGCTACAACGA CCACCAGG 4972 1239 UCCAGGUG G UGGCCUGA 3688 TCAGCCCA GGCTAGCTACAACGA CCACCAGA 4973 1239 UCCAGGUG G CUGAUGAC 3689 GTCATCAG GGCTAGCTACAACGA CCACCAGA 4973 1246 GGCUGAUG A CACAGAAG 3690 CTTGGTCA GGCTAGCTACAACGA CACTCAGCA 4975 1246 GGCUGAUG A CACAGAAG 3691 CTTCTTGG GGCTAGCTACAACGA CACCACCA 4976 1256 CAAGAACA C CACAUUUG 3693 CAAATGTG GGCTAGCTACAACGA CATCAGCC 4976 1256 CAAGAACA C CACAUUGU 3693 CAAATGTG GGCTAGCTACAACGA CTCTTCTT 4979 1251 AGAACAGC A CAUUUGUC 3693 CAAATGTG GGCTAGCTACAACGA CTTCTTCT 4979 1252 AACAGCAC A UUUGUCAG 3695 CTGACAAA GGCTAGCTACAACGA CTGTTCTT 4980 1257 UUGUCAGG G UCCAUGAA 3695 CTGACAAA GGCTAGCTACAACGA CTGTTCT 4981 1257 UUGUCAGG G UCCAUGAA 3697 TTCATGGA GGCTAGCTACAACGA CTGTTCT 4981 1257 CAGGGUCC A UGAAAAAC 3698 GTTTTCA GGCTAGCTACAACGA CTGACAA 4983 1277 CAGGGUCC A UGAAAAAAC 3698 GTTTTCA GGCTAGCTACAACGA CTGACAA 4983 1271 CAGGGUCC A UGAAAAAAC 3698 GTTTTCA GGCTAGCTACAACGA CCTGACAA 4983 1271 CAGGGUCC A UGAAAAAC 3699 ACAAAAGG GGCTAGCTACAACGA CCTGACAA 4983 1271 CAGGGUCC A UGAAAAAC 3699 ACAAAAGG GGCTAGCTACAACGA CCTGACAA 4983 1271 CAGGGUCC A UGAAAAAC 3700 AAAAGGA GGCTAGCTACAACGA AACAAAAG 4983 1271 CAGGGUCC A UGAAAAAC 3700 AAAAGGA GGCTAGCTACAACGA AACAAAAG 4983 1271 CAGGGUCC A UGAAAAAC 3700 AAAAGGA GGCTAGCTACAACGA ACAAAAAG 4983 1271 AUGUCAGG G UGCAUGA 3701 CCCACCG GGCTAGCTACAACGA ACAAAAAG 4983 1301 UGGAAGCC A CGGGGGG 3700 AAAAGGA GGCTAGCTACAACGA ACCACTCC 4990 1314 GGCAAGGA G CUCGAGAA 3701 CCCACCG GGCTAGCTACAACGA					
1217   AGGAUUGU A CACCUGUIG   3682   CACAGGTG GGCTAGCTACAACGA ACAATCCT   4968   1219   GAUUGUAC A CCUGUIGCA   3683   TGCACAGG GGCTAGCTACAACGA AGGTACTACACCU   GUCAGCAU   3685   GATGCTGC GGCTAGCTACAACGA AGGTGTTAC   4969   1228   GUACACCU G UGCAGCAU   3685   GGATGCTG GGCTAGCTACAACGA ACAGTGT   4971   1228   CCUGUIGCA G CAUCCAGU   3686   ACTGGTG GGCTAGCTACAACGA TGCACAGG   4972   1230   UGUGCAGC A UCCAGUIG   3688   TCAGCCCG GGCTAGCTACAACGA TGCACAGG   4973   1225   AGCAUCCA G UGGGCUGA   3688   TCAGCCCA GGCTAGCTACAACGA TGCACAGG   4973   1225   AGCAUCCA G UGGGCUGA   3688   TCAGCCCA GGCTAGCTACAACGA TGCACAGG   4974   1229   UCCAGUIGG G CUGAUGAC   3689   GTCATCAG GGCTAGCTACAACGA CCACTGGA   4975   1224   GUGGGCUGA A UGACCAAG   3690   CTTGGTCA GGCTAGCTACAACGA CCACTGGA   4975   1224   GUGGGCUGA A UGACCAAG   3691   CTTCTTGG GGCTAGCTACAACGA CACTCAGCC   4976   1226   GAGAAGAA A CAGCACAU   3692   ATTTGCTG GGCTAGCTACAACGA CATCAGCC   4977   1256   CAACAAGA A CAGCACAU   3693   CAAATGTG GGCTAGCTACAACGA TCTTCTTG   4978   1251   AGAACAGC A CAUUUGU   3694   GACAAATG GGCTAGCTACAACGA TCTTCTTG   4978   1251   AGAACAGC A UUUGUCAG   3695   CTGACAAA GGCTAGCTACAACGA TCTTCTT   4980   1263   AACAGCAC A UUUGUCAG   3695   GACCCTGA GGCTAGCTACAACGA GTGCTTCT   4981   1267   GUCACAUUU G UCAGGGUU   3699   ACAAAAGG GCTAGCTACAACGA CCTGACAA   4981   1277   CAGGGUCC A UGAAAAAC   3699   TTCATGGA GGCTAGCTACAACGA CCTGACAA   4982   1273   UUGUCAGG G UCCAUGAA   3697   TTCATGGA GGCTAGCTACAACGA CTTTCTAG   4984   1284   CAUGAAAA A CCUUUUG   3699   ACAAAAG GGCTAGCTACAACGA CTTTCTAG   4986   1294   CUUUUGU G UUGUUGU   3700   AAAAGGA GGCTAGCTACAACGA CTTTCTAG   4986   1294   CUUUUGU G UUGUUGU   3700   AAAAGGA GGCTAGCTACAACGA AAAAAG   4987   1294   CUUUUGU G UUGUUGU   3701   ACAAAAG GGCTAGCTACAACGA AACAAAAG   4987   1294   CUUUUGU G UUGUUGU   3701   ACAAAAG GGCTAGCTACAACGA ACAAAAG   4987   1294   CUUUUGU G UUGUUGU   3701   ACAAAAG GGCTAGCTACAACGA ACCAAAAG   4987   1294   CUUUUGGAA G UGGCAGAA   3702   CCATGCCA GGCTAGCTACAACGA ACCATTCCA   4998   1304   GUGAGAGC G UGGGAG					
1219 GAUUGUAC A CCUGUGCA 3683 TGCACAGG GGCTAGCTACAACGA GTACAATC 4969 1223 GUACACCU G UGCAGCAU 3684 ATGCTGCA GGCTAGCTACAACGA AGGTGTAC 4970 1225 ACACCUGU G CAGCAUCC 3685 GGATGCTG GGCTAGCTACAACGA ACGGTGT 4971 1228 CCUGUGCA G CAUCCAGU 3686 ACTGGATG GGCTAGCTACAACGA TGCACAGG 4972 1230 UGUGCAGC A UCCAGUGG 3687 CCACTGGA GGCTAGCTACAACGA TGCACAGG 4973 1235 AGCAUCCA G UGGGCUGA 3688 TCAGCCCA GGCTAGCTACAACGA TGCACAGG 4973 1235 AGCAUCCA G UGGGCUGA 3688 TCAGCCCA GGCTAGCTACAACGA TGGATGCA 4973 1235 UCCAGUGG G CUGAUGAC 3689 GTCATCAG GGCTAGCTACAACGA TGGATGCA 4975 1243 GUGGGCUG A UGACCAAG 3699 CTTGGTCA GGCTAGCTACAACGA CCACTGGA 4975 1243 GUGGGCUG A UGACCAAG 3699 CTTGGTCA GGCTAGCTACAACGA CACCCCAC 4976 1246 GGCUGAUGA CCAAGAAG 3691 CTTCTTGG GGCTAGCTACAACGA CATCAGCC 4976 1256 CAAGAAGA A CAGCACAU 3692 ATGTGCTG GGCTAGCTACAACGA CATCAGCC 4977 1256 CAAGAAGA A CAGCACAU 3692 CATCTGCT GGCTAGCTACAACGA TCTTCTTG 4978 1259 GAAGAACA C ACAUUUGU 3693 CAAATGTG GGCTAGCTACAACGA TCTTCTTC 4979 1251 AGAACAGC A CUUUUGCA 3695 CACACAUUG GCTAGCTACAACGA TGTTCTTC 4979 1261 AGAACAGC A CUUUUGCA 3695 CTGACAAA GGCTAGCTACAACGA GTGCTTCT 4980 1263 AACAGCA A UUUGUCAG 3695 CTGACAAA GGCTAGCTACAACGA GTGCTTCT 4981 1264 CAUGAAAA A CCUUUUGG 3695 CTGACAAA GGCTAGCTACAACGA GTGCTTGT 4981 1277 CAGGGUCC A UGAAAAAC 3698 GTTTTTCA GGCTAGCTACAACGA GACCCTG 4984 1278 UUGUCAGG G UCCAUGAA 3697 TTCATGGA GGCTAGCTACAACGA TTTTCATG 4985 1279 AACCUUU G UUGUCUUU 3700 AAAAGCAA GGCTAGCTACAACGA AAAAGGT TTTCATG 4985 1291 AACCUUU G UUGUCUUU 3700 AAAAGCAA GGCTAGCTACAACGA AAAAGGT 4986 1294 CUUUUGUA G CUUUUGGA 3701 TCCAAAAG GGCTAGCTACAACGA AAAAGGT 4987 1304 UUUUGGAA G UGGCAUGG 3702 CCATGCCA GGCTAGCTACAACGA AAAAGGT 4987 1304 UUUUGAA G UUGCUUUU 3700 AAAAGCAA GGCTAGCTACAACGA AAAAGGT 4987 1309 GAAGUGG C AUGAAAUC 3704 AGATTCCA GGCTAGCTACAACGA CACTTCC 4991 1314 GGCAUGGA A UCCUUGGU 3705 ACCAGGAG GGCTAGCTACAACGA CACTTCC 4991 1321 AAUCUCGG G UGGAAGC 3706 GGCTACCACG GGCTACCAACGA CACTTCC 4991 1321 AAUCUCGG G UGGAAGC 3706 GGCTACCACG GGCTACCAACGA CCCCCC 4991 1324 GUGGGGAG C CUUCAGAA 3709 CCCCCC GGCTAGCTACAACGA CCCCCC					
1223 GUACACCU G UGCAGCALU 3684 ATGCTGCA GGCTAGCTACAACGA AGGTGTAC 4970 1225 ACACCUGU G CAGCAUCC 3685 GGATGCTG GGCTAGCTACAACGA ACAGGTGT 4971 1228 CCUGUIGCA G CAUCCAGU 3686 ACTGGATG GGCTAGCTACAACGA TGCACAGG 4972 1230 UGUIGCAGC A UCCAGUGG 3687 CCACTGGA GGCTAGCTACAACGA TGCACAGG 4973 1235 AGCAUCCA G UGGGCUGA 3688 TCAGCCCA GGCTAGCTACAACGA GCTGCACA 4973 1235 AGCAUCCA G UGGGCUGA 3688 TCAGCCCA GGCTAGCTACAACGA TGGATGCT 4974 1239 UCCAGUGG G CUGAUGAC 3689 GTCATCAG GGCTAGCTACAACGA CCACTGGA 4975 1243 GUGGGCUG A UGACCAAG 3690 CTTGGTCA GGCTAGCTACAACGA CCACTGGA 4976 1246 GGCUGAUG A CCAAGAAG 3691 CTTCTTGG GGCTAGCTACAACGA CACCCAC 4976 1256 CAAGAAGA A CAGCACAU 3692 ATGTGCTG GGCTAGCTACAACGA CATCAGC 4977 1256 CAAGAAGA A CAGCACAU 3692 ATGTGCTG GGCTAGCTACAACGA TCTTCTTG 4978 1259 GAAGAACA G CACAUUUG 3693 CAAATGTG GGCTAGCTACAACGA TCTTCTTG 4979 1261 AGAACAGC A CAUUUGU 3694 GACAAATG GGCTAGCTACAACGA TCTTCTTG 4979 1261 AGAACAGC A CAUUUGU 3694 GACAAATG GGCTAGCTACAACGA GTGCTTCT 4980 1253 AACAGCAC A UUUGUCAG 3695 CTGACAAA GGCTAGCTACAACGA GTGCTTCT 4981 1267 GCACAUUU G UCAGGGUC 3696 GACCCTGA GGCTAGCTACAACGA AAATGTG 4982 1273 UUGUCAGG G UCCAUGAA 3697 TTCATGGA GGCTAGCTACAACGA AAATGTG 4982 1271 AUGUCAGG G UCCAUGAA 3698 GTTTTTCA GGCTAGCTACAACGA AAATGTG 4982 1272 CAGGGUC A UGAAAAAC 3698 GTTTTTCA GGCTAGCTACAACGA ACAAAAG 4983 1274 CAGGGUC A UGAAAAAC 3698 GTTTTTCA GGCTAGCTACAACGA AAATGTG 4984 1284 CAUGAAAA A CCUUUUGU 3700 AAAAGGAA GGCTAGCTACAACGA AAAAGGAT 4985 1291 AACCUUU G UUGCUUU 3700 AAAAGGAA GGCTAGCTACAACGA AAAAAAGGAT 4985 1301 UGGAAGUG G CAUGGAAU 3703 ATTCCAAAG GGCTAGCTACAACGA AACAAAA 4986 1301 UGGAAGUG G CAUGGAAU 3703 ATTCCATG GGCTAGCTACAACGA CACTTCCA 4989 1314 GGCAUGGA G UCGAGAAUC 3704 AGAATCCA GGCTAGCTACAACGA CACTTCCA 4999 1314 GGCAUGGA G UCGAGAAUC 3704 AGATTCCA GGCTAGCTACAACGA CACTTCCA 4999 1314 AGCUUU G G UGGAAGCC 3705 ACCAGGA GGCTAGCTACAACGA CACTTCCA 4991 1314 GGGGGGG G UGGAAGCC 3706 GGCTTCCA GGCTAGCTACAACGA CACTTCCA 4991 1314 GGGGGGG G UGGAAGCC 3706 GGCTACCACG GGCTAGCTACAACGA CCCTCCC 4991 1314 GGGGGGGA G UGCAGAAC 3711 CCACAGG GGCTAGCTACAACGA					
1225 ACACCUGU G CAGCAUCC 3685 GGATGCTG GGCTAGCAACGA ACAGGTGT 4971 1228 CCUGUGCA G CAUCCAGU 3686 ACTGGATG GGCTAGCTACAACGA TGCACAGG 4972 1230 UGUGCAGC A UCCAGUGG 3687 CCACTGGA GGCTAGCTACAACGA TGCACAGG 4973 1235 AGCAUCCA G UGGGCUGA 3688 TCAGCCCA GGCTAGCTACAACGA TGCACCA 4973 1239 UCCAGUGG G CUGAUGAC 3689 GTCACTACA GGCTAGCTACAACGA CCACTGGA 4975 1243 GUGGGCUG A UGACCAAG 3699 GTCATCAG GGCTAGCTACAACGA CCACTGGA 4975 1246 GGCUGAUG A CCAAGAAG 3691 CTTCTTGG GGCTAGCTACAACGA CAGCCCAC 4976 1246 GGCUGAUG A CCAAGAAG 3691 CTTCTTGG GGCTAGCTACAACGA CATCAGCC 4977 1256 CAAGAAGA A CAGCACAU 3692 ATGTGCTG GGCTAGCTACAACGA CATCAGCC 4977 1255 GAAGAACA C CACAUUUG 3693 CAAATGTG GGCTAGCTACAACGA TGTTCTTC 4978 1259 GAAGAACA C CACAUUUG 3693 CAAATGTG GGCTAGCTACAACGA TGTTCTTC 4980 1263 AACAGCCA A UUUGUCAG 3695 CTGACAAA GGCTAGCTACAACGA TGTTCTT 4980 1263 AACAGCAC A UUUGUCAG 3695 CTGACAAA GGCTAGCTACAACGA GTGCTTCT 4981 1267 GCACAUUU G UCAGGGUC 3696 GACCCTGA GGCTAGCTACAACGA GTGCTGTT 4981 1267 GCACAUUU G UCAGGGUC 3696 GACCCTGA GGCTAGCTACAACGA AAATGTGC 4982 1273 UUGUCAGG G UCCAUGAA 3697 TTCATGGA GGCTAGCTACAACGA CGTGACAA 4983 1277 CAGGGUC A UGAAAAAC 3699 GTTTCATGA GGCTAGCTACAACGA CGTGACAA 4983 1277 CAGGGUC A UGAAAAAC 3699 GTTTCTTCA GGCTAGCTACAACGA CTTGACAA 4983 1284 CAUGAAAA A CCUUUUGU 3700 AAAAGGAA GGCTAGCTACAACGA TTTTCATG 4985 1291 AACCUUUU G UUGCUUUU 3700 AAAAGCAA GGCTAGCTACAACGA AAAAAGGT 4986 1294 CUUUUGUA G CUUUUGGA 3701 TCCAAAAA GGCTAGCTACAACGA AACAAAAG 4987 1307 UGGAAGUG C AUGGAAUU 3700 AAAAGCAA GGCTAGCTACAACGA AACAAAAG 4987 1308 UGUUUGAA A UCCUUGGU 3705 ACCAGAGA GGCTAGCTACAACGA AACAAAAG 4989 1314 GGCAUGGA A UCGCAUGG 3706 GGCTTCCA GGCTAGCTACAACGA CACTTCCA 4989 1314 GGCAUGGA A UCCCUGGU 3705 ACCAGAGA GGCTAGCTACAACGA CACTTCCA 4990 1314 GGCAUGGA A UCCCUGGU 3706 GGCTTCCA GGCTAGCTACAACGA CACTTCCA 4991 1321 AAUCUCUG G UGGAAGCC 3706 GGCTTCCA GGCTAGCTACAACGA CACGACTTC 4991 1321 AAUCUCGA G UGGGAGGA 3709 CTCCCCC GGCTAGCTACAACGA CAGAGAT TCCACCA 4991 1333 AAGCCACG G UGGGGAGA 3709 CTCCCCC GGCTAGCTACAACGA CAGAGAT TCCACCA 4991 1334 GGGGGGGA G CUUUCAGAA 3711 CTCAC	<del></del>				
1228   CCUGUIGCA G CAUCCAGU   3686   ACTGGATG GGCTAGCTACAACGA TGCACAGG   4972   1230   UGUIGCAGC A UCCAGUGG   3687   CCACTGGA GGCTAGCTACAACGA GCTGCACA   4973   1235   ASCAUCCA G UGGGCUGA   3688   TCAGCCCA GGCTAGCTACAACGA CCACTGGA   4974   1239   UCCAGUGG G CUGAUGAC   3689   GTCATCAG GGCTAGCTACAACGA CACCCAC   4976   1243   GUGGGCUG A UGACCAAG   3689   GTCATCAG GGCTAGCTACAACGA CAGCCAC   4976   1246   GGCUGAUGA   CCACAGGA   3690   CTTGGTCA GGCTAGCTACAACGA CATCAGCC   4977   1256   CAAGAAGA A CAGCACAU   3692   ATGTGCTG GGCTAGCTACAACGA CATCAGCC   4977   1259   GAAGAACA C CACAUUUG   3693   CAAATGTG GGCTAGCTACAACGA TCTTCTC   4979   1261   AGAACAGC A CAUUUGUC   3694   GACAAATG GGCTAGCTACAACGA CTGTTCT   4980   1263   AACAGCACA UUUGUCAG   3695   CTGACAAA GGCTAGCTACAACGA GTGCTGT   4981   1267   GCACAUUU G UCAGGGUC   3695   GACCCTGA GGCTAGCTACAACGA CATCAGACCA   4982   1273   UUGUCAGG GU UCCAUGAA   3697   TTCATGGA GGCTAGCTACAACGA AAATGTGC   4982   1273   UUGUCAGG GU UCCAUGAA   3698   GTTTTCA GGCTAGCTACAACGA AAATGTGC   4984   1284   CAUGAAAA A CCUUUUGU   3699   ACAAAAGG GGCTAGCTACAACGA AAATGTGC   4985   1291   AACCUUUU G UUUUUGGA   3700   AAAAGGA GGCTAGCTACAACGA AAAAGGTT   4986   1294   CUUUUGUA G CUUUUGGA   3700   AAAAGGA GGCTAGCTACAACGA AAAAGGAT   4986   1294   CUUUUGUA G CUUUUGGA   3701   TCCAAAAG GGCTAGCTACAACGA AAAAAGAT   4988   1307   UGGAAGUG G CACGGAAU   3703   ATTCCATG GGCTAGCTACAACGA AACAAAAA   4988   1309   GAAGUGGC A UGGAAUCU   3704   AGATTCCA GGCTAGCTACAACGA ACCAACGA TCCAACAGA   4988   1309   GAAGUGGC A UGGAAUCU   3704   AGATTCCA GGCTAGCTACAACGA CACTTCCA   4990   1314   GGCAUGG A UCCUUGGU   3705   ACCAGGAG GGCTAGCTACAACGA CACTTCCA   4991   1321   AAUCUCUG G UGGAAGCC   3706   GGCTTCCA GGCTAGCTACAACGA CACTTCCA   4991   1321   AAUCUCUG G UGGAAGCC   3706   GGCTTCCA GGCTAGCTACAACGA CACTTCCA   4991   1321   AAUCUCUG G UUGAGA   3710   CCCAGGGG GGCTAGCTACAACGA CACTTCCA   4991   1321   AAUCUCUG G UUGAGAA   3711   TCTGACA GGCTAGCTACAACGA CAGGACTT   4992   1333   AGGCACG G UGUCAGA   3711   CTGACAG GGCTAGCTACAACGA CAGGACTC					
1230         UGUGCAGC A UCCAGUGG         3687         CCACTGGA GGCTAGCTACAACGA GCTGCACA         4973           1235         AGCAUCCA G UGGGCUGA         3688         TCAGCCCA GGCTAGCTACAACGA TGGATGCT         4974           1239         UCCAGUGG G CUGAUGAC         3689         GTCATCAG GGCTAGCTACAACGA CACCACTGGA         4975           1243         GUGGGCUG A UGACCAAG         3690         CTTCTTGG GGCTAGCTACAACGA CATCAGCC         4976           1246         GGCUGAUG A CCAAGAAG         3691         CTTCTTGG GGCTAGCTACAACGA CATCATCACGC         4977           1256         CAAGAAGA A CAGCACAU         3692         ATGTGCTG GGCTAGCTACAACGA TCTTCTTC         4978           1259         GAAGAACA G CACAUUG         3693         CAAATGTG GGCTAGCTACAACGA TCTTCTTC         4979           1261         AGAACGCA C A CUUUGUCAG         3694         GACAATG GGCTAGCTACAACGA GCTGTTCT         4980           1267         GCACAUUU G UCAGGGUC         3695         GACCCTGA GGCTAGCTACAACGA TCTCTCT         4981           1273         UUGUCAGG G UCCAUGAA         3697         TTCATGGA GGCTAGCTACAACGA AAAAGTT         4983           1271         CAGGGUC A UGAAAAA         3698         GTTTTCTA GGCTACAACGA AAAAAGTTTCATG         4981           1294         CUUUUGU G UUGUUUUU         3700         AAAAGGA GGCTAGCTACAACGA ATCAAAAA					
1235         AGCAUCCA G UGGGCUGA         3688         TCAGCCCA GGCTAGCTACAACGA TGGATGCT         4974           1239         UCCAGUGG G CUGAUGAC         3689         GTCATCAG GGCTAGCTACAACGA CACCCAC         4975           1243         GUGGGCUG A UGACCAAG         3690         CTTGGTCA GGCTAGCTACAACGA CAGCCCAC         4976           1246         GGCUGAUG A CAGCACAU         3692         ATGTGCTG GGCTAGCTACAACGA CATCAGCC         4977           1256         CAAGAAGA A CAGCACAU         3692         ATGTGCTG GGCTAGCTACAACGA TCTTCTTG         4978           1259         GAAGAACA G CACAUUUG         3693         CAAATGTG GGCTAGCTACAACGA TCTTCTTG         4979           1261         AGAACAGC A CAUUUGU         3694         GACCAAATG GGCTAGCTACAACGA GTGTTCTT         4980           1263         AACAGCAC A UUUGUCAG         3695         CTGACAAA GGCTAGCTACAACGA GTGCTTT         4981           1267         GCACAUUU G UCAGGGUC         3696         GACCCTGA GGCTAGCTACAACGA AATGTGC         4982           1277         CAGGGCC C UGAAAAAAC         3698         GTTTTCTAGGA GGCTAGCTACAACGA AATGTGC         4983           1277         CAGGGCC C UGAAAAAAC         3698         GTTTTCTAGGA GGCTAGCTACAACGA TTTTCTAG         4981           1294         CUUUUGU G UUGCUUU         3700         AAAAGCAA GCCTAGCTACAACGA AACAAACGA					
1239         UCCAGUGG G CUGAUGAC         3689         GTCATCAG GGCTAGCTACAACGA CCACTGGA         4975           1243         GUGGCUG A UGACCAAG         3690         CTTGGTCA GGCTAGCTACAACGA CAGCCCAC         4976           1246         GGCUGAUG A CCAAGAAG         3691         CTTCTTGG GGCTAGCTACAACGA CATCAGCC         4977           1256         CAAGAAGA A CAGCACAU         3692         ATGTGCTG GGCTAGCTACAACGA TCTTCTTG         4978           1259         GAAGACA G CACAUUUG         3693         CAAATGTG GGCTAGCTACAACGA TGTTCTTC         4979           1261         AGACACGC A CAUUUGU G 3694         GACAATG GGCTAGCTACAACGA GCTGTTCT         4980           1263         AACAGCAC A UUUGUCAG 3695         CTGACAAA GGCTAGCTACAACGA GTGTGTT         4981           1267         GCACAUUU G UCAGGGUC         3696         GACCCTGA GGCTAGCTACAACGA GTGCTGTACAACGA CTGACAA         4982           1277         CAGGGUCC A UGAAAAAC         3698         GTTTTTCATGGA GGCTAGCTACAACGA CCTGACAA         4983           1277         CAGGGUCC A UGAAAAAC         3699         ACAAAAGG GGCTAGCTACAACGA TTTCATG         4985           1294         CUUUUGU G UUGCUUUGU 3700         ACAAAAGG GGCTAGCTACAACGA TTCCATG         4986           1294         CUUUUGU G CUUUUGGA         3701         TCCAAAAG GGCTAGCTACAACGA ACTTCCA         4987					
1243 GUGGGCUG A UGACCAAG 3690 CTTGGTCA GGCTAGCTACAACGA CAGCCCAC 4976 1246 GGCUGAUG A CCAAGAAG 3691 CTTCTTGG GGCTAGCTACAACGA CATCAGCC 4977 1256 CAAGAAGA A CAGCACAU 3692 ATGTGCTG GGCTAGCTACAACGA CATCAGCC 4977 1259 GAAGAACA G CACAUUUG 3693 CAAATGTG GGCTAGCTACAACGA TCTTCTTG 4978 1259 GAAGAACA C CACAUUUG 3693 CAAATGTG GGCTAGCTACAACGA TCTTCTTC 4979 1261 AGAACAGC A CAUUUGUCAG 3695 CTGACAAA GGCTAGCTACAACGA GTCTGTT 4980 1263 AACAGCAC A UUUGUCAG 3695 CTGACAAA GGCTAGCTACAACGA GTCTGTT 4981 1267 GCACAUUU G UCAGGGUC 3696 GACCCTGA GGCTAGCTACAACGA AAATGTGC 4981 1277 CAGGGUCC A UGAAAAAC 3698 GTTTTCA GGCTAGCTACAACGA AAATGTGC 4982 1273 UUGUCAGG G UCCAUGAA 3697 TTCATGGA GGCTAGCTACAACGA GAACCTTG 4984 1284 CAUGAAAA A CCUUUUGU 3699 ACAAAAGG GGCTAGCTACAACGA CTTCATCAA 4985 1291 AACCUUUU G UUGCUUUU 3700 AAAAGCAA GGCTAGCTACAACGA AAAAGGTT 4986 1294 CUUUUGGU G CUUUUGGA 3701 TCCAAAAG GGCTAGCTACAACGA AACAAAAG 4987 1304 UUUUGGAA G UGGCAUGA 3702 CCATGCCA GGCTAGCTACAACGA AACAAAAG 4987 1307 UGGAAGUG G CAUGGAAU 3703 ATTCCATG GGCTAGCTACAACGA ACCAAAAG 4989 1314 GGCAUGGA A UCGUCUGU 3704 AGATTCCA GGCTAGCTACAACGA CACTTCCA 4989 1314 GGCAUGGA A UCGCAUGGU 3705 ACCAGAGA GGCTAGCTACAACGA CACTTCCA 4991 1314 GACAUGAA G CACGGUG 3706 GGCTTCCA GGCTAGCTACAACGA CACTTCCA 4991 1321 AAUCUCUG G UGGAAGCC 3706 GGCTTCCA GGCTAGCTACAACGA CACTTCCA 4991 1321 AAUCUCUG G UGGAAGCC 3706 GGCTTCCA GGCTAGCTACAACGA CAGAGATT 4992 1327 UGGUGGAA G CCACGGUG 3707 CACCGTGG GGCTAGCTACAACGA CAGAGATT 4992 1328 AGCCACG G UGGGAGG 3708 CCCCCCC GGCTAGCTACAACGA CAGAGATT 4992 1331 AGCCACG G UGGGGGA 3709 CTCCCCCA GGCTAGCTACAACGA CGTGCCCC 4991 1343 GGGGAGCC A CGGUGGG 3708 CCCCCCC GGCTAGCTACAACGA CGTGCCCC 4996 1343 GGGGAGCC G UGCAGAAUC 3712 GATTCTAG GGCTAGCTACAACGA CCTCCCC 4996 1343 GGGGAGC G UGCAGAAUC 3712 GATTCTAG GGCTAGCTACAACGA CCTCCCC 4996 1343 GGGGAGCC G UCCAGAAC 3711 TTCTGACA GGCTAGCTACAACGA CCTCCCC 4996 1351 GUGUCAGA A UCCCUGC 3713 CGCAGGG GGCTAGCTACAACGA CCTCCCC 4996 1357 GAAUCCCU G CGAAGUAC 3712 GATTCTGA GGCTAGCTACAACGA ACGCTCCC 4996 1357 GAAUCCCU G CGAAGUAC 3712 GATTCTGA GGCTAGCTACAACGA AC	<b></b>	<del></del>			
1246         GGCUGAUG A CCAAGAAG         3691         CTTCTTGG GGCTAGCTACAACGA CATCAGCC         4977           1256         CAAGAAGA A CAGCACAU         3692         ATGTGCTG GGCTAGCTACAACGA TCTTCTTG         4978           1259         GAAGAACA G CACAUUUG         3693         CAAATGTG GGCTAGCTACAACGA TGTTCTTC         4979           1261         AGAACAGC A CAUUUGUC         3694         GACAAATG GGCTAGCTACAACGA GTGCTGTT         4980           1263         AACAGCAC A UUUGUCAG         3695         CTGACAAA GGCTAGCTACAACGA GTGCTGTT         4981           1267         GGCACAUUU G UCCAUGAA         3696         GACCCTGA GGCTACAACGA AAATGTGC         4982           1273         UUGUCAGG G UCCAUGAA         3697         TTCATGGA GGCTACAACGA CCTGACAA         4983           1277         CAGGGUCC A UGAAAAAC         3698         GTTTTTCA GGCTACAACGA CTTCATCA         4984           1284         CAUGAAAA A CCUUUUGAA         3699         ACAAAAGG GGCTACAACGA TTTCATG         4985           1294         CUUUUGUU         3700         AAAAGCAA GGCTAGCTACAACGA TTCCAAAAG         4987           1304         UUUUGGAA G UGGCAUGG         3702         CCATGCCA GGCTAGCTACAACGA CACTTCCA         4988           1307         UGGAAGCG         A UGGAAUCU         3704         AGATTCCA GGCTACCAACGA CACTTCCA <td< td=""><td></td><td></td><td></td><td></td><td></td></td<>					
1256 CAAGAAGA A CAGCACAU 3692 ATGTGCTG GGCTAGCTACAACGA TCTTCTTG 4978 1259 GAAGAACA G CACAUUUG 3693 CAAATGTG GGCTAGCTACAACGA TGTTCTTC 4979 1261 AGAACAGC A CAUUUGUC 3694 GACAAATG GGCTAGCTACAACGA GCTGTTCT 4980 1263 AACAGCAC A UUUGUCAG 3695 CTGACAAA GGCTAGCTACAACGA GTGCTGTT 4981 1267 GCACAUUU G UCAGGGUC 3696 GACCCTGA GGCTAGCTACAACGA AAATGTGC 4982 1273 UUGUCAGG G UCCAUGAA 3697 TTCATGGA GGCTAGCTACAACGA AAATGTGC 4982 1273 UUGUCAGG G UCCAUGAA 3697 TTCATGGA GGCTAGCTACAACGA CGTGCTCT 4981 1274 CAGGGUCC A UGAAAAAC 3698 GTTTTTCA GGCTAGCTACAACGA CGACCCTG 4984 1284 CAUGAAAA A CCUUUUGU 3699 ACAAAAGG GGCTAGCTACAACGA TTTTCATG 4985 1291 AACCUUUU G UUGCUUUU 3700 AAAAGCAA GGCTAGCTACAACGA AACAGAT 4986 1294 CUUUUGGU G CUUUUGGA 3701 TCCAAAAG GGCTAGCTACAACGA AACAAAAG 4987 1304 UUUUGGAA G UGGCAUGG 3702 CCATGCCA GGCTAGCTACAACGA AACAAAAG 4987 1307 UGGAAGUG G CAUGGAAU 3703 ATTCCATG GGCTAGCTACAACGA CACTTCCA 4989 1309 GAAGUGGC A UGGAAUCU 3704 AGATTCCA GGCTAGCTACAACGA CACTTCCA 4989 1314 GGCAUGGA A UCUCUGGU 3705 ACCAGAGA GGCTAGCTACAACGA CCACTTCC 4990 1314 GGCAUGGA A UCUCUGGU 3705 ACCAGAGA GGCTAGCTACAACGA CACTTCCA 4991 1321 AAUCUCUG G UGGAACCC 3706 GGCTTCCA GGCTAGCTACAACGA CCACTTCC 4991 1321 AAUCUCUG G UGGAACCC 3706 GGCTTCCA GGCTAGCTACAACGA CAGAGATT 4992 1327 UGGUGGAA G CCACGGUG 3707 CACCGTGG GGCTAGCTACAACGA CGAGATT 4992 1328 UGGAAGCC A CGGUGGGG 3708 CCCCACCG GGCTAGCTACAACGA CGACGTTCCA 4993 1333 AAGCCACG G UGGGGGG 3709 CTCCCCCA GGCTAGCTACAACGA CGTTCCA 4995 1341 GUGGGGAA G CCACGGUG 3710 CTGACACG GGCTAGCTACAACGA CGTTCCA 4995 1342 GGGGAGCG G UGGAGAU 3711 TTCTGACA GGCTAGCTACAACGA CGTGCTTCCA 4996 1343 GGGGGAGC G UGCAGAAUC 3712 GATTCTGA GGCTAGCTACAACGA CGTGCTTCCA 4995 1345 GGGGAGCG G UCCAGAAUC 3712 GATTCTGA GGCTAGCTACAACGA CGTGCTCCC 4997 1345 GGGGAGCG G UCCAGAAUC 3712 GATTCTGA GGCTAGCTACAACGA CGTGCTCCC 4997 1345 GGGGAGCG G UCCAGAAUC 3712 GATTCTGA GGCTAGCTACAACGA CGTGCTCCC 4996 1357 GAAUCCCU G CGAAGUC 3714 GTACTTCG GGCTAGCTACAACGA CGTGCCCC 4999 1357 GAAUCCCU G CGAAGUC 3714 GTACTTCG GGCTAGCTACAACGA CTTCGCC 5002 1360 GUACCUUG G UUACCCAC 3717 GTGGGGTA GC					
1259   GAAGACA G CACAUUUG   3693   CAAATGTG GGCTAGCTACAACGA TGTTCTTC   4979   1261   AGAACAGC A CAUUUGUC   3694   GACAAATG GGCTAGCTACAACGA GCTGTTCT   4980   1263   AACAGCAC A UUUGUCAG   3695   CTGACAAA GGCTAGCTACAACGA GTGCTGTT   4981   1267   GCACAUUU G UCAGGGUC   3696   GACCCTGA GGCTAGCTACAACGA AAATGTGC   4982   1273   UUGUCAGG G UCCAUGAA   3697   TTCATGGA GGCTAGCTACAACGA AAATGTGC   4982   1277   CAGGGUCC A UGAAAAAC   3698   GTTTTTCA GGCTAGCTACAACGA GGACCCTG   4984   1284   CAUGAAAA A CCUUUUGU   3699   ACAAAAGG GGCTAGCTACAACGA GGACCCTG   4985   1291   AACCUUUU G UUGCUUUU   3700   AAAAGGAA GGCTAGCTACAACGA AACAAAAG   4987   1294   CUUUUGUA   3701   TCCAAAAG GGCTAGCTACAACGA AACAAAAG   4987   1304   UUUUGGAA G UGGCAUGG   3702   CCATGCCA GGCTAGCTACAACGA AACAAAAG   4988   1307   UGGAAGUG G CAUGGAAU   3703   ATTCCATG GGCTAGCTACAACGA ACCAAAA   4988   1309   GAAGUGGC A UGGAAUCU   3704   AGATTCCA GGCTAGCTACAACGA CACTTCCA   4990   1314   GGCAUGGA A UCUCUGGU   3705   ACCAGAGA GGCTAGCTACAACGA CCACTTC   4990   1321   AAUCUUCUG G UGGAAGCC   3706   GGCTTCCA GGCTAGCTACAACGA TCCATGC   4991   1321   AAUCUUCUG G UGGAAGCC   3706   GGCTTCCA GGCTAGCTACAACGA TCCATGC   4991   1321   AAUCUUCUG G UGGAAGCC   3706   GGCTTCCA GGCTAGCTACAACGA TCCATGC   4991   1333   AGGCCACG G UGGGGGG   3708   CCCCACCG GGCTAGCTACAACGA TCCACCA   4992   1333   AGGCCACG G UGGGGGG   3708   CCCCACCG GGCTAGCTACAACGA TCCACCA   4994   1333   AGGCCACG G UGGGGGAG   3709   CTCCCCCA GGCTAGCTACAACGA CGTCCACCA   4994   1333   AGGCCACG G UGGGGGAG   3709   CTCCCCCA GGCTAGCTACAACGA CGTCCCC   4997   1345   GGGGAGC G UGUCAGAA   3711   TTCTGACA GGCTAGCTACAACGA CGTCCCC   4997   1345   GGGGAGC G UGUCAGAA   3711   TTCTGACA GGCTAGCTACAACGA CGTCCCC   4998   1351   GUGUCAGA A UCCCUGCG   3713   CGCAGGGA GGCTAGCTACAACGA CGTCCCC   4998   1351   GUGUCAGA A UCCCUGCG   3713   CGCAGGGA GGCTAGCTACAACGA CGTCCCC   4998   1352   GAAUCCCU G CGAAGUAC   3714   GTACTTCG GGCTAGCTACAACGA CGAGGATTC   5000   1362   CUUGGAAGU A CCCUUGGU   3716   AACCAAGG GGCTAGCTACAACGA CTCCGCA   5000   1364   UGCCAA					
1261 AGAACAGC A CAUJUGUC 3694 GACAAATG GGCTAGCTACAACGA GCTGTTCT 4980 1263 AACAGCAC A UJUGUCAG 3695 CTGACAAA GGCTAGCTACAACGA GTGCTGTT 4981 1267 GCACAJUU G UCAGGGUC 3696 GACCCTGA GGCTAGCTACAACGA AAATGTGC 4982 1273 UJUGUCAGG G UCCAJGAA 3697 TTCATGGA GGCTAGCTACAACGA AAATGTGC 4982 1277 CAGGGUCC A UGAAAAAC 3698 GTTTTCA GGCTAGCTACAACGA CGTGCCTG 4984 1284 CAUGAAAA A CCUJUJUGU 3699 ACAAAAGG GGCTAGCTACAACGA GGACCCTG 4984 1291 AACCUJUU G UJUGCUJUU 3700 AAAAGGAA GGCTAGCTACAACGA AAAAGGTT 4986 1294 CUJUJUGU G CUJUJUGGA 3701 TCCAAAAA GGCTAGCTACAACGA AAAAGGTT 4986 1307 UJGAAGUG G CAUGGAAU 3702 CCATGCCA GGCTAGCTACAACGA TCCCAAAA 4988 1307 UJGAAGUG G CAUGGAAU 3703 ATTCCATG GGCTAGCTACAACGA TCCCAAAA 4988 1307 UJGAAGUG G CAUGGAAU 3704 AGATTCCA GGCTAGCTACAACGA CCACTTCC 4980 1314 GGCAUGGA A UCUCUGGU 3704 AGATTCCA GGCTAGCTACAACGA TCCATGCC 4991 1321 AAUCUCUG G UJGAAGCC 3706 GGCTTCCA GGCTAGCTACAACGA TCCATGCC 4991 1321 AAUCUCUG G UJGAAGCC 3706 GGCTTCCA GGCTAGCTACAACGA TCCATGCC 4991 1321 AUGGAGGC A CGGUGGGG 3708 CCCCACGG GGCTAGCTACAACGA TCCACCA 4993 1330 UJGAAGCC A CGGUGGGG 3708 CCCCACCG GGCTAGCTACAACGA TCCACCA 4994 1333 AAGCCACG G UJGGGGGA 3709 CTCCCCCA GGCTAGCTACAACGA TCCACCA 4994 1333 AAGCCACG G UJGGGGAAG 3710 CTGACACG GGCTAGCTACAACGA TCCCCAC 4994 1333 AAGCCACG G UJGGGGAAG 3709 CTCCCCCA GGCTAGCTACAACGA CGTGCCTT 4995 1341 GUGGGGAG G CUJUCAGA 3711 TTCTGACA GGCTAGCTACAACGA TCCCCCC 4997 1345 GGGGGGCG G UJUCAGAA 3711 TTCTGACA GGCTAGCTACAACGA CGTGGCTT 4995 1341 GUGGGAGA A UCCCUGCG 3713 CGCAGGGA GGCTAGCTACAACGA TCCCCCC 4997 1345 GGGAGCGU G UJCAGAAUC 3712 GATTCTGA GGCTAGCTACAACGA TCCCCCC 4997 1345 GGGAGCGU G UCAGAAUC 3712 GATTCTGA GGCTAGCTACAACGA TCCCCCC 4998 1357 GAAUCCCU G CGAAGUAC 3714 GTACTTCG GGCTAGCTACAACGA TCTGACAC 4999 1357 GAAUCCCU G CGAAGUAC 3714 GTACTTCG GGCTAGCTACAACGA ACGGATTC 5000 1362 CUUGCGAA G UACCUUGG 3715 CCCAGGGGA GGCTAGCTACAACGA ACGGATCC 5000 1364 UGCGAAGU A CCUUGGU 3716 AACCAAGG GGCTAGCTACAACGA ACGGATCC 5000 1364 UGCGAAGU A CCUUGGU 3716 AACCAAGG GGCTAGCTACAACGA CAAGGATC 5000 1360 UACCUUG G UUACCCAC 3717 GTGGGTAA GGCTACCAAC	<b></b>				
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1309 GAAGUGGC A UGGAAUCU 3704 AGATTCCA GGCTAGCTACAACGA GCCACTTC 4990 1314 GGCAUGGA A UCUCUGGU 3705 ACCAGAGA GGCTAGCTACAACGA TCCATGCC 4991 1321 AAUCUCUG G UGGAAGCC 3706 GGCTTCCA GGCTAGCTACAACGA CAGAGATT 4992 1327 UGGUGGAA G CCACGGUG 3707 CACCGTGG GGCTAGCTACAACGA TTCCACCA 4993 1330 UGGAAGCC A CGGUGGGG 3708 CCCCACCG GGCTAGCTACAACGA GGCTTCCA 4994 1333 AAGCCACG G UGGGGGAG 3709 CTCCCCCA GGCTAGCTACAACGA CGTGGCTT 4995 1341 GUGGGGGA G CGUGUCAG 3710 CTGACACG GGCTAGCTACAACGA TCCCCCAC 4996 1343 GGGGGAGC G UGUCAGAA 3711 TTCTGACA GGCTAGCTACAACGA CCTCCCC 4997 1345 GGGAGCGU G UCAGAAUC 3712 GATTCTGA GGCTAGCTACAACGA ACGCTCCC 4998 1351 GUGUCAGA A UCCCUGCG 3713 CGCAGGGA GGCTAGCTACAACGA TCTGACAC 4999 1357 GAAUCCCU G CGAAGUAC 3714 GTACTTCG GGCTAGCTACAACGA AGGGATTC 5000 1362 CCUGCGAA G UACCUUGG 3715 CCAAGGTA GGCTAGCTACAACGA TTCGCAGG 5001 1364 UGCGAAGU A CCUUGGUU 3716 AACCAAGG GGCTAGCTACAACGA ACTTCGCA 5002 1370 GUACCUUG G UUACCCAC 3717 GTGGGTAA GGCTAGCTACAACGA CAAGGTAC 5003	<del></del>				
1314 GGCAUGGA A UCUCUGGU 3705 ACCAGAGA GGCTAGCTACAACGA TCCATGCC 4991 1321 AAUCUCUG G UGGAAGCC 3706 GGCTTCCA GGCTAGCTACAACGA CAGAGATT 4992 1327 UGGUGGAA G CCACGGUG 3707 CACCGTGG GGCTAGCTACAACGA TTCCACCA 4993 1330 UGGAAGCC A CGGUGGGG 3708 CCCCACCG GGCTAGCTACAACGA GGCTTCCA 4994 1333 AAGCCACG G UGGGGGAG 3709 CTCCCCCA GGCTAGCTACAACGA CGTGGCTT 4995 1341 GUGGGGGA G CGUGUCAG 3710 CTGACACG GGCTAGCTACAACGA TCCCCCAC 4996 1343 GGGGAGCG G UGUCAGAA 3711 TTCTGACA GGCTAGCTACAACGA TCCCCCCC 4997 1345 GGGAGCGU G UCAGAAUC 3712 GATTCTGA GGCTAGCTACAACGA ACGCTCCC 4998 1351 GUGUCAGA A UCCCUGCG 3713 CGCAGGGA GGCTAGCTACAACGA TCTGACAC 4999 1357 GAAUCCCU G CGAAGUAC 3714 GTACTTCG GGCTAGCTACAACGA AGGGATTC 5000 1362 CCUGCGAA G UACCUUGG 3715 CCAAGGTA GGCTAGCTACAACGA TTCGCAGG 5001 1364 UGCGAAGU A CCUUGGUU 3716 AACCAAGG GGCTAGCTACAACGA ACTTCGCA 5002 1370 GUACCUUG G UUACCCAC 3717 GTGGGTAA GGCTAGCTACAACGA CAAGGTAC 5003				<del> </del>	
1321 AAUCUCUG G UGGAAGCC 3706 GGCTTCCA GGCTAGCTACAACGA CAGAGATT 4992 1327 UGGUGGAA G CCACGGUG 3707 CACCGTGG GGCTAGCTACAACGA TTCCACCA 4993 1330 UGGAAGCC A CGGUGGGG 3708 CCCCACCG GGCTAGCTACAACGA GGCTTCCA 4994 1333 AAGCCACG G UGGGGGAG 3709 CTCCCCCA GGCTAGCTACAACGA CGTGGCTT 4995 1341 GUGGGGAA G CGUGUCAG 3710 CTGACACG GGCTAGCTACAACGA TCCCCCAC 4996 1343 GGGGAGCG G UGUCAGAA 3711 TTCTGACA GGCTAGCTACAACGA GCTCCCC 4997 1345 GGGAGCGU G UCAGAAUC 3712 GATTCTGA GGCTAGCTACAACGA ACGCTCCC 4998 1351 GUGUCAGA A UCCCUGCG 3713 CGCAGGGA GGCTAGCTACAACGA TCTGACAC 4999 1357 GAAUCCCU G CGAAGUAC 3714 GTACTTCG GGCTAGCTACAACGA ACGGATTC 5000 1362 CCUGCGAA G UACCUUGG 3715 CCAAGGTA GGCTAGCTACAACGA TTCGCAGG 5001 1364 UGCGAAGU A CCUUGGUU 3716 AACCAAGG GGCTAGCTACAACGA ACTTCGCA 5002 1370 GUACCUUG G UUACCCAC 3717 GTGGGTAA GGCTAGCTACAACGA CAAGGTAC 5003					
1327 UGGUGGAA G CCACGGUG 3707 CACCGTGG GGCTAGCTACAACGA TTCCACCA 4993 1330 UGGAAGCC A CGGUGGGG 3708 CCCCACCG GGCTAGCTACAACGA GGCTTCCA 4994 1333 AAGCCACG G UGGGGGAG 3709 CTCCCCCA GGCTAGCTACAACGA CGTGGCTT 4995 1341 GUGGGGAA G CGUGUCAG 3710 CTGACACG GGCTAGCTACAACGA TCCCCCAC 4996 1343 GGGGAGCC G UGUCAGAA 3711 TTCTGACA GGCTAGCTACAACGA GCTCCCCC 4997 1345 GGGAGCGU G UCAGAAUC 3712 GATTCTGA GGCTAGCTACAACGA ACGCTCCC 4998 1351 GUGUCAGA A UCCCUGCG 3713 CGCAGGGA GGCTAGCTACAACGA TCTGACAC 4999 1357 GAAUCCCU G CGAAGUAC 3714 GTACTTCG GGCTAGCTACAACGA AGGGATTC 5000 1362 CCUGCGAA G UACCUUGG 3715 CCAAGGTA GGCTAGCTACAACGA TTCGCAGG 5001 1364 UGCGAAGU A CCUUGGUU 3716 AACCAAGG GGCTAGCTACAACGA ACTTCGCA 5002 1370 GUACCUUG G UUACCCAC 3717 GTGGGTAA GGCTAGCTACAACGA CAAGGTAC 5003	<b>-</b>				
1330 UGGAAGCC A CGGUGGGG 3708 CCCCACCG GGCTAGCTACAACGA GGCTTCCA 4994 1333 AAGCCACG G UGGGGGAG 3709 CTCCCCCA GGCTAGCTACAACGA CGTGGCTT 4995 1341 GUGGGGAA G CGUGUCAG 3710 CTGACACG GGCTAGCTACAACGA TCCCCCAC 4996 1343 GGGGAGCG G UGUCAGAA 3711 TTCTGACA GGCTAGCTACAACGA GCTCCCC 4997 1345 GGGAGCGU G UCAGAAUC 3712 GATTCTGA GGCTAGCTACAACGA ACGCTCCC 4998 1351 GUGUCAGA A UCCCUGCG 3713 CGCAGGGA GGCTAGCTACAACGA TCTGACAC 4999 1357 GAAUCCCU G CGAAGUAC 3714 GTACTTCG GGCTAGCTACAACGA AGGGATTC 5000 1362 CCUGCGAA G UACCUUGG 3715 CCAAGGTA GGCTAGCTACAACGA TCCGCAGG 5001 1364 UGCGAAGU A CCUUGGUU 3716 AACCAAGG GGCTAGCTACAACGA ACTTCGCA 5002 1370 GUACCUUG G UUACCCAC 3717 GTGGGTAA GGCTAGCTACAACGA CAAGGTAC 5003					~
1333 AAGCCACG G UGGGGGAG 3709 CTCCCCCA GGCTAGCTACAACGA CGTGGCTT 4995 1341 GUGGGGGA G CGUGUCAG 3710 CTGACACG GGCTAGCTACAACGA TCCCCCAC 4996 1343 GGGGAGCG G UGUCAGAA 3711 TTCTGACA GGCTAGCTACAACGA GCTCCCCC 4997 1345 GGGAGCGU G UCAGAAUC 3712 GATTCTGA GGCTAGCTACAACGA ACGCTCCC 4998 1351 GUGUCAGA A UCCCUGCG 3713 CGCAGGGA GGCTAGCTACAACGA TCTGACAC 4999 1357 GAAUCCCU G CGAAGUAC 3714 GTACTTCG GGCTAGCTACAACGA AGGGATTC 5000 1362 CCUGCGAA G UACCUUGG 3715 CCAAGGTA GGCTAGCTACAACGA TTCGCAGG 5001 1364 UGCGAAGU A CCUUGGUU 3716 AACCAAGG GGCTAGCTACAACGA ACTTCGCA 5002 1370 GUACCUUG G UUACCCAC 3717 GTGGGTAA GGCTAGCTACAACGA CAAGGTAC 5003	<del></del>				
1341 GUGGGGGA G CGUGUCAG 3710 CTGACACG GGCTAGCTACAACGA TCCCCCAC 4996 1343 GGGGGAGC G UGUCAGAA 3711 TTCTGACA GGCTAGCTACAACGA GCTCCCC 4997 1345 GGGAGCGU G UCAGAAUC 3712 GATTCTGA GGCTAGCTACAACGA ACGCTCCC 4998 1351 GUGUCAGA A UCCCUGCG 3713 CGCAGGGA GGCTAGCTACAACGA TCTGACAC 4999 1357 GAAUCCCU G CGAAGUAC 3714 GTACTTCG GGCTAGCTACAACGA AGGGATTC 5000 1362 CCUGCGAA G UACCUUGG 3715 CCAAGGTA GGCTAGCTACAACGA TTCGCAGG 5001 1364 UGCGAAGU A CCUUGGUU 3716 AACCAAGG GGCTAGCTACAACGA ACTTCGCA 5002 1370 GUACCUUG G UUACCCAC 3717 GTGGGTAA GGCTAGCTACAACGA CAAGGTAC 5003					
1343 GGGGAGC G UGUCAGAA 3711 TTCTGACA GGCTAGCTACAACGA GCTCCCCC 4997 1345 GGGAGCGU G UCAGAAUC 3712 GATTCTGA GGCTAGCTACAACGA ACGCTCCC 4998 1351 GUGUCAGA A UCCCUGCG 3713 CGCAGGGA GGCTAGCTACAACGA TCTGACAC 4999 1357 GAAUCCCU G CGAAGUAC 3714 GTACTTCG GGCTAGCTACAACGA AGGGATTC 5000 1362 CCUGCGAA G UACCUUGG 3715 CCAAGGTA GGCTAGCTACAACGA TTCGCAGG 5001 1364 UGCGAAGU A CCUUGGUU 3716 AACCAAGG GGCTAGCTACAACGA ACTTCGCA 5002 1370 GUACCUUG G UUACCCAC 3717 GTGGGTAA GGCTAGCTACAACGA CAAGGTAC 5003					
1345 GGGAGCGU G UCAGAAUC 3712 GATTCTGA GGCTAGCTACAACGA ACGCTCCC 4998 1351 GUGUCAGA A UCCCUGCG 3713 CGCAGGGA GGCTAGCTACAACGA TCTGACAC 4999 1357 GAAUCCCU G CGAAGUAC 3714 GTACTTCG GGCTAGCTACAACGA AGGGATTC 5000 1362 CCUGCGAA G UACCUUGG 3715 CCAAGGTA GGCTAGCTACAACGA TTCGCAGG 5001 1364 UGCGAAGU A CCUUGGUU 3716 AACCAAGG GGCTAGCTACAACGA ACTTCGCA 5002 1370 GUACCUUG G UUACCCAC 3717 GTGGGTAA GGCTAGCTACAACGA CAAGGTAC 5003	$\vdash$				
1351 GUGUCAGA A UCCCUGCG 3713 CGCAGGGA GGCTAGCTACAACGA TCTGACAC 4999 1357 GAAUCCCU G CGAAGUAC 3714 GTACTTCG GGCTAGCTACAACGA AGGGATTC 5000 1362 CCUGCGAA G UACCUUGG 3715 CCAAGGTA GGCTAGCTACAACGA TTCGCAGG 5001 1364 UGCGAAGU A CCUUGGUU 3716 AACCAAGG GGCTAGCTACAACGA ACTTCGCA 5002 1370 GUACCUUG G UUACCCAC 3717 GTGGGTAA GGCTAGCTACAACGA CAAGGTAC 5003					
1357 GAAUCCCU G CGAAGUAC 3714 GTACTTCG GGCTAGCTACAACGA AGGGATTC 5000 1362 CCUGCGAA G UACCUUGG 3715 CCAAGGTA GGCTAGCTACAACGA TTCGCAGG 5001 1364 UGCGAAGU A CCUUGGUU 3716 AACCAAGG GGCTAGCTACAACGA ACTTCGCA 5002 1370 GUACCUUG G UUACCCAC 3717 GTGGGTAA GGCTAGCTACAACGA CAAGGTAC 5003		<del></del>			4998
1362 CCUGCGAA G UACCUUGG 3715 CCAAGGTA GGCTAGCTACAACGA TTCGCAGG 5001 1364 UGCGAAGU A CCUUGGUU 3716 AACCAAGG GGCTAGCTACAACGA ACTTCGCA 5002 1370 GUACCUUG G UUACCCAC 3717 GTGGGTAA GGCTAGCTACAACGA CAAGGTAC 5003					4999
1364 UGCGAAGU A CCUUGGUU 3716 AACCAAGG GGCTAGCTACAACGA ACTTCGCA 5002 1370 GUACCUUG G UUACCCAC 3717 GTGGGTAA GGCTAGCTACAACGA CAAGGTAC 5003					5000
1370 GUACCUUG G UUACCCAC 3717 GTGGGTAA GGCTAGCTACAACGA CAAGGTAC 5003			3715		5001
	_		3716		5002
1373 CCUUGGUU A CCCACCCC 3718   GGGTGGG GGCTAGCTACAACGA AACCAAGG 5004			3717		5003
	1373	CCUUGGUU A CCCACCCC	3718	GGGGTGGG GGCTAGCTACAACGA AACCAAGG	5004

		133	
1377 GGUUACCC A CCCCCAGA	3719	TCTGGGGG GGCTAGCTACAACGA GGGTAACC	5005
1387 CCCCAGAA A UAAAAUGG	3720	CCATTITA GGCTAGCTACAACGA TTCTGGGG	5006
1392 GAAAUAAA A UGGUAUAA	3721	TTATACCA GGCTAGCTACAACGA TTTATTTC	5007
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1453 AUGUACUG A CGAUUAUG	3737	CATAATCG GGCTAGCTACAACGA CAGTACAT	5023
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1459 UGACGAUU A UGGAAGUG	3739	CACTTCCA GGCTAGCTACAACGA AATCGTCA	5025
1465 UUAUGGAA G UGAGUGAA	3740	TTCACTCA GGCTAGCTACAACGA TTCCATAA	5026
1469 GGAAGUGA G UGAAAGAG	3741	CTCTTTCA GGCTAGCTACAACGA TCACTTCC	5027
1478 UGAAAGAG A CACAGGAA	3742	TTCCTGTG GGCTAGCTACAACGA CTCTTTCA	5028
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1490 AGGAAAUU A CACUGUCA	3745	TGACAGTG GGCTAGCTACAACGA AATTTCCT	5031
1492 GAAAUUAC A CUGUCAUC	3746	GATGACAG GGCTAGCTACAACGA GTAATTTC	5032
1495 AUUACACU G UCAUCCUU	3747	AAGGATGA GGCTAGCTACAACGA AGTGTAAT	5033
1498 ACACUGUC A UCCUUACC	3748	GGTAAGGA GGCTAGCTACAACGA GACAGTGT	5034
1504 UCAUCCUU A CCAAUCCC	3749	GGGATTGG GGCTAGCTACAACGA AAGGATGA	5035
1508 CCUUACCA A UCCCAUUU	3750	AAATGGGA GGCTAGCTACAACGA TGGTAAGG	5036
1513 CCAAUCCC A UUUCAAAG	3751	CTTTGAAA GGCTAGCTACAACGA GGGATTGG	5037
1527 AAGGAGAA G CAGAGCCA	3752	TGGCTCTG GGCTAGCTACAACGA TTCTCCTT	5038
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1535 GCAGAGCC A UGUGGUCU	3754	AGACCACA GGCTAGCTACAACGA GGCTCTGC	5040
1537 AGAGCCAU G UGGUCUCU	3755	AGAGACCA GGCTAGCTACAACGA ATGGCTCT	5041
1540 GCCAUGUG G UCUCUCUG	3756	CAGAGAGA GGCTAGCTACAACGA CACATGGC	5042
1549 UCUCUCUG G UUGUGUAU	3757	ATACACAA GGCTAGCTACAACGA CAGAGAGA	5043
1552 CUCUGGUU G UGUAUGUC	3758	GACATACA GGCTAGCTACAACGA AACCAGAG	5044
1554 CUGGUUGU G UAUGUCCC	3759	GGGACATA GGCTAGCTACAACGA ACAACCAG	5045
1556 GGUUGUGU A UGUCCCAC	3760	GTGGGACA GGCTAGCTACAACGA ACACAACC	5046
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1563 UAUGUCCC A CCCCAGAU	3762	ATCTGGGG GGCTAGCTACAACGA GGGACATA	5048
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1574 CCAGAUUG G UGAGAAAU	3764	ATTTCTCA GGCTAGCTACAACGA CAATCTGG	5050
1581 GGUGAGAA A UCUCUAAU	3765	ATTAGAGA GGCTAGCTACAACGA TTCTCACC	5051
1588 AAUCUCUA A UCUCUCCU		AGGAGAGA GGCTAGCTACAACGA TAGAGATT	5052
1597 UCUCUCCU G UGGAUUCC		GGAATCCA GGCTAGCTACAACGA AGGAGAGA	5053
1601 UCCUGUGG A UUCCUACC	3768	GGTAGGAA GGCTAGCTACAACGA CCACAGGA	5054
1607 GGAUUCCU A CCAGUACG	3769	CGTACTGG GGCTAGCTACAACGA AGGAATCC	5055
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1613 CUACCAGU A CGGCACCA	<del></del>	TGGTGCCG GGCTAGCTACAACGA ACTGGTAG	5057
<u> </u>			

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1616	CCAGUACG G CACCACUC	3772	GAGTGGTG GGCTAGCTACAACGA CGTACTGG	5058
1618	AGUACGGC A CCACUCAA	3773	TTGAGTGG GGCTAGCTACAACGA GCCGTACT	5059
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1627	CCACUCAA A CGCUGACA	3775	TGTCAGCG GGCTAGCTACAACGA TTGAGTGG	5061
1629	ACUCAAAC G CUGACAUG	3776	CATGTCAG GGCTAGCTACAACGA GTTTGAGT	5062
1633	AAACGCUG A CAUGUACG	3777	CGTACATG GGCTAGCTACAACGA CAGCGTTT	5063
1635	ACGCUGAC A UGUACGGU	3778	ACCGTACA GGCTAGCTACAACGA GTCAGCGT	5064
1637	GCUGACAU G UACGGUCU	3779	AGACCGTA GGCTAGCTACAACGA ATGTCAGC	5065
1639	UGACAUGU A CGGUCUAU	3780	ATAGACCG GGCTAGCTACAACGA ACATGTCA	5066
1642	CAUGUACG G UCUAUGCC	3781	GGCATAGA GGCTAGCTACAACGA CGTACATG	5067
1646	UACGGUCU A UGCCAUUC	3782	GAATGGCA GGCTAGCTACAACGA AGACCGTA	5068
1648	CGGUCUAU G CCAUUCCU	3783	AGGAATGG GGCTAGCTACAACGA ATAGACCG	5069
1651	UCUAUGCC A UUCCUCCC	3784	GGGAGGAA GGCTAGCTACAACGA GGCATAGA	5070
1662	CCUCCCCC G CAUCACAU	3785	ATGTGATG GGCTAGCTACAACGA GGGGGAGG	5071
1664	UCCCCCGC A UCACAUCC	3786	GGATGTGA GGCTAGCTACAACGA GCGGGGGA	5072
1667	CCCGCAUC A CAUCCACU	3787	AGTGGATG GGCTAGCTACAACGA GATGCGGG	5073
1669	CGCAUCAC A UCCACUGG	3788	CCAGTGGA GGCTAGCTACAACGA GTGATGCG	5074
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1677	AUCCACUG G UAUUGGCA	3790	TGCCAATA GGCTAGCTACAACGA CAGTGGAT	5076
	CCACUGGU A UUGGCAGU	3791	ACTGCCAA GGCTAGCTACAACGA ACCAGTGG	5077
	UGGUAUUG G CAGUUGGA	3792	TCCAACTG GGCTAGCTACAACGA CAATACCA	5078
-	UAUUGGCA G UUGGAGGA	3793	TCCTCCAA GGCTAGCTACAACGA TGCCAATA	5079
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	AAGAGUGC G CCAACGAG	3796	CTCGTTGG GGCTAGCTACAACGA GCACTCTT	5082
_	GUGCGCCA A CGAGCCCA	3797	TGGGCTCG GGCTAGCTACAACGA TGGCGCAC	5083
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	CGAGCCCA G CCAAGCUG	3799	CAGCTTGG GGCTAGCTACAACGA TGGGCTCG	5085
├──-	CCAGCCAA G CUGUCUCA	3800	TGAGACAG GGCTAGCTACAACGA TTGGCTGG	5086
<del></del>	GCCAAGCU G UCUCAGUG	3801	CACTGAGA GGCTAGCTACAACGA AGCTTGGC	5087
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<del></del>	UCUCAGUG A CAAACCCA	3803	TGGGTTTG GGCTAGCTACAACGA CACTGAGA	5089
	AGUGACAA A CCCAUACC	3804	GGTATGGG GGCTAGCTACAACGA TTGTCACT	5090
	ACAAACCC A UACCCUUG		CAAGGGTA GGCTAGCTACAACGA GGGTTTGT	5091
	AAACCCAU A CCCUUGUG		CACAAGGG GGCTAGCTACAACGA ATGGGTTT	5092
	AUACCCUU G UGAAGAAU	3807	ATTCTTCA GGCTAGCTACAACGA AAGGGTAT	5093
	UGUGAAGA A UGGAGAAG	3808	CTTCTCCA GGCTAGCTACAACGA TCTTCACA	5094
	AUGGAGAA G UGUGGAGG	3809	CCTCCACA GGCTAGCTACAACGA TTCTCCAT	5095
	GGAGAAGU G UGGAGGAC	3810	GTCCTCCA GGCTAGCTACAACGA ACTTCTCC	5096
<u> </u>	UGUGGAGG A CUUCCAGG		CCTGGAAG GGCTAGCTACAACGA CCTCCACA	5097
	GGGAGGAA A UAAAAUUG		CAATTTTA GGCTAGCTACAACGA TTCCTCCC	5098
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	AAAUUGAA G UUAAUAAA	3814	TTTATTAA GGCTAGCTACAACGA TTCAATTT	
	UGAAGUUA A UAAAAAUC		· · · · · · · · · · · · · · · · · · ·	5100
	UAAUAAAA A UCAAUUUG		GATTTTTA GGCTAGCTACAACGA TAACTTCA	5101
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	ACAAAACU G UAAGUACC	3822	GGTACTTA GGCTAGCTACAACGA AGTTTTGT	5108
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1864	UUAUCCAA G CGGCAAAU	3827	ATTIGCCG GGCTAG	CTACAACGA	TTGGATAA	5113
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1873	CGGCAAAU G UGUCAGCU	3830	AGCTGACA GGCTAGO	CTACAACGA	ATTTGCCG	5116
1875	GCAAAUGU G UCAGCUUU	3831	AAAGCTGA GGCTAGG	TACAACGA	ACATTTGC	5117
1879	AUGUGUCA G CUUUGUAC	3832	GTACAAAG GGCTAGO	TACAACGA	TGACACAT	5118
1884	UCAGCUUU G UACAAAUG	3833	CATTTGTA GGCTAGO	TACAACGA	AAAGCTGA	5119
1886	AGCUUUGU A CAAAUGUG	3834	CACATTTG GGCTAGO	TACAACGA	ACAAAGCT	5120
1890	UUGUACAA A UGUGAAGC	3835	GCTTCACA GGCTAGO	TACAACGA	TTGTACAA	5121
1892	GUACAAAU G UGAAGCGG	3836	CCGCTTCA GGCTAGO	TACAACGA	ATTTGTAC	5122
1897	AAUGUGAA G CGGUCAAC	3837	GTTGACCG GGCTAGO	TACAACGA	TTCACATT	5123
1900	GUGAAGCG G UCAACAAA	3838	TTTGTTGA GGCTAGO			5124
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	UCCACGUG A CCAGGGGU	3845	ACCCCTGG GGCTAGG			5131
-	GACCAGGG G UCCUGAAA	3846	TTTCAGGA GGCTAGG			
	GUCCUGAA A UUACUUUG	3847	CAAAGTAA GGCTAGG			5132
<b>—</b>	CUGAAAUU A CUUUGCAA	3848				5133
	AUUACUUU G CAACCUGA	3849	TTGCAAAG GGCTAGO			5134
<b>—</b>	ACUUUGCA A CCUGACAU		TCAGGTTG GGCTAGC			5135
		3850	ATGTCAGG GGCTAGC			5136
	GCAACCUG A CAUGCAGC	3851	GCTGCATG GGCTAGO			5137
	AACCUGAC A UGCAGCCC	3852	GGGCTGCA GGCTAGC			5138
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	GAGAGCGU G UCUUUGUG	3859	CACAAAGA GGCTAGO		· · · · · · · · · · · · · · · · · · ·	5145
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	UUUGUGGU G CACUGCAG	3862	CTGCAGTG GGCTAGC			5148
	UGUGGUGC A CUGCAGAC	3863	GTCTGCAG GGCTAGC			5149
	GGUGCACU G CAGACAGA		TCTGTCTG GGCTAGO			5150
	CACUGCAG A CAGAUCUA		TAGATCTG GGCTAGC			5151
	GCAGACAG A UCUACGUU		AACGTAGA GGCTAGO			5152
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	AGAUCUAC G UUUGAGAA	3868	TTCTCAAA GGCTAGC	CTACAACGA	GTAGATCT	5154
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	CUCACAUG G VACAAGCU	3872	AGCTTGTA GGCTAGO	TACAACGA	CATGTGAG	5158
2054	CACAUGGU A CAAGCUUG	3873	CAAGCTTG GGCTAGC	TACAACGA	ACCATGTG	5159
2058	UGGUACAA G CUUGGCCC	3874	GGGCCAAG GGCTAGC	TACAACGA	TTGTACCA	5160
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2067	CUUGGCCC A CAGCCUCU	3876	AGAGGCTG GGCTAGC	TACAACGA	GGGCCAAG	5162
2070	GGCCCACA G CCUCUGCC	3877	GGCAGAGG GGCTAGC	TACAACGA	TGTGGGCC	5163

2076	CAGCCUCU G CCAAUCCA	3878	TGGATTGG GGCTAGCTACAACGA AGAGGCTG	5164
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2086	CAAUCCAU G UGGGAGAG	3881	CTCTCCCA GGCTAGCTACAACGA ATGGATTG	5167
2094	GUGGGAGA G UUGCCCAC	3882	GTGGGCAA GGCTAGCTACAACGA TCTCCCAC	5168
2097	GGAGAGUU G CCCACACC	3883	GGTGTGGG GGCTAGCTACAACGA AACTCTCC	5169
2101	AGUUGCCC A CACCUGUU	3884	AACAGGTG GGCTAGCTACAACGA GGGCAACT	5170
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2107	CCACACCU G UUUGCAAG	3886	CTTGCAAA GGCTAGCTACAACGA AGGTGTGG	5172
2111	ACCUGUUU G CAAGAACU	3887	AGTTCTTG GGCTAGCTACAACGA AAACAGGT	5173
2117	UUGCAAGA A CUUGGAUA	3888		5174
2123	GAACUUGG A UACUCUUU	3889		5175
	ACUUGGAU A CUCUUUGG	3890		5176
	CUUUGGAA A UUGAAUGC	3891		5177
	GAAAUUGA A UGCCACCA	3892		5178
	AAUUGAAU G CCACCAUG	3893		5179
	UGAAUGCC A CCAUGUUC	3894		5180
$\overline{}$	AUGCCACC A UGUUCUCU	3895		
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	CUCUAAUA G CACAAAUG CUAAUAGC A CAAAUGAC	3898	<del></del>	5184
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}	CAAAUGAC A UUUUGAUC	3902		5188
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	AUCAUGGA G CUUAAGAA	3905		5191
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	AAGAAUGC A UCCUUGCA	3908		5194
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$\vdash$	CCAAGGAG A CUAUGUCU	3911		5197
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-	UCUGCCUU G CUCAAGAC	3915		5201
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	ACAGGAAG A CCAAGAAA	3917		5203
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	AAGACAUU G CGUGGUCA	3920	TGACCACG GGCTAGCTACAACGA AATGTCTT	5206
2266	GACAUUGC G UGGUCAGG	3921	CCTGACCA GGCTAGCTACAACGA GCAATGTC	5207
2269	AUUGCGUG G UCAGGCAG	3922	CTGCCTGA GGCTAGCTACAACGA CACGCAAT	5208
2274	GUGGUCAG G CAGCUCAC	3923	GTGAGCTG GGCTAGCTACAACGA CTGACCAC	5209
2277	GUCAGGCA G CUCACAGU	3924	ACTGTGAG GGCTAGCTACAACGA TGCCTGAC	5210
2281	GGCAGCUC A CAGUCCUA	3925	TAGGACTG GGCTAGCTACAACGA GAGCTGCC	5211
2284	AGCUCACA G UCCUAGAG	3926	CTCTAGGA GGCTAGCTACAACGA TGTGAGCT	5212
2292	GUCCUAGA G CGUGUGGC	3927		5213
2294	CCUAGAGC G UGUGGCAC	3928		5214
2296	UAGAGCGU G UGGCACCC	3929		5215
2299	AGCGUGUG G CACCCACG	3930		5216
			<u> </u>	

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2305 UGGCACCC A CGAUCACA	3932	TGTGATCG	GGCTAGCTACAACGA	GGGTGCCA	5218
2308 CACCCACG A UCACAGGA	3933	TCCTGTGA	GGCTAGCTACAACGA	CGTGGGTG	5219
2311 CCACGAUC A CAGGAAAC	3934	GTTTCCTG	GGCTAGCTACAACGA	GATCGTGG	5220
2318 CACAGGAA A CCUGGAGA	3935	TCTCCAGG	GGCTAGCTACAACGA	TTCCTGTG	5221
2327 CCUGGAGA A UCAGACGA	3936	TCGTCTGA	GGCTAGCTACAACGA	TCTCCAGG	5222
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2335 AUCAGACG A CAAGUAUU	3938	AATACTTG	GGCTAGCTACAACGA	CGTCTGAT	5224
2339 GACGACAA G UAUUGGGG	3939	CCCCAATA	GGCTAGCTACAACGA	TTGTCGTC	5225
2341 CGACAAGU A UUGGGGAA	3940	TTCCCCAA	GGCTAGCTACAACGA	ACTTGTCG	5226
2351 UGGGGAAA G CAUCGAAG	3941	CTTCGATG	GGCTAGCTACAACGA	TTTCCCCA	5227
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2518 CCUGCCAG G CAUGCAGU			GGCTAGCTACAACGA		5262
	3977		GGCTAGCTACAACGA		5263
TOUGHT A COCKGOOD	3978		GGCTAGCTACAACGA		5264
2522 CCAGGCAII G CAGIGITICE .	J 7 1 0	WARLIG	ACTURCIVE CHACGY	PIRCLIRE	3204
	3970	CDDCDDCD	CCCTACCTACAACCA	TOCATOCO	E26E
2525 GGCAUGCA G UGUUCUUG :	3979		GGCTAGCTACAACGA		5265
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2525 GGCAUGCA G UGUUCUUG : 2527 CAUGCAGU G UUCUUGGC : 2534 UGUUCUUG G CUGUGCAA : 2537 UCUUGGCU G UGCAAAAG :	3980	GCCAAGAA TTGCACAG CTTTTGCA	GGCTAGCTACAACGA	ACTGCATG CAAGAACA AGCCAAGA	5266

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2545   AGUGGARAA G UGGARGECA 3984   TSCCTTCA GSCTAGCTACAACGA TITTOCAC 5270 2551   AGUGGAGG C AUUUUUCU 3985   ATGANAN GGCTAGCTACACCAC TCCCACT 5271 2553   GUGGAGGC A UUUUUCU 3985   ATGANAN GGCTAGCTACACGA CTCCACT 5272 2553   GUUGUUC A UAAUGGAN 3987   TCTATTA GGCTAGCTACACGA GAAAAATG 5273 2553   UUUUCU A UAAUGGAN 3987   TCTATTA GGCTAGCTACACGA GAAAAATG 5273 2553   UUUCUAU A UAAUGGAN 3989   CCTGGGCA GGCTACCTACACGA TATGANAN 5274 2553   UUUCUAU A UACAAAA 3990   TTCCTAGG GGCTAGCTACACGA CATCATCTT 5276 2554   AGGANAGA A CGAACUUG 3991   CAAGTTCG GGCTAGCTACAACGA CTTCTCTT 5276 2558   AGGAAAGA A CGAACUUG 3991   CAAGTTCG GGCTAGCTACAACGA CTTCTCTT 5276 2558   AGGAAAGA A UAUUAUUUU 3993   AATAATGA GGCTAGCTACAACGA CTTCTCTT 5278 2595   ACUUGGAA A UAUUAUUUU 3993   AATAATGA GGCTAGCTACAACGA CTTCTCTT 5279 2595   CAGGAAACA A UAUUAUUUU 3993   AATAATGA GGCTAGCTACAACGA CTTCTCTT 5279 2595   DUGGAAAUC A UUUCUAGA 3995   TACCAAGA GGCTAGCTACAACGA AATAATTT 5281 2608   UUAUUUUU A G UAGGCGG 3995   CCGTGCCTA GGCTAGCTACAACGA CATCATCAG 5280 2612   UUCUGUUU A G UAGGCGG 3995   CCGTGCCTA GGCTAGCTACAACGA CATCATCAG 5282 2612   UUCUGGCC G GGGGGAUU 3999   AACCAGCG GGCTAGCTACAACGA CTACCTAG 5284 2614   UUCUGGCC G GGGGGAUU 3999   AACCAGCG GGCTAGCTACAACGA CTACCTAG 5284 2615   UUCUGCC G GGGGGAUU 3999   AACCAGCG GGCTAGCTACAACGA CCTACCTA 5284 2616   UUCUGUU G COACUUUU 4005   GAACATGG GGCTAGCTACAACGA CCGCGCG 5287 2621   GGGGGGU A UUCUCUU G 4001   GAACATGG GGCTAGCTACAACGA CCGCGCG 5287 2622   GGGGGGU A UUCUCUU G 4001   GAACATGG GGCTAGCTACAACGA CATCACCGC 5288 2623   UUCUUCUG G CUACUUUU 4005   GAACATGG GGCTAGCTACAACGA CATCACCGA CAGAAGAA CAGAACGA GGCTAGCTACAACGA CACCAGAA 6391 2631   AUUCUGU G CUACUUUU 4005   GAACATGG GGCTAGCTACAACGA CACCAGAA 5291 2652   UUCUUCU G CUACUUUU 4005   AGAACATG GGCTAGCTACAACGA CACCAGAA 5291 2653   UUCUUCU G CUACUUUU 4005   AGAACATG GGCTAGCTACAACGA CACCAGAA 5291 2654   UUCUGGC C CUACUUUU 4005   AGAACATG GGCTAGCTACAACGA CACGAAGA 5291 2655   UUCUGUU G CUACUUU 4005   AGAACATG GGCTAGCTACAACGA CACCAGAA 5291 2656   UUCUGUU G CUACUUU 4005   AGAACATG GGC			138	
2553 GUGGAGGC A UUUUUCAU 3986 ATGAAAAA GGCTACCTACAACGA GCCTCCAC 5272 2560 CAUUUUUC A UAAUAGAA 3987 TTCTATTA GGCTACCTACAACGA GAAAAATT 5273 2570 AAUAGAAG GUGCCCAGG 3989 CCTGGGCA GGCTACCTACAACGA TATGAAAAA 5274 2570 AAUAGAAG G UGCCCAGG 3989 CCTGGGCA GGCTAGCTACAACGA CTTCTATT 5275 2572 UAGAAGGU G CCCAGGAA 3990 CTCTGGG GGCTAGCTACAACGA CTTCTATT 5276 2584 AGGAAAAAA G CCAACGUUG 3991 CAAGTTCG GGCTAGCTACAACGA CTTCTATT 5276 2584 AGGAAAAA G CCAACGUUG 3991 CAAGTTCG GGCTAGCTACAACGA CTTCTTAT 5276 2588 AAAGACGA A CUUGGAAA 3992 TTCCCAAG GGCTAGCTACAACGA CTTCTTCT 5276 2588 AAAGAACA A CUUGGAAA 3992 TTCCCAAG GGCTAGCTACAACGA CTTCTCT 5276 2589 UGGAAAUC A UUAUUUU 3994 AATAATGA GGCTAGCTACAACGA TTCCAAGT 5279 2599 UGGAAAUCAU 3 PUCUAGUA 3995 TACCAAGA GGCTAGCTACAACGA ATTCCTAC 5280 2500 UUAUUCUU G UAAGCACA 3995 CGTGCCAC AGGCTACCTACAACGA AATCATT 5281 2501 UUAUUCUA G UAAGCACA 3995 CGTGCCAC GGCTAGCTACAACGA CATTCTAC 5280 2512 UCUAUUCUA G UAAGCACA 3996 CGTGCCAC GGCTAGCTACAACGA CACTCTAC 5282 2512 UCUAUUCUA G UAAGCACA 3999 CACCGCCG GGCTAGCTACAACGA CACCACTAC 5282 2514 UAGGACAC G CGGUGAUU 3999 AATCACCG GGCTAGCTACAACGA CCGCCCG 5287 2523 CGGCGGGG G UAAUUCUU 4001 GGCAATCA GGCTAGCTACAACGA CCGCCCG 5287 2523 CGGCGGGG G UACUUCUU 4002 GAACATGA GGCTAGCTACAACGA CCGCCCG 5287 2524 CGGUGAUU G CCAUGUUC 4001 GAACATGA GGCTAGCTACAACGA CACCGCCC 5287 2525 CGGUGAUU G CCAUGUUC 4002 GAACATGA GGCTAGCTACAACGA CACCGCC 5287 2526 CGGUGAUU G CUACUUCU 4005 AAAGAACA GGCTAGCTACAACGA AATCACCG 5289 2521 UACUUCUU G UUCUUCU 4005 AAAGAACA GGCTAGCTACAACGA AATCACCG 5289 2521 UACUUCUU G UCAUCUUC 4004 CAGAAGAA GGCTAGCTACAACGA AATCACCG 5289 2523 UACUUCUU G UCAUCUUC 4005 AAAGAACA GGCTAGCTACAACGA AGGAACA 5292 2526 CGGUGAUU C UCCUUCU 4005 AAAGAACA GGCTAGCTACAACGA AGGAACA 5292 2526 UACUUCUU G UCAUCUUC 4005 AGAACATGA GGCTAGCTACAACGA AGGAACA 5293 2526 UACUUCUU G UCAUCUUC 4005 AGAACATGA GGCTAGCTACAACGA AGGAACAA 5293 2526 UACUUCUU G UCAUCUUC 4005 AGAACATGA GGCTAGCTACAACGA AGGAACA 5293 2526 CGGGGGG A UUCUUCU 4005 AGAACATGA GGCTAGCTACAACGA AGGAACA 5293 2526 CGGGGGG A UUCUUCU 4005 AGAACATGA GGCTAGCTACA	2545 GUGCAAAA G UGGAGGCA	3984	TGCCTCCA GGCTAGCTACAACGA TTTTGCAC	5270
2560         CAUUUUUU A UANUAGAA         3987         TTCTATTA GGCTAGCTACAACGA GAAAAATO         5273           2563         JUUUUCAIDA A UAQAAGGU         3988         ACCTTCTA GGCTAGCTACAACGA TATGAAAA         5274           2570         RAUAGAAG G         UACCAGAGGA         3999         CCTGGGGA GGCTAGCTACAACGA ACCTTCTA         5276           2572         UAGAAGGU         CCCAGGAA         3990         TTCCTGGG GGCTAGCTACAACGA ACCTTCTA         5276           2584         AAAGACGA A CUUGGAAA         3991         TTCCATGG GGCTAGCTACAACGA TTCCAAGT         5277           2595         ACUUGGAA         A UUAUUUUA         3994         TAGAAATA GGCTAGCTACAACGA TTCCAAGT         5279           2599         LUGABAUC A UUAUUUA         3994         TAGAAATA GGCTAGCTACAACGA ATTCCA         5280           2612         LUCUAGUU A UUCUAGUA         3995         TACCAGCG GGCTAGCTACAACGA ATTCCA         5280           2612         LUCUAGUU A UUCUAGUA         3995         CCGCCGT GGCTAGCTACAACGA ATTCAAGA         5282           2612         LUCUAGUAG G         CACGGCGG GGGGG GGGGGGGGGGGGGGGGGGGGGGGG	2551 AAGUGGAG G CAUUUUUC	3985	GAAAAATG GGCTAGCTACAACGA CTCCACTT	5271
2563 UUUUCAUA A UAGAAGGU 3988 ACCTTCTA GGCTAGCTACAACGA TATGAAAA 5274 2570 AANJAGAAG U GCCCAGG 3989 CCTGGGCA GGCTAGCTACAACGA CCTTCTATT 5275 2572 UAGAAGGU G CCCAGGAA 3999 TTCCTGGG GGCTAGCTACAACGA CCTTCTATT 5275 2584 AGGAAAG A CGAACUUG 3991 CAAGTTCG GGCTAGCTACAACGA CCTTTCCT 5276 2584 AAGGACGA A CUUGGAAA 3992 TTCCCAG GGCTAGCTACAACGA CCTTTCCT 5276 2585 AAAGGAAA A UCAUUUUU 3994 AATAATGA GGCTAGCTACAACGA TCCTCTAT 5276 2595 ACUUGGAA A UCAUUUUU 3994 AATAATGA GGCTAGCTACAACGA TCCTCAT 5276 2596 ACUUGGAA A UCAUUUUU 3994 AATAATGA GGCTAGCTACAACGA TCCTATG 5278 2599 UGGAAAUC A UUAUUCUA 3994 TAGAATAA GGCTAGCTACAACGA AATGAATT 5229 2590 UGGAAAUC A UUAUUCUA 3995 TACTAGAA GGCTAGCTACAACGA AATGAATT 5281 2508 UUUUCUUCU G UAGGACGG 3996 CGTGGCTAGCTACAACGA AATGAATT 5281 2508 UUUUCUUCU G UAGGACGG 3996 CACGGCGG GGCTAGCTACAACGA TAGATAA 5282 2512 UCUAGUAG G CACGGCGG 3997 CCGCCGTG GGCTAGCTACAACGA CTACTAGA 5283 2514 UUGGACACG C GGGGAUU 3999 AATCAACCG GGCTAGCTACAACGA CTACTAGA 5283 2520 GCACGGCG G UGAUUGCC 4000 GGCAATCA GGCTAGCTACAACGA CCCACCTA 5285 2520 GCACGGCG G UGAUUGCC 4001 GGCAATCA GGCTAGCTACAACGA CCCACCCG 5286 2523 GCAGCGUG A UUGCCUUC 4001 GACGAGCA GGCTAGCTACAACGA ACCGCCC 5286 2523 UUCUUCUC G CUACUUCU 4003 GAACATGG GGCTAGCTACAACGA ACCGCCC 5286 2524 CGGUGGAUU G CCCUGUCU 4004 CAGAAGAA GGCTAGCTACAACGA ATGCACCC 5288 2525 CGGUGGAUU G CUCUUCU 4004 CAGAAGAA GGCTAGCTACAACGA ATGCACAC 5286 2524 CUUUUCUC G CUACUUCU 4005 GAACATGG GGCTAGCTACAACGA AGGAAA 5291 2525 UUCUUCUC G CUACUUCU 4005 GAACATGG GGCTAGCTACAACGA AGGAAA 5291 2526 CGGUGAUU G UCUUCUC 4004 CAGAAGAA GGCTAGCTACAACGA AGGAAAA 5292 2526 CGGUGAUU G UCUUCUC 4005 GAACATGG GGCTAGCTACAACGA AGGAAAA 5292 2526 CGGUGAUU G UCUUCUC 4005 GAACATGG GGCTAGCTACAACGA AGGAAAA 5293 2526 CGGUGAUA A CUUCUUCU 4005 GAACATGG GGCTAGCTACAACGA AGGAAAA 5293 2526 CGGUGAUA C UCUUCUCU 4005 GAACATGG GGCTAGCTACAACGA AGGAAAA 5293 2526 CGGUGAAU A UCUUCUCU 4005 GAACATGG GGCTAGCTACAACGA AGGAAAA 5293 2526 CGGCGAACTACAACGA ACGAACAA 5293 2527 CAUCUUCU G UCAUCUCU 4006 CACAAGAG GGCTAGCTACAACGA AGGAAAA 5293 2526 CGGGGAACTACAACGA ACGAACAC	2553 GUGGAGGC A UUUUUCAU	3986	ATGAAAAA GGCTAGCTACAACGA GCCTCCAC	5272
2570         AAUAGAAG G UGCCCAGGA         3989         CCTGGGCA GGCTAGCTACAACGA CTTCTAT         5275           2572         UAGAAGGU G CCCAGGAA         3990         TTCCTGGG GGCTAGCTACAACGA ACCTTCTA         5276           2584         AGGAAAAGA C CAGGAA         3990         TTCCTGG GGCTAGCTACAACGA CTTTTCCT         5277           2588         AAAGACGA A CUUGGAAA         3992         TTTCCAAG GGCTAGCTACAACGA CTGCTTT         5278           2599         BGAAAACAU A UAUUUUU 3994         TAGAATAA GGCTAGCTACAACGA CATTCCAAGCA         5280           2602         AAAUCAUU A UUCUAGUA         3995         TACTAGAA GGCTAGCTACAACGA AATGATTT         5281           2603         MUAUUCUA G UAGGCACG         3996         CGTGCCTA GGCTAGCTACAACGA AATGATTT         5281           2612         LUCAGUAG G CACGGGG         3997         CCGCCGTG GGCTAGCTACAACGA CTACTAGA         5282           2612         LUCAGUAG G CACGGGG         3997         ACCCGCCG GGCTAGCTACAACGA CTACTAGA         26720 CACGGGG G UGAUUGC         4001         CACGGCGG GCCACGGG G UGAUUGC         4001         CACGGCGG GCCACGGG G UGAUGUCC         4002         CACAGGGA G CACGGCGG         5286           2629         UGAUUCUC         AUUCUCCA         4002         CAACAGGG GCTAGCTACAACGA ATCCACCA         5288           2629         UGAUUCUC         AUUCUCCA	2560 CAUUUUUC A UAAUAGAA	3987	TTCTATTA GGCTAGCTACAACGA GAAAAATG	5273
2572 UAGANAGGU G CCCAGGAN 3990 TTCCTGGG GGCTAGCTACAAGGA ACCTTCTA 5276 2584 AGGANAAG A CGAACUUG 3991 CAAGTTCG GGCTAGCTACAACGA CCTTTTCCT 5277 2585 AAGAGGA A CUJUGGAN 3992 TTTCCAMG GGCTAGCTACAACGA TCGTCTTT 5278 2595 ACUJUGGAA A UCAUUAUU 3993 AATAATGA GGCTAGCTACAACGA TCGTCTTT 5278 2596 ACUJUGGAA A UCAUUAUU 3993 AATAATGA GGCTAGCTACAACGA TCCTACTT 5279 2599 UGGANAUC A UJUCUUGU 3994 TACAAGAA GGCTAGCTACAACGA AATGATTC 5280 2602 AAAUCAUU A UJCUJAGU 3995 TACTAGAA GGCTAGCTACAACGA AATGATT 5281 2603 UUAUUCUA G UAGGCACG 3996 CGTGCCTA GGCTAGCTACAACGA AATGATTA 5281 2614 UUAUJAGGA CA CGGCGGU 3997 CCGCCGTG GGCTAGCTACAACGA TAGAATAA 5282 2612 UCUAGUAGA G CAGGCGGU 3999 ACCACCGCG GGCTAGCTACAACGA TAGAATAA 5282 2614 UUAGUAGGC A CGGCGGU 3998 CACCGCCG GGCTAGCTACAACGA CGCTACTA 5284 2617 UAGGCACG G CGGUGAUU 3999 AATCACCG GGCTAGCTACAACGA CGCCGTGC 5286 2623 CGGCGGUG A UUGCAUG 4000 GGCAATCA GGCTAGCTACAACGA CCCCCCC 5287 2624 CGGGGGUG A UUGCAUG 4001 CATGGCA GGCTAGCTACAACGA CACCACCG 5287 2625 CGGGGAUU G CAUGUUC 4002 GAACATGA GGCTAGCTACAACGA ATCACCG 5288 2629 UGAUUGCC A UGUUCUUC 4003 GAAGAAC GGCTAGCTACAACGA ATCACCG 5288 2629 UGAUUGCC A UGUUCUUC 4003 GAAGAAC GGCTAGCTACAACGA ATCACCG 5288 2631 UUCUUCUUG G CUACUUCU 4004 CAGAAGAA GGCTAGCTACAACGA ATCACCG 5288 2640 UUCUUCUG G CUACUUCU 4005 AACAGGA GGCTAGCTACAACGA ATCACCA 5289 2651 UACUUCUU G CUACUUCU 4006 ACAAGAA GGCTAGCTACAACGA ATCACCA 5292 2652 UUCUUCUU G CUACUUCU 4006 ACAAGAA GGCTAGCTACAACGA ACGAAGAA 5291 2653 UUCUUCUU G CUACUUCU 4006 ACAAGAA GGCTAGCTACAACGA ACGAAGAA 5291 2654 CUACUUCU G CUACUUCU 4006 ACAAGAA GGCTAGCTACAACGA ACGAAGAA 5291 2655 UUCUUCUU G CUACUCU 4007 AGATGATG GGCTAGCTACAACGA AGAAGAA 5291 2656 UUCUUCUU G CUACUCU 4007 AGATGATG GGCTAGCTACAACGA AGAAGAA 5291 2656 UUCUUCUU G CUACUCU 4007 AGATGATG GGCTAGCTACAACGA AGAAGAA 5291 2656 UUCUUCU G CUACUCU 4007 AGATGATG AGGCTAGCTACAACGA AGCAAGAA 5292 2657 ACGGGGA A CCGUUAGGA 4011 CTTACACG GGCTAGCTACAACGA AGCAAGAA 5293 2658 ACCGAGG A CCGUUAGGA 4011 CTTACACG GGCTAGCTACAACGA AGCAAGAA 5295 2658 LUCUUCU G CUACUCGA 4012 CTCACTGG GGCTAGCTACAACGA AGCAGAGA 5	2563 UUUUCAUA A UAGAAGGU	3988	ACCTTCTA GGCTAGCTACAACGA TATGAAAA	5274
2584         AGGARANAG A COGACUUG         3991         CAAGTTCG GCTAGCTACAACGA CTTTTCCT         5277           2588         AAAGACGA A CUUGAAA         3992         TTTCCAAG GCTTACTACAACGA TCGTTTT         5278           2596         ACUUGAGAA A UUAUUCUA         3994         TATGAATGA GCTTACTACAACGA TCCCAAGT         5279           2599         UIGGAAAUC A UUAUUCUA         3994         TAGAATAA GGCTTACGTACAACGA ATGATTTCA         5280           2602         JAANUCUU A UUCUAGUA         3995         TACTAGAA GGCTTACGTACAACGA ATGATTA         5281           2608         UUAUUCUA         3996         CGTGCCTA GGCTAGCTACAACGA TAGAATAA         5282           2612         UUCUGUAGUAG G UAGGCACG         3997         CCGCCGTG GCTAGCTACAACGA CTCCTACTA         5283           2614         UAGGCACG         G CGGUGAUU         3999         AATCACCG GGCTAGCTACAACGA CTCCTACTA         5284           2617         UAGGCACG         G UAGUUCU         4000         GCACATCA GCTAGCTACAACGA CTCCCCCC         5286           2623         CGGUGAUU G CCAUGUUC         4001         CATAGGCAA GGCTAGCTACAACGA CACCACCC         5287           2626         CGGUGAUU G UUCUUCUG         4003         GAAGAACA GGCTAGCTACAACGA CACGAA         5289           2631         JAUCUUCUG G UACUUCU         4003         GAAGAAA GGCTAG	2570 AAUAGAAG G UGCCCAGG	3989	CCTGGGCA GGCTAGCTACAACGA CTTCTATT	5275
2588         AAAGACGA A CUUGGANA         3992         TTTCCAAG GGCTAGCTACAACGA TCCACTT         5278           2596         ACUUGAA A UCAUUAUU         3993         AATAATGA GGCTAGCTACAACGA GATTCCAAGT         5279           2592         IAAUCAUU A UUCUAGUA         3994         TAGAATAA GGCTAGCTACAACGA AATGATT         5280           2602         IAAUCAUU A UUCUAGUA         3995         TACTAGAA GGCTAGCTACAACGA AATGATT         5281           2602         IUUAUUCUA GUAGGACG         3996         CGTGCCTA GGCTAGCTACAACGA CTACTAGA         5283           2612         UCUAGUAG         A CACGGCGG         3996         CGTGCCTG GGCTAGCTACAACGA CTACTAGA         5283           2612         UCAGGAGG         A CACGGCGG GGCTAGCTACAACGA CTACTAGA         5283         2620         GCACGGCG         GUAGUGCC         4000         GGCAACGA GG GUAGUGCC         4001         CACGGCAG GG GUAGUGCC         4001         CATGGCAA GGCTAGCTACAACGA CGCCCCCCCCC         5286           2623         IGGGGGUB A UUGCCAUC         4001         CATGGCAA GGCTAGCTACAACGA ATCACCCC         5288           2623         IGGGGGUB A UUGCCAUC         4001         CARAAGAA GGCTAGCTACAACGA ATCACCC         5288           2623         IUGAUCACC A UGUUCUC         4001         CAGAAGAA GGCTAGCTACAACGA ATCACACA         5292           2631         <	2572 UAGAAGGU G CCCAGGAA	3990	TTCCTGGG GGCTAGCTACAACGA ACCTTCTA	5276
2595 ACUUGGAA A UCAULAUU 3993 AATAATGA GCTAGCTACAACGA TTCCAACT 5279 2599 UGGAAAUC A UUAUUCUA 3994 TAGAATTA GGCTAGCTACAACGA GATTTCCA 5280 2602 AAAUCAUU A UUCUAGUA 3995 TACTAGAA GGCTAGCTACAACGA AATGATTT 5281 2608 UUAUUCUA G UAGGCACG 3996 CGTGCCTA GGCTAGCTACAACGA TAGAATTA 5282 2612 UCUAGUAG G CACGGCGG 3997 CCGCCGTG GGCTAGCTACAACGA CTACTAGA 5283 2614 UAGGCACG G CGGGGUAUU 3999 ACCCGCCG GGCTAGCTACAACGA CCTCATGA 5284 2617 UAGGCACG G CGGGAUU 3999 AATCACCG GGCTAGCTACAACGA CCTGCCTA 5284 2618 GCACGCAC G CGGGAUU 3999 AATCACCG GGCTAGCTACAACGA CCTGCCTA 5284 2619 GCACGGCG G UGAUUGCC 4000 GGCAATCA GGCTACTACAACGA CCTGCCTA 5285 2620 GCACGGCG G UGAUUGCC 4000 GGCAATCA GGCTACTACAACGA CCTGCCTA 5286 2621 GCACGGCG G UGAUUGCC 4001 CATGGCAA GGCTACTACAACGA CACGCCCG 5287 2622 GCGCGGUG A UUGCCAUG 4001 CATGGCAA GGCTAGCTACAACGA AATCACCC 5288 2623 UGAUUGCC A UGUUCC 4002 GAACATGG GGCTAGCTACAACGA AATCACCC 5288 2624 UUCUUCCU G CUACUUCU 4005 GAACATGG GGCTAGCTACAACGA AATCACCC 5288 2625 UUCUUCUC G CUACUUCU 4005 GAACATGG GGCTAGCTACAACGA AATCACCC 5288 2626 UUCUUCUC G CUACUUCU 4005 ACAAGGAA GGCTAGCTACAACGA AATCACCC 5288 2627 UUCUUCUU G CUACUUCU 4006 ACAAGGAA GGCTAGCTACAACGA AAGAATTA 5290 2628 UUCUUCUU G UCAUCAUC 4007 GATGATGA GGCTAGCTACAACGA AAGAATA 5291 2629 UACUUCUU G UCAUCAUC 4007 GATGATGA GGCTAGCTACAACGA AAGAAGTA 5291 2626 UUCUUCUU G UCAUCAUC 4007 GATGATGA GGCTAGCTACAACGA AAGAAGAA 5291 2626 UUGUUCU A UCCUACGG 4009 CCGTAGGA GGCTAGCTACAACGA AAGAAGAA 5292 2626 UUGUUCU A UCCUACGG 4009 CCGTAGGA GGCTAGCTACAACGA GACAAGAA 5292 2626 UUGUUCU A UCCUACGG 4009 CCGTAGGA GGCTAGCTACAACGA GACAAGAA 5292 2626 UUGUUCU A UCCUACGG 4009 CCGTAGGA GGCTAGCTACAACGA GACAACGA 5292 2626 UUGUUCU A UCCUACGG 4009 CCGTAGGA GGCTAGCTACAACGA GACAACAA 5295 2626 UUGUUCU A UCCUACGG 4009 CCGTAGGA GGCTAGCTACAACGA GACAACAA 5295 2627 UUAAGCG G CCAUUGAG 4010 CCGCTAG GGCTAGCTACAACGA GACAACAA 5295 2628 AACUACGU A UCCUACGG 4010 CCGCTAG GGCTAGCTACAACGA GACGACAA 5296 2629 AACUACGA C UUAAGAGA 4011 CCTATAGG GGCTAGCTACAACGA AGGACAA 5297 2629 GAACGAC A UGAACACC 4010 CCCCTACA GGCTAGCTACAACGA CCGCTTAA	2584 AGGAAAAG A CGAACUUG	3991	CAAGTTCG GGCTAGCTACAACGA CTTTTCCT	5277
2599   UGQAARUC A UUAUUCUA 3994   TAGAATAA GGCTAGCTACAACGA GATTTCCA 5280   2602   AAAUCAUU A UUCUAGUA 3995   TACTAGAA GGCTAGCTACAACGA AATGATTT 5281   2612   UUAUUCUA G UAGGCACG 3996   CGTGGCTA GGCTAGCTACAACGA TAGAATAA 5282   2612   UUAUUCUA G UAGGCACG 3996   CGTGGCTA GGCTAGCTACAACGA CTACTACAA 5283   2614   UAGUAGGC A CGCGGUG 3998   CACCGCCG GGCTAGCTACAACGA CTACTACAA 5283   2614   UAGUAGGC A CGCGGUGU 3999   AATCACCG GGCTAGCTACAACGA CTACTACAA 5284   2617   UAGGCACG G CGGUGAUU 3999   AATCACCG GGCTAGCTACAACGA CGCGTTAC 5286   2620   GCACGGCG G UGADUGCC 4000   GGCAATCA GGCTAGCACACGA CGCGTTAC 5286   2621   CGCGGUG A UUGCCAUG 4001   CATGGCAA GGCTAGCTACAACGA CACCGCCG 5287   2622   CGCGGUU G CCAUGUUC 4001   CATGGCAA GGCTAGCTACAACGA CACCGCCG 5287   2623   CGCUAUU G CCAUGUUC 4003   GAACATGA GGCTAGCTACAACGA AATCACCG 5288   2629   UGAUUCCC A UUCUUCU 4003   GAACATGA GGCTAGCTACAACGA AATCACCG 5289   2631   AUUCCGAU G UUCUUCU 4005   AGAAGAA GGCTAGCTACAACGA ATGCCACCG 5289   2643   UUCUUCUG G CUACUUCU 4005   AGAAGAA GGCTAGCTACAACGA ATGCCAACGA 5290   2644   UUCUUCUG G CUACUUCU 4005   AGAAGAA GGCTAGCTACAACGA AGCCAGAA 5291   2655   UUCUUCUU G UCAUCAUC 4007   GATGATGA GGCTAGCTACAACGA AGCCAGAA 5291   2656   UUGUUCUC A UCCUACGA 4007   GATGATGA GGCTAGCTACAACGA AGCCAGAA 5292   2656   UUGUUCUC A UCCUACGA 4008   TAGGATGA GGCTAGCTACAACGA AGCCAGAA 5293   2656   UUGUUCUC A UCCUACGA 4006   TAGGATGA GGCTAGCTACAACGA AGCCAGAA 5295   2666   AUCCUACGA A UCCUACGA 4010   ACGGTCAG GGCTAGCTACAACGA AGGCAGAA 5295   2667   AUCAUCCU A CGGACCGU 4010   ACGGTCAG GGCTAGCTACAACGA AGGCACAA 5295   2668   UACGGCAC A UCCUACGA 4011   CTTAACGG GCTAGCTACAACGA AGGAACAA 5296   2669   UACGCAC G UUAAGCGG 4012   CCCTTCAG GCTAGCTACAACGA GGTCTACAACGA 5297   2670   UUAAGCGG G CCAAUGAA 4013   TTGGCCG GCTAGCTACAACGA TCACCGTA 5298   2671   UUAAGCGG G CCAAUGAA 4014   TCCATTGG GCTAGCTACAACGA TCCACTGC 5209   2682   AACGGAC G UUAAGCGA 4015   TGGCCGG GCTAGCTACAACGA TCCCCTC 5302   2683   AACUGACA G UUGAGCA 4016   TGCATTGG GCTAGCTACAACGA TCCACTGC 5301   2709   GGCAGGA A UGAAGAAC 4016	2588 AAAGACGA A CUUGGAAA	3992	TTTCCAAG GGCTAGCTACAACGA TCGTCTTT	5278
2602 AAAUCAUU A UUCUAGUA 3995 TACTAGAA GGCTAGCTACAACGA AATGATTT 5281 2608 UUAUUCUA G UAGGCAGG 3996 CGTGCCTA GGCTAGCTACAACGA TACAATAA 5282 2614 UAGUAGGAG G CACGGCGG 3997 CCGCCGTG GGCTAGCTACAACGA CTACTAGA 5283 2614 UAGUAGGAC A CGGCGGUG 3997 CCGCCGTG GGCTAGCTACAACGA CCTACTAGA 5284 2617 UAGGCACG G CGGUGNUU 3999 AATCACCG GGCTAGCTACAACGA CCTACTAGA 5284 2617 UAGGCACG G CGGUGNUU 3999 AATCACCG GGCTAGCTACAACGA CCCTACTA 5285 2620 GCACGGCG G UGAUUGCC 4000 GGCAATCA GGCTAGCTACAACGA CCCGCCG 5287 2622 GGCACGGUG A UUGCCCUU 4001 CATGGCAA GGCTAGCTACAACGA CCCCGCCG 5287 2623 CGGCGGUG A UUGCCCUU 4001 CATGGCAA GGCTAGCTACAACGA CACCGCCG 5287 2624 UGAUUGCC A UUUCUUC 4003 GAACATGG GCCTAGCTACAACGA AATCACCG 5288 2629 UGAUUGCC A UUUCUUCU 4003 GAACATGG GCCTAGCTACAACGA AATCACCG 5288 2631 AUUGCCAU G UUCUUCU 4005 AGAAGTAG GGCTAGCTACAACGA ATCACAAC 5289 2640 UUCUUCUU G CUACUUCU 4005 AGAAGTAG GGCTAGCTACAACGA ATGACAAT 5290 2640 UUCUUCUU G UCAUCUUC 4007 AGAAGTAG GGCTAGCTACAACGA AGCCAGAA 5291 2650 UUCUUCUU G UCAUCUUC 4007 GATGATGA GGCTAGCTACAACGA AGCCAGAA 5291 2651 UUCUUCUU A UCAUCCUU 4006 ACAAGAAG GGCTAGCTACAACGA AGCCAGAA 5292 2652 UUCUUCUU A UCAUCCUU 4006 ACAAGAAG GGCTAGCTACAACGA AGCAAGAA 5292 2653 UUCUUCUU A UCAUCCUU 4007 GATGATGA GGCTAGCTACAACGA AGCAAGAA 5292 2656 UUCUCAUC A UCCUUCUG 4007 CATGAGAA GGCTAGCTACAACGA AGCAAGAA 5292 2656 UUCUCAUC A UCCUUCUG 4007 CATGAGAA GGCTAGCTACAACGA AGCAAGAA 5292 2656 UUCUCAUC A UCCUUCUG 4009 CCCTAGGA GGCTAGCTACAACGA AGCAAGAA 5292 2656 UUCUCAUC A UCCUACGG 4009 CCCTAGGA GGCTAGCTACAACGA AGCAAGAA 5295 2661 AUCAUCCU A CGGACCGU 4010 ACGGTCCG GGCTAGCTACAACGA AGCAAGAA 5295 2662 UUCUCAUC A UCCUACGG 4011 CTACACG GGCTAGCTACAACGA AGCAAGAA 5295 2663 ACUGAGAA C GUUAACCGG 4011 CTACACG GGCTAGCTACAACGA AGGAAGAA 5295 2664 UUCAACCGG A CUGAUGAA 4011 CTACACG GGCTAGCTACAACGA AGGAACGA 5298 2673 ACCGUUAA G CGGCCAA 4013 TTGGCCCG GGCTAGCTACAACGA AGGACCTA 5298 2673 ACCGUUAA G CGGACCAA 4013 TTGGCCCG GGCTAGCTACAACGA CCGTTAGA 5298 2679 GAACGACU A UUGAACGAC 4011 CTACACG GGCTAGCTACAACGA TCCCTCC 5302 2698 AACUGAGA A UGAACACU 4014 CACACACGA GGCTAG	2596 ACUUGGAA A UCAUUAUU	3993	AATAATGA GGCTAGCTACAACGA TTCCAAGT	5279
2608 UUNUUCUA G UAGGCACG 3996 CGTGCCTA GGCTAGCTACAACGA TAGAATAA 5282 2612 UCUAGUAG G CACGGCGG 3997 CCGCCGTG GGCTAGCTACAACGA CTACTACAA 5283 2614 UAGUAGGC A CGGCGGUG 3998 CACCGCCG GGCTAGCTACAACGA CCTACTACA 5284 2617 UAGCACGC G CGGUGAUU 3999 AATCACCG GGCTAGCTACAACGA CGTGCTAC 5284 2617 UAGCACGC G CGGUGAUU 3999 AATCACCG GGCTAGCTACAACGA CGTGCTAC 5285 2620 GCACGGCG G UGAUUCC 4000 GGCAATCA GGCTAGCTACAACGA CGCCGCG 5286 2621 CGGUGAUU G CCAUGUUC 4001 CATGGCAA GGCTAGCTACAACGA CACCGCCG 5286 2622 CGGUGAUU G CCAUGUUC 4002 GAACATGG GGCTAGCTACAACGA CACCGCCG 5288 2623 UAGUUCUCC A UGUUCUC 4003 GAACATGG GGCTAGCTACAACGA AATCACCC 5288 2624 UUCUUCUC G CUACUUCU 4003 GAACATGG GGCTAGCTACAACGA AATCACCC 5288 2625 UUCUUCUC G CUACUUCU 4005 AGAAGAAG GGCTAGCTACAACGA AATCACCC 5289 2631 AUUGCCAU G UUCUUCUC 4004 CAGAAGAA GGCTAGCTACAACGA AATCACCC 5289 2643 UUCUUCUC G CUACUUCU 4005 AGAAGAAG GGCTAGCTACAACGA AGCCAGAA 5291 2653 UUCUUCUC G CUACUUCU 4006 ACAGAAAG GGCTAGCTACAACGA AGCCAGAA 5292 26543 UUCUUGU A CUACUCUU 4006 ACAGAAAG GGCTAGCTACAACGA AGCCAGAA 5292 26550 UUCUUCUC A UCAUCCUU 4006 TAGGAATGA GGCTAGCTACAACGA AGCCAGAA 5292 26561 AUCUUCUU G UCAUCAUC 4007 GATGAATGA GGCTAGCTACAACGA AGCCAGAA 5293 26561 AUCUUCUU A UCCACCGU 4007 CATGAATGA GGCTAGCTACAACGA AGCCAGAA 5293 26561 AUCUUCUU A UCCACCGU 4008 TAGGAATGA GGCTAGCTACAACGA AGCCAGAA 5295 26561 AUCUUCUU A UCCACCGU 4010 ACGGTCAG AGCTACAACGA AGGATGA 5295 26561 AUCAUCCU A CGGACCGU 4010 ACGGTCAG AGCTACAACGA GGTTACAACGA 5297 26681 AACGAAGA A CCGGUAAG 4011 CTTAACGG GGCTAGCTACAACGA GGTTACAACGA 5297 2679 UAAACGG A CCGUUAAG 4011 CTTAACGG GGCTAGCTACAACGA GGTCCGTA 5298 2673 ACCGUUAA C CGGCAA 4011 TTGGCCCG GCTAGCTACAACGA TGGCCCCC 5301 2681 GCGGGCCA A UGGAGGG 4012 CCGCTTAG GGCTAGCTACAACGA TGGCCCCC 5301 2691 AACGAAGA A CGGGCAA 4013 TCGCCCCC GCCTAGCAACAGA TTCACCCC 5302 2692 AACGAAGA A CAGGCAU 4017 TCGCCCG GCCTAGCTACAACGA TGCCCCCC 5302 2702 GAAGACAG G CUACUGU 4024 CACATGGA GGCTAGCTACAACGA TGCCCCC 5302 2703 GACGGAC A UGGAGGA 4014 TCCCATGG GCCTAGCTACAACGA AGCCCTC 5302 2704 GACGACC A UGGAGCA 4017 TCGCCCG GCCTAGCTACAACGA	2599 UGGAAAUC A UUAUUCUA	3994	TAGAATAA GGCTAGCTACAACGA GATTTCCA	5280
2612 UCUAGUAG G CACGGCGU 3997 CCGCCGTG GGCTAGCTACAACGA CTACTAGA 5283 2614 UAGUAGGC A CGGCGUUG 3998 CACCGCCG GGCTAGCTACAACGA CCTACTA 5284 2617 UAGGCACG G CGGUGAUU 3999 AATCACCG GGCTAGCTACAACGA CCTACTA 5284 2620 GCACGGCG G UGAUUGCC 4000 GGCAATCA GGCTAGCTAACGA CGTCGCTG 5287 2620 GCACGGCG G UGAUUGCC 4001 CATGGCAA GGCTAGCTAACGA CGCCGTGC 5287 2622 GCGCGUG A UUGCCAUG 4001 CATGGCAA GGCTAGCTAACGA CACCGCCG 5287 2625 UGAUUGCC A UUUCUUC 4002 GAACATGG GGCTAGCTACAACGA CACCGCCG 5287 2626 UGAUUGCC A UUUCUUCU 4002 GAACATGG GGCTAGCTACAACGA AATCACCG 5288 2629 UGAUUGCC A UUUCUUCU 4004 CAGAAGAA GGCTAGCTACAACGA AATCACCA 5289 2621 AUUGCCAU G UUCUUCUU 4005 AGAAGAA GGCTAGCTACAACGA ATGCCAAT 5290 2640 UUCUUCUG G CUACUUCU 4005 AGAAGAA GGCTAGCTACAACGA ATGCCAAA 5291 2643 UUCUGGCU A CUUCUUGU 4005 ACAAGAA GGCTAGCTACAACGA ATGCCAAA 5292 2650 UACUUCUU G UCAUCUUC 4007 GATGATGA GGCTAGCTACAACGA AGCCAGAA 5292 2650 UACUUCUU G UCAUCAUC 4007 GATGATGA GGCTAGCTACAACGA AGCCAGAA 5292 2650 UACUUCUU A UCAUCCUA 4008 TAGGATGA GGCTAGCTACAACGA AGCAAGAA 5294 2650 UACUUCUU A UCAUCCUA 4008 TAGGATGA GGCTAGCTACAACGA AGCAAGAA 5294 2651 UUCUUGUC A UCAUCCUA 4008 TAGGATGA GGCTAGCTACAACGA AGCACAAA 5295 2656 UUGUCAUC A UCGACGG 4009 CCGTAGGTAGCTACAACGA AGCACAAA 5295 2666 UUGUCAUC A UCGACGG 4009 CCGTAGGTAGCTACAACGA AGCACAAA 5295 2666 UUCUGAGC A CGGUCAA 4011 CTTAACGG GGCTAGCTACACGA AGCAGTAGA 5297 2666 UACGGCCC G UUAAGCGG 4012 CCCGCTTAA GGCTAGCTACACGA CGTAGGAA 5297 2666 UACGGCC G UUAAGCGG 4012 CCCGCTTAA GGCTAGCTACACGA CGTAGGAA 5297 2667 UUAAGCGG C CCAUGGA 4011 CTTAACGG GGCTAGCTACAACGA CTGTAGGA 5297 2668 UACGGACC A UGGAACA 4011 CTTAACGG GGCTAGCTACAACGA CTGTACAGA 5297 2679 UUAAGCGG C CCAUGGA 4011 CTTAACGG GGCTAGCTACAACGA CTGCTACA 5298 2671 CUACGGG A CUGAAGAC 4012 CCCCCCC GGCTAGCTACAACGA CTCCCC 5302 2679 UUAAGCGG C CAUGGAA 4011 CTTAACGG GGCTAGCTACAACGA CTCCCC 5302 2679 UUAAGCGG C CAUGGAA 4011 CTTAACGG GGCTAGCTACAACGA CTCCCC 5302 2679 CUACGGC A UGGAACA 4016 GTCTCG GGCTAGCTACAACGA CTCCTCC 5302 2670 GAAGACAU G UCAACGGU 4018 CAACTAG GGCTAGCTACAACGA CTCCTCC 5302 2770 GAAGAGG A CUGAGAC	2602 AAAUCAUU A UUCUAGUA	3995	TACTAGAA GGCTAGCTACAACGA AATGATTT	5281
2614 UAGUAGGC A CGGCGGUG 3998 CACCGCCG GGCTAGCTACAACGA GCCTACTA 5284 2617 UAGGCACG G CGGUGAUU 3999 AATCACCG GGCTAGCTACAACGA CGTGCCTA 5285 2620 GCACGGCG G UGAUUGCC 4000 GGCAATCA GGCTAGCTACAACGA CGTGCCTA 5285 2623 CGGCGGUG A UUGCCAUG 4001 CATGGCAA GGCTAGCTACAACGA CGCCGTG 5287 2626 CGGUGAUU G CCAUGUUC 4002 GAACATGG GGCTAGCTACAACGA CACCGCCG 5288 2629 UGAUUGCC A UGUUCUUC 4003 GAACATGG GGCTAGCTACAACGA AATCACCG 5288 2631 AUUGCCAU G UUCUUCU 4003 GAACATGG GGCTAGCTACAACGA AATCACCG 5288 2631 AUUGCCAU G UUCUUCU 4005 AGAAGAA GGCTAGCTACAACGA ATGGCAAC 5289 2640 UUCUUCUG G CUACUUCU 4005 AGAAGAA GGCTAGCTACAACGA ATGGCAACA 5290 2640 UUCUUCUG G CUACUUCU 4005 AGAAGAA GGCTAGCTACAACGA ATGGCAACA 5291 2640 UUCUUCUG G CUACUUCU 4005 AGAAGAA GGCTAGCTACAACGA AGGCAAGAA 5292 2650 UACUUCUU G UCAUCAUC 4007 GATGATGA GGCTAGCTACAACGA AGGCAAGAA 5292 2651 UUCUUCUC A UCAUCAU 4008 ACAAGAA GGCTAGCTACAACGA AGGCAAGAA 5292 2653 UUCUUCUU C UCAUCAUC 4007 GATGATGA GGCTAGCTACAACGA AGGCAAGAA 5294 2655 UUCUUCUU C UCAUCAGG 4009 CCGTAGGA GGCTAGCTACAACGA AGGAAGAA 5294 2656 UUCUUCUU A UCAUCAU 4008 ACGGTCG GGCTAGCTACAACGA AGGAAGAA 5294 2656 UUCUUCUU A UCAUCAU 4008 ACGGTCG GGCTAGCTACAACGA AGGATGAT 5296 2656 UUCUCACGG A CCGUUAAGG 4011 CTTAACGG GGCTAGCTACAACGA AGGATGAT 5296 2667 ACCGUCAGG A CCGUUAAGG 4011 CTTAACGG GGCTAGCTACAACGA AGGATGAT 5296 2668 UACGGACC G UUAAGGG 4012 CCGCTTAA GGCTAGCTACAACGA CTGTCAGA 5297 2673 ACCGUUAA G CGGGCCAA 4013 TTGGCCCG GGCTAGCTACAACGA CCGCTTAA 5300 2671 UUAAGCGG G CCAAUGGA 4014 TCCATTGG GGCTAGCTACAACGA TTAACGT 5299 2673 ACCGUUAA G CGGGCCAA 4013 TTGGCCCG GGCTAGCTACAACGA TCCCCTC 5302 2699 AACUGAAG A CUGACGG 4015 CCCCTCC GGCTAGCTACAACGA TCCCCTC 5302 2691 GAGGGGA A UGGAGGG 4015 CCCCTCC GGCTAGCTACAACGA TCCCTCC 5302 2692 ACUGAGA A CUGACGU 4019 TGGACAAG GGCTAGCTACAACGA TCCCTCC 5302 2709 GAAGACAG C UCCUUGU 4018 ACAAGTAG GGCTAGCTACAACGA TCTCCTTC 5304 2719 GACCGCU A CUUGUCA 4019 TGGACAAG GGCTAGCTACAACGA CCTGTCTC 5302 2719 GACCGCU A UGGAUCAU 4021 ACCTACGA GGCTAGCTACAACGA CTGTCTC 5301 2719 CAUCGUC A UGGAUCAU 4021 TCATGAG GGCTAGCTACAACGA CTGTCTC 5311	2608 UUAUUCUA G UAGGCACG	3996	CGTGCCTA GGCTAGCTACAACGA TAGAATAA	5282
2617 UAGGCACG G CGGUGAUU 3999 AATCACCG GGCTAGCTACAACGA CGTGCCTA 5285 2620 GCACGGCG G UGAUUGCC 4000 GGCAATCA GGCTAGCTACAACGA CGCCGGC 5286 2623 CGGCGGUG A UUGCCAUG 4001 CATGGCAA GGCTAGCTACAACGA CACCGCCG 5287 2626 CGGUGAUU G CCAUGUUC 4002 GAACATGG GGCTAGCTACAACGA CACCGCCG 5287 2629 UGAUUGCC A UGUUCUCUC 4003 GAACATGG GGCTAGCTACAACGA AATCACCG 5288 2629 UGAUUGCC A UGUUCUUC 4003 GAACATGG GGCTAGCTACAACGA AATCACCG 5288 2620 UUCUUCUG G UUCUUCUG 4004 CAGAAGAA GGCTAGCTACAACGA ATGCAAT 5289 2631 AUUCUGCU G UUCUUCUG 4004 CAGAAGAA GGCTAGCTACAACGA ATGCAAT 5290 2640 UUCUUCUG G CUACUUCU 4005 AGAAGTAG GGCTAGCTACAACGA ATGCAAT 5291 2651 UUCUUGUU G UCAUCUUC 4005 AGAAGTAG GGCTAGCTACAACGA AGCAAGTA 5291 2652 UUCUUGUU G UCAUCUUC 4007 GATGATGA GGCTAGCTACAACGA AGCAAGTA 5291 2653 UUCUUGUU G UCAUCCUA 4008 TAGGATGA GGCTAGCTACAACGA AGCAAGTA 5293 2653 UUCUUGUC A UCAUCCUA 4008 TAGGATGA GGCTAGCTACAACGA AGCAAGTA 5293 2654 UUGUUGUC A UCAUCCUA 4008 TAGGATGA GGCTAGCTACAACGA AGCAAGTA 5295 2655 UCGUUCAU A UCGACGG 4009 CCGTAGGA GGCTAGCTACAACGA AGGAAGTA 5295 2656 UUGUUCAUC A CGGACCGA 4019 CCGTAGGA GGCTAGCTACAACGA AGGATGAT 5295 2656 UUGUCAUC A CGGACCGA 4011 CTTAACGG GGCTAGCTACAACGA AGGATGAT 5295 2656 UACGGACC G UUAAGCGG 4012 CCGCTTAA GGCTAGCTACAACGA AGGATGAT 5296 2650 UCCUACGG A CCGUUAAG 4011 CTTAACGG GGCTAGCTACAACGA CGGTAGGA 5297 2661 UAAGCGG C CAAUGGA 4011 TTGGCCCG GGCTAGCTACAACGA CGGTAGGA 5297 2677 UUAAGCG G CCAAUGGA 4011 TCCATTGG GGCTAGCTACAACGA CGCTATGA 5209 2679 UUAAGCGG A CUGAAGCA 4016 GTCTTCA GGCTAGCTACAACGA TCCCCTCC 5302 2698 AACUGAAG A CUGAAGAC 4016 GTCTTCA GGCTAGCTACAACGA TCCCCTCC 5302 2698 AACUGAAG A CUGAUCUU 4018 ACAAGTAG GGCTAGCTACAACGA TCCCCTCC 5302 2709 GGCUACUU G UCCAUCGU 4019 ACAAGTAG GGCTAGCTACAACGA TCCCCTCC 5302 2709 GGCUACUU G UCCAUCGU 4020 ACGATGG GGCTAGCTACAACGA AGCATGC 5310 2719 CCAUCGU A UCGAUCGU 4021 ACCATGA GGCTAGCTACAACGA AGCATGC 5310 2720 GAAGACA C UUGGACA 4019 TTGACCAG GGCTAGCTACAACGA AGCATGC 5310 2721 GUUCUGCA C UCGAUCGU 4021 ACCATGA GGCTAGCTACAACGA AGCATGC 5310 2722 GAAGACA A UUGAACAU 4022 ATCCATGA GGCTAGCTACAACGA AGCATGC 5	2612 UCUAGUAG G CACGGCGG	3997	CCGCCGTG GGCTAGCTACAACGA CTACTAGA	5283
2620 GCACGGCG G UGAUUGCC 4000 GGCAATCA GGCTAGCTACAACGA CGCCCGTGC 5286 2623 GGGGGGIG A UUGCCAUG 4001 CATTGGCAA GGCTAGCTACAACGA CACCGCCG 5287 2626 CGGUGALU G CCAUGUUC 4002 GAACATGG GGCTAGCTACAACGA AATCACCG 5288 2629 UGAUUGCC A UGUUCUUC 4003 GAAGAGA GGCTAGCTACAACGA AATCACCG 5289 2631 AUUGCCAU G UUCUUCUG 4004 CAGAAGAA GGCTAGCTACAACGA GACAAGCA 5289 2631 AUUGCCAU G UUCUUCUG 4004 CAGAAGAA GGCTAGCTACAACGA ATGGCAATT 5290 2640 UUCUUCUG G CUACUUCU 4005 AGAAGAA GGCTAGCTACAACGA AGGCAATCA 5299 2641 UUCUUGUG A CUUCUUGU 4005 ACAAGAAG GGCTAGCTACAACGA AGGAAGAA 5291 2643 UUCUUGUG A CUUCUUGU 4006 ACAAGAAG GGCTAGCTACAACGA AGGAAGAA 5292 2650 UACUUCUU G UCAUCAUC 4007 GATGATGA GGCTAGCTACAACGA AGGAAGAA 5293 2651 UUCUUGUC A UCCUACGG 4009 CCGTAGGA GGCTAGCTACAACGA AGAAGAA 5293 2652 UUCUUGUC A UCCUACGG 4009 CCGTAGGA GGCTAGCTACAACGA AGAAGAA 5295 2651 UUCUUGUC A UCCUACGG 4009 CCGTAGGA GGCTAGCTACAACGA AGAAGAA 5295 2651 UUCUUGUC A UCCUACGG 4009 CCGTAGGA GGCTAGCTACAACGA AGGATGAT 5296 2655 UUCUACGG A CCGUAAGA 4011 CTTAACGG GGCTAGCTACAACGA AGGATGAT 5296 2665 UUCUACGG A CCGUAAGA 4011 CTTAACGG GGCTAGCTACAACGA CGCTAGGA 5297 26668 UACGGACC G UUAAGCGG 4012 CCGCTTAA GGCTAGCTACAACGA CGCTAGGA 5297 2677 UUAAGCGG G CCAAUGGA 4011 TTGGCCCG GGCTAGCTACAACGA CGCCTAGA 5299 2677 UUAAGCGG G CCAAUGGA 4014 TCCATTGG GGCTAGCTACAACGA TCGCCTA 5300 2681 GCGGGCCA A UGGAGGGG 4014 TCCATTGG GGCTAGCTACAACGA TCGCCCTC 5301 2698 AACUGAAG A CUGAAGAA 4014 TCCATTGG GGCTAGCTACAACGA TCGCCCC 5301 2698 AACUGAAG A CUGAAGAA 4016 GTCTTCAG GGCTAGCTACAACGA TCGCCTC 5302 2709 GGCUACUU G UCCAUCGU 4017 GTAGCCTG GGCTAGCTACAACGA CGTCTCTC 5302 2719 GCAUGGC A UUGAGAGA 4016 GTCTTCAG GGCTAGCTACAACGA CGTCTCTC 5302 2720 GAAGACAG A CUGACGAU 4021 ACGATGGA GGCTAGCTACAACGA AGGACAGT 5306 2713 ACUUGUC A UUGAACA 4021 ACGATGGA GGCTAGCTACAACGA AGGACAGT 5307 2716 UUCAGCC A UUGAGAU 4021 ACGATGGA GGCTAGCTACAACGA AGGACAGT 5307 2727 GACAGCU A UUGAACA 4021 ACGATGGA GGCTAGCTACAACGA AGGACAGT 5307 2728 GAUGCGU A UUGAACA 4021 ACGATGGA GGCTAGCTACAACGA AGGACAGT 5307 2729 GAUCACC A UUGAGAU 4022 ATCCATGG GGCTAGCTACAACGA CCAT	2614 UAGUAGGC A CGGCGGUG	3998	CACCGCCG GGCTAGCTACAACGA GCCTACTA	5284
2623 CGGCGGUG À UUGCCAUG 4001 CATGGCAA GGCTAGCTACAACGA CACCGCCG 5287 2626 CGGUGAUU G CCAUGUUC 4002 GAACATGG GGCTAGCTACAACGA AATCACCG 5288 2629 UGAUUGCC À UGUUCUUC 4003 GAAGAACA GGCTAGCTACAACGA AATCACCG 5288 2631 AUUGCCAU G UUCUUCUC 4004 CAGAAGAA GGCTAGCTACAACGA ATGGCAAT 5290 2640 UUCUUCUG G CUACUUCU 4005 AGAAGTAG GGCTAGCTACAACGA ATGGCAAT 5290 2640 UUCUUCUG G CUACUUCU 4005 AGAAGTAG GGCTAGCTACAACGA AGGCAAGAA 5291 2643 UUCUUCUG G CUACUUCU 4006 ACAAGAAG GGCTAGCTACAACGA AGGCAAGAA 5292 2650 UACUUCUU G UCAUCAUC 4007 GATGATGA GGCTAGCTACAACGA AGGCAAGAA 5293 2653 UUCUUUCU A UCCUACGG 4009 CCGTAGGA GGCTAGCTACAACGA AAGAAGAA 5293 2656 UUGUCAUC A UCCUACGG 4009 CCGTAGGA GGCTAGCTACAACGA GACAAGAA 5295 2656 UUGUCAUC A UCCUACGG 4009 CCGTAGGA GGCTAGCTACAACGA GATGACAA 5295 2656 UUGUCAUC A UCCUACGG 4009 CCGTAGGA GGCTAGCTACAACGA GATGACAA 5295 2657 AUCAUCCU A CGGACCGU 4010 ACGGTCCG GGCTAGCTACAACGA GATGACAA 5295 2658 UUCUUGG A CCGUUAAG 4011 CTTAACGG GGCTAGCTACAACGA GATGACAA 5295 2659 UCCUACGG A CCGUUAAG 4011 CTTAACGG GGCTAGCTACAACGA GGTCCGTA 5298 2669 UACAGCGC G UUAAGCGG 4012 CCGCTTAA GGCTACCTACAACGA GGTCCGTA 5298 2673 ACCGUUAA G CGGCCCAA 4011 TCCCATTGG GGCTAGCTACAACGA CGGCTACAA 5299 2673 UAAAGCGG G CCAAUGGA 4014 TCCCATTGG GGCTAGCTACAACGA CCGCTTAA 5300 2681 GCGGCCA A UGGAGAGA 4014 TCCCATTGG GGCTAGCTACAACGA TGCCCGC 5301 2698 AACUGAAGA C CUGUUGU 4016 GTCTTCAG GGCTAGCTACAACGA CTGCTCCC 5302 2698 AACUGAAG A CUGAAGAC 4016 GTCTTCAG GGCTAGCTACAACGA CTGCTTCA 5304 2702 GAAGACAG G CUACUUGU 4018 ACAAGTAG GGCTAGCTACAACGA CTGTCTTC 5304 2703 GACAGGCU A CUUGUCCA 4019 TGGACCAG GGCTAGCTACAACGA CTGTCTTC 5304 2704 GACAGGCU A CUUGUCCA 4021 TGGACCAG GGCTAGCTACAACGA CTGTCTTC 5304 2705 GACAGGCU A CUUGUCCA 4021 TGGACCAG GGCTAGCTACAACGA CTGTCTTC 5302 2706 GGCUACUU G UCCAUCGU 4020 ACGATGG GGCTAGCTACAACGA CTGTCTC 5302 2719 CCAUCGU C UCGAGAGG 4021 CATGACGA GGCTAGCTACAACGA CTGTCTC 5306 2719 CCAUCGU C UCGAGAGA 4021 CATGAGGA GGCTAGCTACAACGA CTGTCTC 5306 2719 CCAUCGU C UCGAGAGA 4021 CATGAGGA GGCTAGCTACAACGA CTGTCTC 5316 2729 GAUCCAG A UGGACAU 4020 ACGATGG GGCTAGCTACAAC	2617 UAGGCACG G CGGUGAUU	3999	AATCACCG GGCTAGCTACAACGA CGTGCCTA	5285
2623         CGGCGGUG A UUGCCAUG         4001         CATGGCAA GGCTACTACAACGA CACCGCCC         5287           2626         CGGUGAUU G CCAUGUUC         4002         GAACATGG GGCTACCAACGA AATCACCG         5288           2629         UGALUGCC A UGUUCUUC         4003         GAAGATGA GGCTACAACGA AATCACCG         5288           2631         AUUGCCAU G UUCUUCUU GU CACAAGAA GGCTAGCTACAACGA ATGCCAAT         5290           2640         UUCUUCUG G CUACUUCU COS         ACAAGAAG GGCTAGCTACAACGA AGCCAGAA         5291           2643         UUCUUCUG G CUACUUCU COS         ACAAGAAG GGCTAGCTACAACGA AGCAGAA         5292           2650         UACUUCUU G UCAUCAUC COS         ACAGAGAG GGCTAGCTACAACGA AGCAGAA         5292           2651         UUCUUCU G UCAUCAUC COS         ACAGAGAG GGCTAGCTACAACGA AGCAGAA         5292           2655         UUCUUCU G UCAUCAUC COSCAGG         4007         CATTAGGA GGCTAGCTACAACGA GATGACAA         5294           2656         AUCGUACU A UCGUACGG         4010         ACGGTAGGTACAACAGA GATGACAAA         5292           2661         AUCAUCCU A CGGACCGU A011         CTTAACGG GCTAGCTACAACGA GTGCTACAACGA CCGTTAGA         5297           2668         UUCUCCGG A CCGUAAGA         4011         CTTAACGG GCTAGCTACAACGA CCGCTTAA         5298           2673         ACCGUAAGA         4012         T	2620 GCACGGCG G UGAUUGCC	4000	<u> </u>	
2626 GGGUGAUU G CCAUGUUC 4002 GAACATG GGCTAGCTACAACGA AATCACCG 5288 2629 UGAUUGCC A UGUUCUUC 4003 GAAGAACA GGCTAGCTACAACGA AGCAATCA 5289 2631 AUUGCCAU G UUCUUCUG 4004 CAGAAGAA GGCTAGCTACAACGA ATGGCAAT 5290 2640 UUCUUCUG G CUACUUCU 4005 AGAAGTAG GGCTAGCTACAACGA ATGGCAAT 5290 2640 UUCUUCUG G CUACUUCU 4005 AGAAGTAG GGCTAGCTACAACGA AGGAAGAA 5291 2643 UUCUUGCG C CUACUUCU 4006 ACAAGAAG GGCTAGCTACAACGA CAGAAGAA 5291 2653 UUCUUGUC A UCAUCCU 4007 GATGATGA GGCTAGCTACAACGA AGGAGAA 5292 2650 UACUUCUU G UCAUCCU 4008 TAGGATGA GGCTAGCTACAACGA AAGAAGTA 5292 2651 AUCUUCUC A UCCAUCGU 4008 TAGGATGA GGCTAGCTACAACGA AAGAAGA 5295 2651 AUCAUCCU A CGGACCGU 4010 ACGGTCG GGCTAGCTACAACGA GACAAGAA 5295 2661 AUCAUCCU A CGGACCGU 4010 ACGGTCG GGCTAGCTACAACGA GACAAGAA 5295 2661 AUCAUCCU A CGGACCGU 4010 ACGGTCG GGCTAGCTACAACGA GATGACAA 5295 2662 UCCUACGG A CCGUUAAG 4011 CTTAACGG GGCTAGCTACAACGA GATGACAA 5295 2663 UACGGCC G UUAAGCGG 4012 CCGCTTAA GGCTAGCTACAACGA GGTCCGTA 5298 2664 UACGGCC G UUAAGCGG 4012 CCGCTTAA GGCTAGCTACAACGA TAGACGA 5297 2665 UACGGCC G UUAAGCGG 4012 CCGCTTAA GGCTAGCTACAACGA TAGACGA 5299 2667 UUAAGCGG G CCAAUGGA 4013 TTGGCCCG GGCTAGCTACAACGA TCGCCCGC 5300 2668 UACGGCCA A UGGAGCAA 4013 TTGGCCCG GGCTAGCTACAACGA TCCCCTCC 5302 2669 AACUGAAG A CUGAAGAC 4016 GTCTTCAG GGCTAGCTACAACGA TCCCCTCC 5302 2698 AACUGAAG A CUGAAGAC 4017 GTAGACTA GGCTAGCTACAACGA TCCCCTCC 5302 2698 AACUGAAG A CUGAUCUU 4018 ACAAGTAG GGCTAGCTACAACGA CTCTCAGTT 5303 2702 GAAGAGCU A CUGUCCAA 4019 TGGACAAG GGCTAGCTACAACGA AGCCTGTC 5302 2703 GACAGGCU A CUGUCCAA 4021 TGGACCAG GGCTAGCTACAACGA AGCCTGTC 5302 2713 ACUUGUC A UCGAUCGU 4021 ACCATGGA GGCTAGCTACAACGA AGCCTGTC 5302 2714 CUUCUCC A UCGAUCGU 4021 ACCATGGA GGCTAGCTACAACGA AGCCTGTC 5302 2715 CACAGGCU A UGGAUCCA 4021 TGGACCA GGCTAGCTACAACGA AGCCTGTC 5302 2716 GUCCAUC G UCAUCGAU 4021 ACCATGGA GGCTAGCTACAACGA CACGTAG GGCTAGCTACAACGA CACGTAGG GGCTAGCTACAA	2623 CGGCGGUG A UUGCCAUG		<del> </del>	
2629 UGAUUGCC A UGUUCUUC 4003 GAAGAACA GGCTAGCTACAACGA GGCAATCA 5289 2631 AUUGCCAU G UUCUUCUG 4004 CAGAAGAA GGCTAGCTACAACGA ATGGCAAT 5290 2640 UUCUUCUG G CUACUUCU 4005 AGAAGTAG GGCTAGCTACAACGA ATGGCAAT 5290 2643 UUCUGGCU A CUUCUUGU 4006 ACAAGAAG GGCTAGCTACAACGA AGCCAGAA 5291 2650 UACUUCUU G UCAUCUUGU 4006 ACAAGAAG GGCTAGCTACAACGA AGCCAGAA 5292 2650 UACUUCUU G UCAUCUUGU 4007 GATGATGA GGCTAGCTACAACGA AGAAGTA 5293 2651 UUCUUGUC A UCAUCUU 4008 TAGGATGA GGCTAGCTACAACGA AGAAGTA 5293 2652 UUCUUGUC A UCAUCCUA 4008 TAGGATGA GGCTAGCTACAACGA AGAAGTA 5294 2653 UUCUUGUC A UCAUCCUA 4008 TAGGATGA GGCTAGCTACAACGA GACAAGAA 5294 2656 UUGUCAUC A UCCUACGG 4009 CCGTAGGA GGCTAGCTACAACGA GACAAGAA 5295 2651 AUCAUCUU A CGGACCGU 4010 ACCGTCCG GGCTAGCTACAACGA GATGACAA 5295 2652 UCCUACGG A CCGUUAAG 4011 CTTAACGG GGCTAGCTACAACGA GGTCGTTA 5296 2653 UCCUACGG A CCGUUAAG 4011 CTTAACGG GGCTAGCTACAACGA GTCCGTTA 5296 2656 UCCUACGG A CCGUUAAG 4012 TTGGCCCG GGCTAGCTACAACGA GTCCGTTA 5298 26673 ACCGUUAA G CGGGCCAA 4013 TTGGCCCG GGCTAGCTACAACGA GTCCGTTA 5300 2668 UACGGACC G UUAAGCGG 4012 CCGCTTAA GGCTAGCTACAACGA TTAACGGT 5299 2671 UUAAGCGG G CCAAUGGA 4014 TCCATTGG GGCTAGCTACAACGA TCGCCCCC 5301 2691 GGAGGGAA A CUGAAGGA 4016 GTCTTCAG GGCTAGCTACAACGA TCCCCTCC 5302 2692 AACUGAAGA A CUGAAGAA 4016 GTCTTCAG GGCTAGCTACAACGA TCCCCTC 5302 2702 GAAGACAG G CUACUUGU 4018 ACAAGTAG GGCTAGCTACAACGA TCTCCTTC 5302 2703 GACAGGCU A CUUGUCCA 4019 TGGACAAG GGCTAGCTACAACGA AGCTCTTC 5304 2705 GACAGGCU A CUUGUCCA 4019 TGGACAAG GGCTAGCTACAACGA AGCTCTTC 5304 2713 ACUUGUCC A UCCAUCGU 4021 ACCATGAG GGCTAGCTACAACGA AGCTCTTC 5302 2713 CUUCAUC G UCCAUCGU 4021 ACCATGAG GGCTAGCTACAACGA AGCTCTC 5302 2713 CUUCAUC G UCCAUCGU 4021 ACCATGAG GGCTAGCTACAACGA AGCTCTC 5302 2714 CUUCCAUC G UCCAUCGU 4021 ACCATGAG GGCTAGCTACAACGA AGCTAGCA GAGCACGA GAGCACGA GACAAGA ACCACACGA GGCTAGCTACAACGA GACGAACGA GAGCACGA GAGCACGA GACAACGA GGCTAGCTACAACGA GACGAACGA GAGCACGA GAGCACGA GACAACGA GCCAACGA GGCTAGCTACAACGA GACGAACGA GACAACGA GCCAACGA GCCAACGA GCCAACGA GCCAACGA GCCAACGA GCCAACGA GCCAACGA GCCAACGA GCCA	2626 CGGUGAUU G CCAUGUUC	4002		5288
2631 AUUGCCAU G UUCUUCUG 4004 CAGAAGAA GGCTAGCTACAACGA ATGCCAAT 5290 2640 UUCUUCUG G CUACUUCU 4005 AGAAGTAG GGCTAGCTACAACGA CAGAAGAA 5291 2643 UUCUGCU A CUUCUUGU 4006 ACAAGAAG GGCTAGCTACAACGA AGCCAGAA 5292 2650 UACUUCUU G UCAUCAUC 4007 GATGATGA GGCTAGCTACAACGA AGCAAGAA 5292 2653 UUCUUGUC A UCAUCCUU 4008 TAGGATGA GGCTAGCTACAACGA AGCAAGAA 5294 2656 UUGUCAUC A UCCUCACGG 4009 CCGTAGGA GGCTAGCTACAACGA GACAAGAA 5294 2656 UUGUCAUC A CGGACCGU 4010 ACGGTCG GGCTAGCTACAACGA AGGATGAT 5295 2661 AUCAUCCU A CGGACCGU 4010 ACGGTCG GGCTAGCTACAACGA AGGATGAT 5296 2662 UUCUGCG A CCGUUAAG 4011 CTTAACGG GGCTAGCTACAACGA AGGATGAT 5296 2663 UACGGACC G UUAAGGCG 4012 CCGCTTAA GGCTAGCTACAACGA GGTCGTA 5298 2663 UACGGACC G UUAAGGCG 4012 CCGCTTAA GGCTAGCTACAACGA GGTCGTA 5298 2664 UACGGACC G UUAAGGCG 4012 CCGCTTAA GGCTAGCTACAACGA CCGCTTAA 5299 2677 UUAAGCGG G CCAAUGGA 4014 TCCATTGG GGCTAGCTACAACGA CCGCTTAA 5300 2691 GGGGGCCA A UGGAGGGG 4015 CCCCTCCC GGCTAGCTACAACGA CCGCTTAA 5300 2691 GGAGGGGA A CUGAAGAC 4016 GTCTTCAG GGCTAGCTACAACGA TCCCCTCC 5302 2698 AACUGAAG A CAGGCUAC 4017 GTAGCCTG GGCTAGCTACAACGA TCCCCTCC 5302 2698 AACUGAAG A CAGGCUAC 4017 GTAGCCTG GGCTAGCTACAACGA CTCCTCTC 5302 2709 GGCUACUU G UCCAUCGU 4019 TGGACAAG GGCTAGCTACAACGA AGCCTTCC 5302 2713 ACUUGUCC A UCGUCCA 4019 TGGACAAG GGCTAGCTACAACGA AGCCTTCC 5305 2714 GUGCCAUC G UCAUCGUC 4020 ACGATGGA GGCTAGCTACAACGA AGCCTTCC 5306 2713 ACUUGUCC A UCGUCACU 4020 ACGATGGA GGCTAGCTACAACGA AGCCTTCC 5307 2716 UGUCCAUC G UCAUCGU 4021 CATGACGA GGCTAGCTACAACGA AGCCTTCC 5307 2717 CCAUCGUC A UCGUCACU 4020 ACGATGGA GGCTAGCTACAACGA AGCCTTCC 5307 2718 CCUUCUC A UCGUCAUG 4021 CATGACGA GGCTAGCTACAACGA AGCCTTCC 5307 2719 GCCAUCGU A UCGUCACU 4020 ACGATGGA GGCTAGCTACAACGA AGCCATGG 5307 2719 CCAUCGUC A UCGUCAUG 4021 CATGACGA GGCTAGCTACAACGA CGACAGGT 5307 2729 GGCUCAUG A UCGUCAUG 4021 CATGACGA GGCTAGCTACAACGA CGACAGGT 5307 2733 CCCAUCGUC A UCGUCAU 4026 ACGATGA GGCTAGCTACAACGA CCATGACG 5310 2733 CCCAUCGUC A UCGAGAAC 4023 TGGATCCA GGCTAGCTACAACGA CCATGACG 5312 2739 GAACUCC A UUGAACAA 4025 GACGTTCA GGCTAGCTACAACGA	<del></del>	<del>  </del>	<del> </del>	
2640 UUCUUCUG G CUACUUCU 4005 AGAAGTAG GGCTAGCTACAACGA CAGAAGAA 5291 2643 UUCUGGCU A CUUCUUGU 4006 ACAAGAAG GGCTAGCTACAACGA AGCCAGAA 5292 2650 UACUUCUU G UCAUCAUC 4007 GATGATGA GGCTAGCTACAACGA AGCCAGAA 5293 2653 UUCUUGUC A UCAUCAUC 4007 GATGATGA GGCTAGCTACAACGA AGAAGTA 5294 2656 UUGUCAUC A UCCUCACGG 4009 CCGTAGGA GGCTAGCTACAACGA GACAAGAA 5295 2661 AUCAUCCU A UCCUCACGG 4009 CCGTAGGA GGCTAGCTACAACGA GATGACAA 5295 2661 AUCAUCCU A CGGACCGU 4010 ACCGTCG GGCTAGCTACAACGA GATGACAA 5295 2665 UUCUCACGG A CCGUUAAG 4011 CTTAACGG GGCTAGCTACAACGA CGGTAGGA 5297 2668 UACGGACC G UUAAGCGG 4012 CCGCTTAA GGCTAGCTACAACGA GGTCGTA 5298 2673 ACCGUUAA G CGGGCCCAA 4013 TTGGCCCG GGCTAGCTACAACGA GGTCCGTA 5298 2673 UUAAGCGG C CAAUGGA 4014 TCCATTGG GGCTAGCTACAACGA TTAACGGT 5299 2671 UUAAGCGG CCAAUGGA 4014 TCCATTGG GGCTAGCTACAACGA TGGCCCGC 5301 2691 GGAGGGCA A UGGAGGGG 4015 CCCCTCCA GGCTAGCTACAACGA TGGCCCGC 5302 2698 AACUGAAG A CUGAAGAC 4016 GTCTTCAG GGCTAGCTACAACGA TGGCCCGC 5302 2698 AACUGAAG A CAGGCUAC 4017 GTAGCCTG GGCTAGCTACAACGA TCCCTCC 5302 2702 GAAGACAG G CUACUUGU 4018 ACAAGTAG GGCTAGCTACAACGA TGCCCTCC 5302 2705 GACAGGCU A CUUGUCCA 4019 TGGACAAG GGCTAGCTACAACGA AGCTCTTC 5304 2719 GGCUACUU G UCCAUCGU 4020 ACGATGG GGCTAGCTACAACGA AGCTCTTC 5305 2719 CCAUCGU C UCCAUCGU 4020 ACGATGG GGCTAGCTACAACGA AGCTAGTC 5305 2719 CCAUCGU C UCCAUCGU 4021 CATGACGA GGCTAGCTACAACGA AGTAGCC 5307 2716 UGUCCAUC G UCAUCGU 4021 CATGACGA GGCTAGCTACAACGA AGTAGCC 5307 2717 CCAUCGU C UCAUCGU 4022 ATCCATGA GGCTAGCTACAACGA AGTAGCC 5307 2718 CCAUCGU C UCAUCGAU 4021 CATGACGA GGCTAGCTACAACGA GACGATGG 5307 2719 CCAUCGU C UCAUCGAU 4022 ATCCATGA GGCTAGCTACAACGA GACGATGG 5307 2719 CCAUCGU C UCAUCGAU 4021 CATGACGA GGCTAGCTACAACGA CCATGACG 5310 2729 GGAUCCAG A UGAACUC 4023 TGGATCA GGCTAGCTACAACGA CCATGACG 5310 2733 CCUCAUGG A UCAGGAUG 4023 TGGATCA GGCTAGCTACAACGA CCATGACG 5310 2739 GAACUCC A UUGGAUGA 4024 CATCTGGA GGCTAGCTACAACGA CCATGACG 5312 2739 GAACUCC A UUGGAUGA 4026 AATGGGAG GGCTAGCTACAACGA TCATCCTAG 5312 2739 GAACUCC A UUGGAUGA 4029 TCACAAG GGCTAGCTACAACGA TCATCCAA 531				
2643         UUCUGGCU A CUUCUUGU         4006         ACAAGAAG GGCTAGCTACAACGA AGCCAGAA         5292           2650         UACUUCUU G UCAUCAUC         4007         GATGATGA         GGCTAGCTACAACGA AAGAAGTA         5293           2653         UUCUUGUCAU CA UCAUCCUA         4008         TAGGATGA         GGCTAGCTACAACGA GACAGAA         5294           2656         UUGUCAUC A UCCUACGG         4009         CCGTAGGA         GGCTAGCTACAACGA GAGATGAT         5295           2661         AUCAUCCU A CGGACCGU         4010         ACGGTCCG GGCTAGCTACAACGA AGGATGAT         5296           2665         UCCUACGG A CCGUUAAG         4011         CTTAACGG GGCTAGCTACAACGA CCGCTAGGA         5297           2668         UACGGACC G UUAAGCGG         4012         CCCGCTTAA         GGCTAGCTACAACGA CGGTTCGTA         5298           2677         UUAAGCGG G CCAAUGGA         4014         TCCATTGG GGCTAGCTACAACGA CCGCTTAA         5300           2691         GGAGGGA A CUGAAGAC         4016         GTCTTCCA GGCTAGCTACAACGA TGCCCCC         5301           2692         GAAGAGAGA C CUGAUGA         4017         GTAGCTACAACGA CTGCTCTCAACGA CTGCTCTC         5302           2702         GAAGACGA C CUGAUGUA         4017         GTAGACTACAACGA CTGTCTCTC         5304           2703         GACAGGCUA C AUGGUCAA				
2650         UACUUCUU G UCAUCAUC         4007         GATGATGA GGCTAGCTACAACGA AAGAAGTA         5293           2653         UUCUUGUC A UCAUCCUA         4008         TAGGATGA GGCTAGCTACAACGA GACAAGAA         5294           2655         UUGUCAUC A UCCUACGG         4009         CCGTAGGA GGCTAGCTACAACGA GATGACAA         5295           2661         AUCAUCCU A CGGACCGU         4010         ACGGTCG GGCTAGCTACAACGA AGGATGAT         5296           2665         UCCUACGG A CCGUUAAG         4011         CTTAACGG GGCTAGCTACAACGA AGGATCGAT         5296           2668         UACGGACC G UUAAGCGG 4012         CCCCTTAA GGCTAGCTACAACGA GGTCCGTA         5298           2673         ACCGUUAG C GGGCCAA         4013         TTGGCCGG GGCTAGCTACAACGA GGTCCGTA         5299           2671         UUAAGCGG G CCAAUGGA         4014         TCCATTGG GGCTAGCTACAACGA TTAACGGT         5299           2671         UUAAGCGG G CCAAUGGA         4014         TCCATTGG GGCTAGCTACAACGA TTAACGGT         5300           2681         GCGGGCCA A UGGAGGG         4015         CCCCTCCA GGCTAGCTACAACGA TTCCCCTCC         5302           2698         AACUGAAG A CAGGCUAC         4016         GTTCTCAG GGCTAGCTACAACGA CTTCCTCT         5302           2702         GAAGACGA A CUUCUGU A018         ACAAGTAG GGCTAGCTACAACGA CTGTCTTC         5304		<del></del>		
2655 UUCUUGUC A UCAUCCUA 4008 TAGGATGA GGCTAGCTACAACGA GACAAGAA 5294 2656 UUGUCAUC A UCCUACGG 4009 CCGTAGGA GGCTAGCTACAACGA GATGACAA 5295 2661 AUCAUCCU A CGGACCGU 4010 ACGGTCCG GGCTAGCTACAACGA AGGATGAT 5296 2665 UCCUACGG A CCGUUAAG 4011 CTTAACGG GGCTAGCTACAACGA AGGATGAT 5296 2666 UACGGACC G UUAAGCGG 4012 CCGCTTAA GGCTAGCTACAACGA GGTCCGTA 5298 2673 ACCGUUAA G CGGCCAA 4013 TTGGCCCG GGCTAGCTACAACGA TTAACGGT 5299 2677 UUAAGCGG G CCAAUGGA 4014 TCCATTGG GGCTAGCTACAACGA TTAACGGT 5299 2681 GCGGGCCA A UGGAAGGA 4015 CCCCTCCA GGCTAGCTACAACGA TGACCGC 5300 2681 GCGGGCCA A UGGAAGGAG 4016 GTCTTCAG GGCTAGCTACAACGA TGCCCCCC 5302 2698 AACUGAAG A CUGAAGAC 4016 GTCTTCAG GGCTAGCTACAACGA TCCCCTCC 5302 2698 AACUGAAG A CUGAAGAC 4017 GTAGCCTG GGCTAGCTACAACGA TCCCCTCC 5302 2702 GAAGACAG G CUACUUGU 4018 ACAAGTAG GGCTAGCTACAACGA TCCCCTCC 5304 2705 GACAGGCU A CUUGUCCA 4019 TGGACAAG GGCTAGCTACAACGA CTTCAGTT 5303 2702 GAAGACAG G CUACUUGU 4018 ACAAGTAG GGCTAGCTACAACGA AGCCTTCC 5305 2705 GACAGGCU A CUUGUCCA 4019 TGGACAAG GGCTAGCTACAACGA AGCCTTCC 5305 2713 ACUUGUCC A UCGUCAUG 4021 CATGACGA GGCTAGCTACAACGA AGCTTCC 5307 2714 CUGUCCAUC G UCAUGGAU 4022 ATCCATGA GGCTAGCTACAACGA GACGAAGT 5307 2715 CCAUCGUC A UGGAUCCA 4022 ATCCATGA GGCTAGCTACAACGA GACGAAGT 5307 2716 UGUCCAUC G UCAUGGAU 4022 ATCCATGA GGCTAGCTACAACGA GACGAAGT 5307 2719 CCAUCGUC A UGGAUCCA 4023 TGGATCCA GGCTAGCTACAACGA GACGAATGG 5310 2729 GAUCCAG A UGAACUCC 4025 GGAGTTCC GGCTAGCTACAACGA GACGATGG 5310 2729 GAUCCAG A UGAACUCC 4025 GGAGTTCA GGCTAGCTACAACGA CCATGACG 5311 2733 CCAGAUGA A CUCCAUU 4026 AATGGGAG GGCTAGCTACAACGA CCATGACG 5312 2739 GAACCACC A UUGGAUCA 4021 TCATCAA GGCTAGCTACAACGA CCATGACG 5312 2739 GAACCACG A UGAACUCC 4025 GGAGTTCA GGCTAGCTACAACGA CCATGACG 5312 2739 GAACCACG A UGAACCC 4025 GGAGTTCA GGCTAGCTACAACGA CCATGACG 5312 2739 GAACCACG A UGAACCC 4026 GACGATGG GGCTAGCTACAACGA CCATGACG 5312 2739 GAACCACG A UGAACCC 4026 GACGATGG GGCTAGCTACAACGA CCATGACG 5314 2744 CCCAUUGG A UGAACGAC 4031 GTCTCCAA GGCTAGCTACAACGA TCATCCAA 5315 2750 GGAUGAAC A UUGUGAAC 4031 GTCTCTCA GGCTAGCTACAAC				
2656         UUGUCAUC A UCCUACGG         4009         CCGTAGGA GGCTACAACGA GATGACAA         5295           2661         AUCAUCCU A CGGACCGU         4010         ACGGTCCG GGCTAGCTACAACGA AGGATGAT         5296           2665         UCCUACGG A CCGUUAAG         4011         CTTAACGG GGCTACAACGA CCGTAGGA         5297           2668         UACGGACC G UUAAGCGG         4012         CCGCTTAA GGCTACAACGA GGTCGTA         5298           2673         ACCGUUAA G CGGCCAA         4013         TTGGCCG GGCTACAACGA TTAACGGT         5299           2677         DUAAGCGG G CCAAUGGA         4014         TCCATTGG GGCTACAACGA CCGCCTTAA         5300           2681         GCGGGCCA A UGGAGGGG         4015         CCCCTCCA GGCTACAACGA TCCCCTC         5302           2691         GGAGGGA A CUGAAGAC         4016         GTCTTCAG GGCTACAACGA TCCCCTC         5302           2692         GAAGGACAG A CUGAUGUU         4018         ACAAGTAG GGCTACAACGA TCTCCTC         5302           2702         GAAGAGCA A CUUGUCCA         4019         TGGACAAG GGCTACAACGA AGCCCTTC         5305           2703         GACAGGUA A CUUGUCCA         4019         TGGACAAG GGCTACAACGA AGCCCTTC         5305           2704         GGCUACUU G UCCAUCGU AUCAUCAGA GGCTACACAGA GGCTACAACGA AGCACAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA				
2661         AUCAUCCU A CGGACCGU 4010         ACGGTCCG GGCTAGCTACAACGA AGGATGAT 5296           2665         UCCUACGG A CCGUUAAG 4011         CTTAACGG GGCTAGCTACAACGA CCGTAGGA 5297           2668         UACGGACC G UUAAGCGG 4012         CCGCTTAA GGCTAGCTACAACGA GGTCCGTA 5298           2673         ACCGUUAA G CGGCCAA 4013         TTGGCCCG GGCTAGCTACAACGA TTAACGGT 5299           2677         UUAAGCGG G CCAAUGGA 4014         TCCATTGG GGCTAGCTACAACGA CGCTTAA 5300           2681         GCGGGCCA A UGGAGGGG 4015         CCCCTCCA GGCTAGCTACAACGA TCCCCTCC 5301           2691         GAAGGGGA A CUGAAGAC 4016         GTCTTCAG GGCTAGCTACAACGA TCCCCTCC 5302           2698         AACUGAAG A CAGCUAC 4017         GTAGCTTA GACCTACAACGA TCTCATCT 5303           2702         GAAGACAG G CUACUUGU 4018         ACAAGTAG GGCTAGCTACAACGA CTTCATCT 5305           2705         GACAGGCU A CUUGUCCA 4019         TGGACAAG GGCTAGCTACAACGA AGCCTGTC 5305           2709         GGCUACUU G UCCAUCGU 4020         ACGATGGA GGCTAGCTACAACGA AGCTGTC 5305           2713         ACUUGUCC A UCGUCUGU 4021         CATGACGA GGCTAGCTACAACGA AGCTAGCACGA CTGCTGC           2714         UUCCAUCG G UCAUGGAU 4022         ATCCATGA GGCTAGCTACAACGA GACGATGG 5308           2719         CCAUCGU A UGGAAU 4023         TGGATCCA GGCTAGCTACAACGA CCATGACG 5310           2723         CGUCAUGG A UCCAGAUG ACCAGAGG GAGGTACCAACGA CCATGACG CCATGAC		<del> </del>		
2665         UCCUACGG A CCGUUAAG         4011         CTTAACGG GGCTAGCTACAACGA CCGTAGGA         5297           2668         UACGGACC G UUAAGCGG         4012         CCGCTTAA GGCTACTACAACGA GGTCCGTA         5298           2673         ACCGUUAA G CGGGCCAA         4013         TTGGCCCG GGCTACATACAACGA TTAACGGT         5299           2677         UUAAGCGG G CCAAUGGA         4014         TCCATTGG GGCTACAACGA CGCCTTAA         5300           2681         GCGGGCCA A UGGAGGG         4015         CCCCTCCA GGCTACACACGA TGGCCCGC         5301           2691         GGAGGGGA A CUGAAGAC         4016         GTCTTCAG GGCTAGCTACAACGA TCCCCTCC         5302           2698         AACUGAAG A CAGGCUAC         4017         GTAGCCTG GGCTAGCTACAACGA CTCCACTC         5303           2702         GAAGACAG G CUACUUGU         4018         ACAAGTAG GGCTAGCTACAACGA CTGTCTC         5304           2705         GACAGGCU A CUUGUCA         4019         TGGACAAG GGCTAGCTACAACGA AGCTTCT         5305           2713         ACUUGUCA U GUCCAUCGU         4020         ACGATGGA GGCTAGCTACAACGA AGCAAGT         5307           2716         UGUCCAUC G UCAUGGAU         4021         CATGAGGA GGCTAGCTACAACGA AGCAAGGA ACAGAGA CAATGGACAAGAACAACAAGAACAACAACAACAACAACAACAAC		<del> </del>		
2668         UACGGACC G UUAAGCGG         4012         CCGCTTAA GGCTAGCTACAACGA GGTCCGTA         5298           2673         ACCGUUAA G CGGGCCAA         4013         TTGGCCCG GGCTAGCTACAACGA TTAACGGT         5299           2677         UUAAGCGG G CCAAUGGA         4014         TCCATTGG GGCTAGCTACAACGA CCGCTTAA         5300           2681         GCGGGCCA A UGGAGGG         4015         CCCCTCCA GGCTAGCTACAACGA TGGCCCGC         5301           2691         GGAGGGGA A CUGAAGAC         4016         GTCTTCAG GGCTAGCTACAACGA TCCCCTCC         5302           2698         AACUGAAG A CAGGCUAC         4017         GTAGCCTG GGCTAGCTACAACGA CTCTCAGTT         5303           2702         GAAGACAG G CUACUUGU 4018         ACAAGTAG GGCTAGCTACAACGA CTGTCTC         5304           2705         GACAGGCU A CUUGUCCA 4019         TGGACAGA GGCTAGCTACAACGA AGCCTTC         5305           2709         GGCUACUU G UCCAUCGU 4020         ACGATGGA GGCTAGCTACAACGA AGCACTC         5306           2713         ACUUCCAU G UCAUGGAU 4021         CATGACGA GGCTAGCTACAACGA GATGGAC         5307           2716         UGUCCAUC G UCAUGGAU 4022         ATCCATGA GGCTAGCTACAACGA GATGGAC         5310           2729         CGAUCGA G UCAGAGAC         4023         TGGATCCA GGCTAGCTACAACGA CCATGACG         5310           2729         GGAUCCAG A UGAAC		<del></del>		———
2673         ACCGUUAA G CGGGCCAA         4013         TTGGCCCG GGCTAGCTACAACGA TTAACGGT         5299           2677         UUAAGCGG G CCAAUGGA         4014         TCCATTGG GGCTAGCTACAACGA CGGCTTAA         5300           2681         GCGGGCCA A UGGAGGGG         4015         CCCCTCCA GGCTAGCTACAACGA TGGCCCGC         5301           2691         GGAGGGGA A CUGAAGAC         4016         GTCTTCAG GGCTAGCTACAACGA TCCCCTCC         5302           2698         AACUGAAG A CAGGCUAC         4017         GTAGCCTG GGCTAGCTACAACGA CTTCTAGTT         5303           2702         GAAGACAG G CUACUUGU         4018         ACAAGTAG GGCTAGCTACAACGA CTGTCTTC         5304           2705         GACAGGCU A CUUGUCCA         4019         TGGACAAG GGCTAGCTACAACGA AGCCTGTC         5305           2709         GGCUACUU G UCCAUCGU         4020         ACGATGGA GGCTAGCTACAACGA AGCTAGTA         5306           2713         ACUUGUCC A UCGUCAUG         4021         CATGACGA GGCTAGCTACAACGA GACAAGT         5307           2716         UGUCCAUC G UCAUGGAU         4022         ATCCATGA GGCTAGCTACAACGA GACGATGG         5308           2719         CCAUCGUC A UGGAUGA         4023         TGGATCCA GGCTAGCTACAACGA GACGATGG         5310           2729         GGAUCAGA A UGAACUCC         4024         CATCTGGA GGCTAGCTACAACGA CTGGATCC		<del> </del>		
2677         UUAAGCGG         G         CCAAUGGA         4014         TCCATTGG         GGCTAGCTACAACGA         CCGCTTAA         5300           2681         GCGGGCCA         A         UGGAGGGG         4015         CCCCTCCA         GGCTAGCTACAACGA         TGGCCCGC         5301           2691         GGAGGGGA         A         CUGAGGAC         4016         GTCTTCAG         GGCTAGCTACAACGA         CTCCAGTT         5302           2698         AACUGAAG         A         CAGGCUAC         4017         GTAGCCTG         GGCTAGCTACAACGA         CTTCAGTT         5303           2702         GAAGACAG         G         CUACUUGU         4018         ACAAGTAG         GGCTAGCTACAACGA         AGCCTGTC         5304           2705         GACAGGCU         A         CUUGUCCA         4019         TGGACAAG         GGCTAGCTACAACGA         AGCCTGTC         5305           2709         GGCUACUU         G         UCCAUCGU         4021         CATGACGA         GGCTAGCTACAACGA         AGCAAGT         5306           2713         ACUGUCCA         G         UCAUGGAU         4021         CATGACGA         GGCTAGCTACAACGA         GACATGGCACA         5308           2719         CCAUCGGA         A         UCGAGAUG		<del></del>		
2681         GCGGGCCA A UGGAGGGG         4015         CCCTCCA GGCTAGCTACAACGA TGGCCCGC         5301           2691         GGAGGGA A CUGAAGAC         4016         GTCTTCAG GGCTAGCTACAACGA TCCCCTCC         5302           2698         AACUGAAG A CAGGCUAC         4017         GTAGCCTG GGCTAGCTACAACGA CTGTCTTC         5303           2702         GAAGACAG G CUACUUGU         4018         ACAAGTAG GGCTAGCTACAACGA CTGTCTC         5304           2705         GACAGGCU A CUUGUCCA         4019         TGGACAAG GGCTAGCTACAACGA AGCTTCC         5305           2709         GGCUACUU G UCCAUCGU         4020         ACGATGGA GGCTAGCTACAACGA AAGTAGCC         5306           2713         ACUUGUCC A UCGUCAUG         4021         CATGACGA GGCTAGCTACAACGA GACAAGT         5307           2716         UGUCCAUC G UCAUGGAU         4022         ATCCATGA GGCTAGCTACAACGA GACGATGG         5308           2719         CCAUCGUC A UGGAUCA         4023         TGGATCCA GGCTAGCTACAACGA GACGATGG         5309           2723         CGUCAUGG A UCAGAUGA         4024         CATCTGA GGCTAGCTACAACGA CCATGACG         5310           2729         GGAUCCAG A UGAACUCC         4025         GGAGTTCA GGCTAGCTACAACGA CTACTACG         5312           2733         CCAGAUGA A CUCCCAUU         4026         AATGGGA GGCTAGCTACAACGA CCATTCGG		<del></del>		
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2768 ACUGCCUU A UGAUGCCA 4035 TGGCATCA GGCTAGCTACAACGA AAGGCAGT 5321				
		<del></del>		
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5038 UAGAGUUC G UUGUGCUG	4511	CAGCACAA GGCTAGCTACAACGA GAACTCTA	5797
5041 AGUUCGUU G UGCUGUUU	4512	AAACAGCA GGCTAGCTACAACGA AACGAACT	5798
5043 UUCGUUGU G CUGUUUCU	4513	AGAAACAG GGCTAGCTACAACGA ACAACGAA	5799
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				148		
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5802	UUGAUGUC A	UUUUAUUA	4687	TAATAAAA GGCTAGCTACAACGA GACATCAA	5973
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Input Sequence = AF035121. Cut Site = R/Y

Arm Length = 8. Core Sequence = GGCTAGCTACAACGA

AF035121 (Homo sapiens KDR/flk-1 protein mRNA, complete cds.; Acc# AF035121; 5830 bp)

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## **CLAIMS**

- 1. A compound having Formula II: (SEQ ID NO: 5978)
  - 5'-usascs asau uc<u>U</u> GAu Gag geg aaa gee Gaa Aag aca aB-3'
- wherein each a is 2'-O-methyl adenosine nucleotide, each g is a 2'-O-methyl guanosine nucleotide, each c is a 2'-O-methyl cytidine nucleotide, each u is a 2'-O-methyl uridine nucleotide, each A is adenosine, each G is guanosine, each s individually represents a phosphorothioate internucleotide linkage, U is 2'-deoxy-2'-C-allyl uridine, and B is an inverted deoxyabasic moiety.
  - A composition comprising the compound of claim 1 and a pharmaceutically acceptable carrier or diluent.
  - 3. A method of administering to a cell the compound of claim 1 comprising contacting said cell with the compound under conditions suitable for said administration.
    - 4. The method of claim 3, wherein said cell is a mammalian cell.
    - 5. The method of claim 3, wherein said cell is a human cell.
  - 6. The method of claim 3, wherein said administration is in the presence of a delivery reagent.
- 7. The method of claim 6, wherein said delivery reagent is a lipid.
  - 8. The method of claim 7, wherein said lipid is a cationic lipid.
  - 9. The method of claim 7, wherein said lipid is a phospholipid.
  - 10. The method of claim 6, wherein said delivery reagent is a liposome.
- 11. A method of administering to a cell the compound of claim 1 in conjunction with one or more other drug comprising contacting said cell

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- with the compound and the other drug(s) under conditions suitable for said administration.
- 12. A method of inhibiting ocular angiogenesis in a subject comprising the step of contacting said subject with the compound of claim 1 under conditions suitable for said inhibition.
- 13. The method of claim 12, wherein said angiogenesis is associated with diabetic retinopathy.
- 14. The method of claim 12, wherein said angiogenesis is associated with age related diabetic retinopathy.
- 10 15. A method of cleaving RNA comprising a sequence of KDR RNA comprising contacting the compound of claim 1 with said RNA under conditions suitable for the cleavage of said RNA.
  - 16. The method of claim 15, wherein said cleavage is carried out in the presence of a divalent cation.
- 15 17. The method of claim 16, wherein said divalent cation is Mg2+.
  - 18. A method of administering to a mammal the compound of claim 1 comprising contacting said mammal with the compound under conditions suitable for said administration.
  - 19. The method of claim 18, wherein said mammal is a human.
- 20 20. The method of claim 18 wherein said administration is in the presence of a delivery reagent.
  - 21. The method of claim 18, wherein said delivery reagent is a lipid.
  - 22. The method of claim 21, wherein said lipid is a cationic lipid.
  - 23. The method of claim 21, wherein said lipid is a phospholipid.
- 25 24. The method of claim 20, wherein said delivery reagent is a liposome.

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- 25. A method for treating a subject having endometriosis, comprising contacting said subject with a nucleic acid molecule that modulates the expression of VEGF, VEGFR1, and/or VEGFR2, under conditions suitable for said treatment.
- 5 26. The method of claim 25, wherein said nucleic acid molecule is an enzymatic nucleic acid molecule.
  - 27. The method of claim 25, wherein said nucleic acid molecule is an antisense nucleic acid molecule.
- 28. The method of claim 25, wherein said nucleic acid molecule is a dsRNA nucleic acid molecule.
  - 29. The method of claim 25, wherein said nucleic acid molecule is a nucleic acid aptamer.
  - 30. The method of claim 25, wherein said nucleic acid molecule comprises a sequence having SEQ ID NO: 5977.
- 15 31. The method of claim 26, wherein said enzymatic nucleic acid molecule has an endonuclease activity to cleave RNA encoded by an VEGFR1 and/or VEGFR2 gene.
  - 32. The method of claim 26, wherein said enzymatic nucleic acid molecule is in a hammerhead configuration.
- 20 33. The method of claim 26, wherein said enzymatic nucleic acid molecule is in an Inozyme configuration.
  - 34. The method of claim 26, wherein said enzymatic nucleic acid molecule is in a Zinzyme configuration.
- The method of claim 26, wherein said enzymatic nucleic acid molecule is in a DNAzyme configuration.
  - 36. The method of claim 26, wherein said enzymatic nucleic acid molecule is in a G-cleaver configuration.
  - 37. The method of claim 26, wherein said enzymatic nucleic acid molecule is in an Amberzyme configuration.

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- 38. The method of claim 26, wherein said enzymatic nucleic acid molecule is an allozyme.
- 39. The method of claim 25, wherein said nucleic acid molecule is chemically synthesized.
- 5 40. The method of claim 25, wherein said nucleic acid molecule comprises at least one 2'-sugar modification.
  - 41. The method of claim 25, wherein said nucleic acid molecule comprises at least one nucleic acid base modification.
- 42. The method of claim 25, wherein said nucleic acid molecule comprises at least one phosphate backbone modification.
  - 43. The method of claim 25, wherein said subject is a human.
- 44. A method for treating a subject having endometriosis, comprising administering to the subject a nucleic acid molecule that modulates the expression of VEGF, VEGFR1, and/or VEGFR2, under conditions suitable for said treatment.
  - 45. The method of claim 44 wherein said administration is in the presence of a delivery reagent.
  - 46. The method of claim 45, wherein said delivery reagent is a lipid.
  - 47. The method of claim 46, wherein said lipid is a cationic lipid.
- 20 48. The method of claim 46, wherein said lipid is a phospholipid.
  - 49. The method of claim 45, wherein said delivery reagent is a liposome.
  - 50. The method of claim 44, further comprising administering one or more other drug(s).
- 51. The method of claim 50, wherein said other drug(s) are chosen from GnRH
  25 (gonadotropin releasing hormone) agonists, Lupron Depot (Leuprolide Acetate), Synarel (naferalin acetate), Zolodex (goserelin acetate), Suprefact (buserelin acetate), Danazol, and oral contraceptives.
  - 52. A compound having Formula I: (SEQ ID NO: 5977)

5

## 5' gsasgsusugcUGAuGagg ccgaaa ggccGaaAgucugB 3'

wherein each a is 2'-O-methyl adenosine nucleotide, each g is a 2'-O-methyl guanosine nucleotide, each c is a 2'-O-methyl cytidine nucleotide, each u is a 2'-O-methyl uridine nucleotide, each A is adenosine, each G is guanosine, each s individually represents a phosphorothioate internucleotide linkage,  $\underline{U}$  is 2'-deoxy-2'-C-allyl uridine, and B is an inverted deoxyabasic moiety.

- 53. A composition comprising a compound of claim 52 in a pharmaceutically acceptable carrier or diluent.
- 10 54. A method of administering to a cell the compound of claim 52 comprising contacting said cell with the compound under conditions suitable for said administration.
  - 55. The method of claim 54, wherein said cell is a mammalian cell.
  - 56. The method of claim 54, wherein said cell is a human cell.
- 15 57. The method of claim 54, wherein said administration is in the presence of a delivery reagent.
  - 58. The method of claim 57, wherein said delivery reagent is a lipid.
  - 59. The method of claim 58, wherein said lipid is a cationic lipid.
  - 60. The method of claim 58, wherein said lipid is a phospholipid.
- 20 61. The method of claim 57, wherein said delivery reagent is a liposome.
  - 62. A method of administering to a cell the compound of claim 52 in conjunction with a chemotherapeutic agent comprising contacting said cell with the compound and the chemotherapeutic agent under conditions suitable for said administration.
- 25 63. The method of claim 62, wherein said chemotherapeutic agent is 5-fluoro uridine.

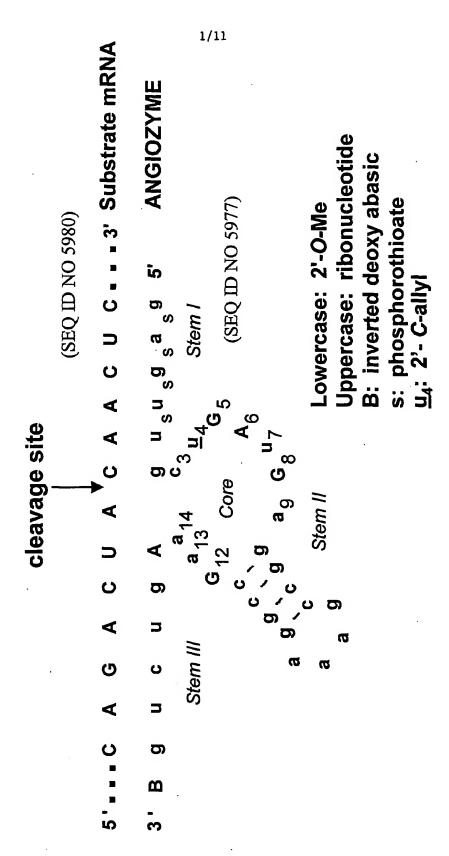
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- 64. The method of claim 62, wherein said chemotherapeutic agent is Leucovorin.
- 65. The method of claim 62, wherein said chemotherapeutic agent is chosen from Irinotecan, CAMPTOSAR®, CPT-11, Camptothecin-11, or Campto.
- 5 66. The method of claim 62, wherein said chemotherapeutic agent is Paclitaxel.
  - 67. The method of claim 62, wherein said chemotherapeutic agent is Carboplatin.
  - 68. A mammalian cell comprising the compound of claim 52...
- 69. The mammalian cell of claim 68, wherein said mammalian cell is a human 10 cell.
  - 70. A method of inhibiting angiogenesis in a subject, comprising the step of contacting said subject with the compound of claim 52, under conditions suitable for said inhibition.
  - 71. The method of claim 70, wherein said angiogenesis is tumor angiogenesis.
- 15 72. A method of treatment of a subject having a condition associated with an increased level of VEGF receptor comprising contacting cells of said subject with the compound of claim 52, under conditions suitable for said treatment.
- 73. The method of claim 72 further comprising the use of one or more drug 20 therapies under conditions suitable for said treatment.
  - 74. A method of cleaving RNA comprising a sequence of VEGFR1 (fit-1), comprising contacting the compound of claim 52 with said RNA under conditions suitable for the cleavage of said RNA.
- *7*5. The method of claim 74, wherein said cleavage is carried out in the 25 presence of a divalent cation.
  - 76. The method of claim 75, wherein said divalent cation is Mg2+.

- 77. The method of claim 72, wherein said condition is cancer.
- 78. The method of claim 77, wherein said cancer is breast cancer.
- 79. The method of claim 77, wherein said cancer is lung cancer.
- 80. The method of claim 77, wherein said cancer is colorectal cancer.
- 5 81. The method of claim 77, wherein said cancer is renal cancer.
  - 82. The method of claim 77, wherein said cancer is melanoma.
  - 83. The method of claim 77, wherein said cancer is pancreatic cancer.
  - 84. The method of claim 79, wherein said lung cancer is non-small cell lung carcinoma.
- 10 85. The method of claim 81, wherein said renal cancer is renal cell carcinoma.
  - 86. The method of claim 73, wherein said other therapy is 5-fluoro uridine.
  - 87. The method of claim 73, wherein said other therapy is Leucovorin.
  - 88. The method of claim 73, wherein said other therapy is Irinotecan, CAMPTOSAR®, CPT-11, Camptothecin-11, or Campto.
- 15 89. The method of claim 73, wherein said other therapy is Paclitaxel.
  - 90. The method of claim 73, wherein said other therapy is Carboplatin.
  - 91. A method of administering to a mammal the compound of claim 52 comprising contacting said mammal with the compound under conditions suitable for said administration.
- 20 92. The method of claim 91, wherein said mammal is a human.
  - 93. The method of claim 91, wherein said administration is in the presence of a delivery reagent.
  - 94. The method of claim 93, wherein said delivery reagent is a lipid.

- 95. The method of claim 94, wherein said lipid is a cationic lipid.
- 96. The method of claim 94, wherein said lipid is a phospholipid.
- 97. The method of claim 93, wherein said delivery reagent is a liposome.
- 98. A method of administering to a mammal the compound of claim 52 in conjunction with a chemotherapeutic agent comprising contacting said mammal with the compound and the chemotherapeutic agent under conditions suitable for said administration.
  - 99. The method of claim 98, wherein said chemotherapeutic agent is 5-fluoro uridine.
- 10 100. The method of claim 98, wherein said chemotherapeutic agent is Leucovorin.
  - 101. The method of claim 98, wherein said chemotherapeutic agent is Irinotecan, CAMPTOSAR®, CPT-11, Camptothecin-11, or Campto.
  - 102. The method of claim 98, wherein said chemotherapeutic agent is Paclitaxel.
- 15 103. The method of claim 98, wherein said chemotherapeutic agent is Carboplatin.

Figure 1: Anti-Flt-1 Ribozyme: ANGIOZYME



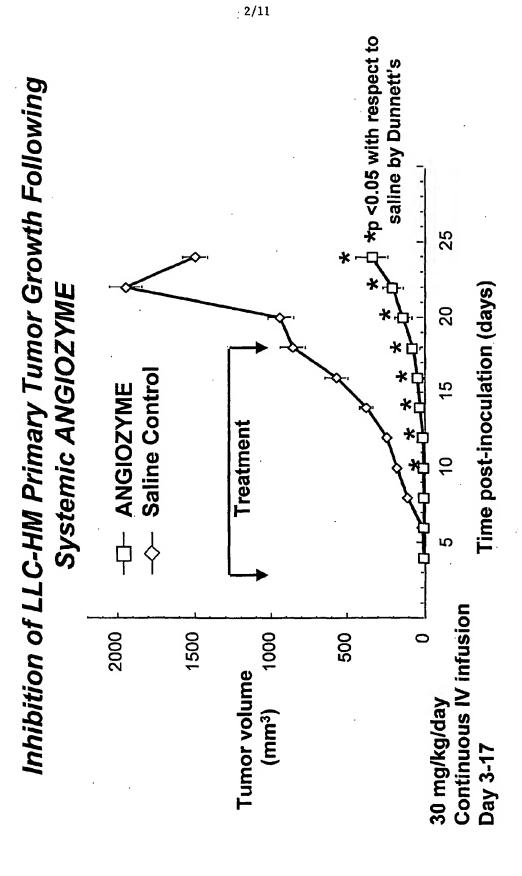


Figure 2

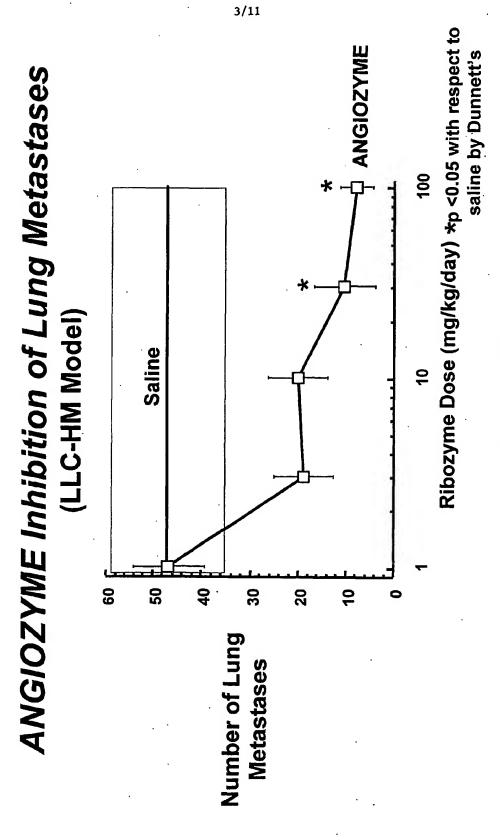
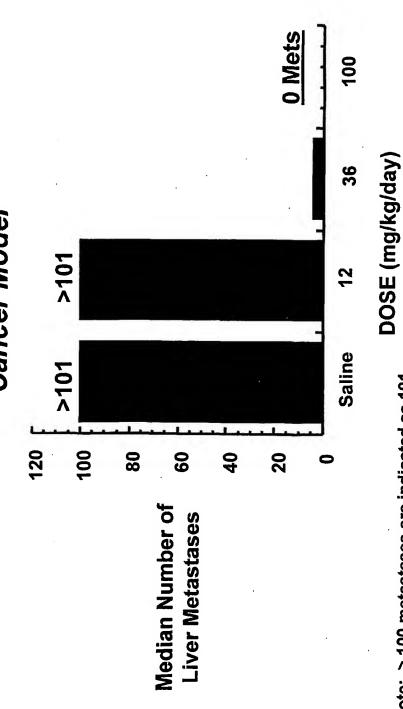


Figure 3

Effect of ANGIOZYME on Liver Metastases in a Colorectal Cancer Model



Note: > 100 metastases are indicated as 101.

Figure 4

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Figure 5: Plasma concentration profile of ANGIOZYME after a single subcutaneous dose of 10, 30, 100 or 300 mg/m<sup>2</sup>

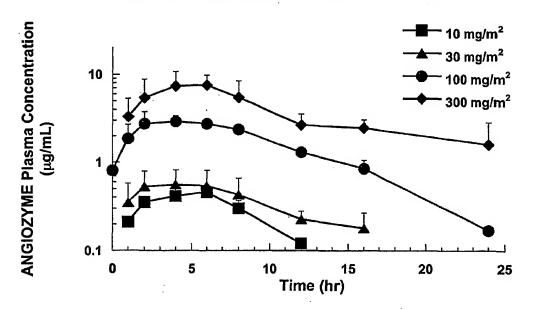
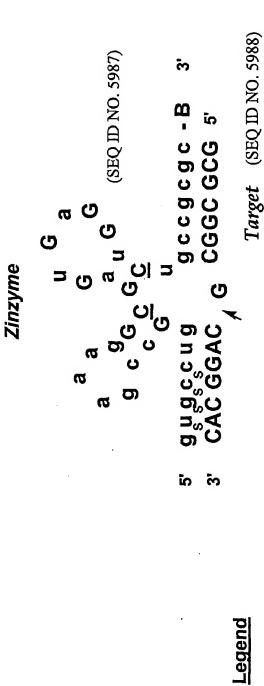


Figure 6: Examples of Nuclease Stable Ribozyme Motifs



Figure 7: Stabilized Zinzyme Ribozyme Motif



Uppercase: indicates natural ribo residues

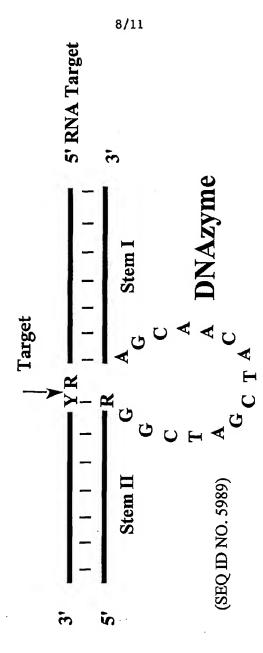
**C**: indicates 2'-deoxy-2'-amino Cytidine

Lowercase: 2'-0-methyl

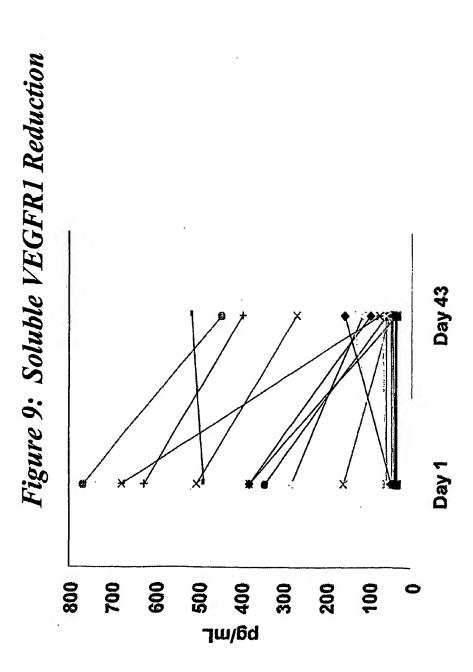
S: phosphorothioate/phosphorodithioate linkage

B: 3'-3' abasic moiety

Figure 8: DNAzyme Motif

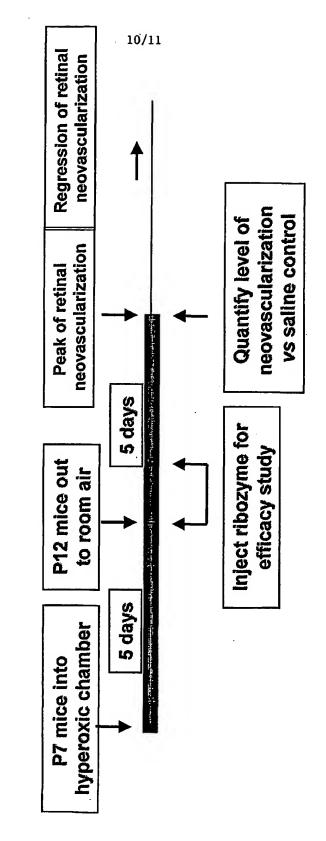


Y=UorC R=AorG



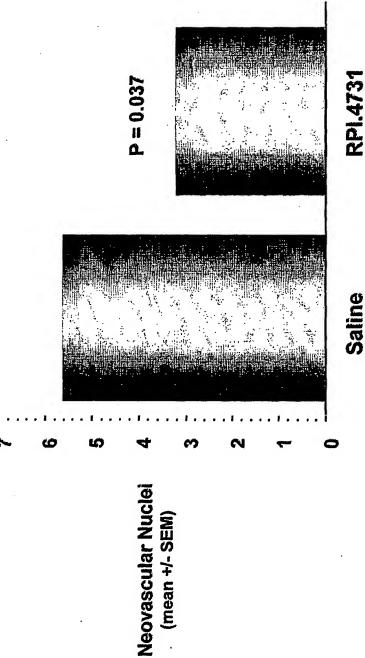
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Figure 10: Mouse Model of Proliferative Retinopathy



Note: Peak VEGF levels noted 12 hr after exposure to room air

Figure 11: RPI.4731 Reduces Hypoxia-Induced Retinal Neovascularization in Neonatal Mice



SEQ ID NO: 5978 Results: ~40% decrease in retinal neovascularization following two intraocular injections of RPI.4731